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| (21) International Application Number: PCT/US98/06954 (22) International Filing Date: 10 April 1998 (10.04.98) (30) Priority Data: 08/835,913 10 April 1997 (10.04.97) US (71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US). (72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). (74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US). | | (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). |
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(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)**(57) Abstract**

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

FIELD OF THE INVENTION

5 The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

10 Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely
15 to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

20 Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST
25 library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-
30 secreted "chaff", wasting effort and resources in the process.

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Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted proteins,
5 namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide
5 comprising a nucleotide sequence selected from the group consisting of:
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10 NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

In other embodiments, the present invention provides an isolated polynucleotide
consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide
 consisting essentially of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide
 comprising a nucleotide sequence which hybridizes to a sequence selected from the group
 30 consisting of:

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NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
25 NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
30 NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID

NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500; or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described
5 polynucleotides.

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each
10 SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

| | | | | | | | | |
|----|----|------|----|------|----|------|----|------|
| 15 | 1 | B11 | 21 | C3 | 41 | C639 | 61 | D148 |
| | 2 | B18 | 22 | C32 | 42 | C641 | 62 | D154 |
| | 3 | B21 | 23 | C141 | 43 | C642 | 63 | D167 |
| | 4 | B26 | 24 | C143 | 44 | C645 | 64 | D179 |
| | 5 | B40 | 25 | C180 | 45 | D4 | 65 | D188 |
| 20 | 6 | B115 | 26 | C195 | 46 | D7 | 66 | D196 |
| | 7 | B121 | 27 | C293 | 47 | D14 | 67 | D200 |
| | 8 | B124 | 28 | C312 | 48 | D15 | 68 | D203 |
| | 9 | B125 | 29 | C539 | 49 | D27 | 69 | D233 |
| | 10 | B142 | 30 | C544 | 50 | D68 | 70 | D252 |
| 25 | 11 | B196 | 31 | C547 | 51 | D69 | 71 | D286 |
| | 12 | B208 | 32 | C571 | 52 | D81 | 72 | D303 |
| | 13 | B224 | 33 | C604 | 53 | D100 | 73 | D304 |
| | 14 | B227 | 34 | C607 | 54 | D101 | 74 | D305 |
| | 15 | B232 | 35 | C608 | 55 | D104 | 75 | D310 |
| 30 | 16 | B236 | 36 | C610 | 56 | D105 | 76 | D311 |
| | 17 | B238 | 37 | C617 | 57 | D115 | 77 | D318 |
| | 18 | B255 | 38 | C626 | 58 | D121 | 78 | D327 |
| | 19 | C1 | 39 | C627 | 59 | D133 | 79 | D329 |
| | 20 | C2 | 40 | C636 | 60 | D143 | 80 | E1 |

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|----|-----|------|-----|-------|-----|------|-----|------|
| | 81 | E4 | 115 | H291 | 149 | J139 | 183 | M141 |
| | 82 | E5 | 116 | H306 | 150 | J143 | 184 | M152 |
| | 83 | E11 | 117 | H383 | 151 | J156 | 185 | M194 |
| | 84 | E12 | 118 | H426 | 152 | J168 | 186 | M230 |
| 5 | 85 | E14 | 119 | H438 | 153 | J297 | 187 | M273 |
| | 86 | E18 | 120 | H541 | 154 | J317 | 188 | M292 |
| | 87 | G1 | 121 | H545 | 155 | J322 | 189 | M301 |
| | 88 | G12 | 122 | H657 | 156 | J422 | 190 | M313 |
| | 89 | G16 | 123 | H698 | 157 | J435 | 191 | M328 |
| 10 | 90 | G20 | 124 | H758 | 158 | J509 | 192 | M338 |
| | 91 | G21 | 125 | H770 | 159 | J512 | 193 | O7 |
| | 92 | G26 | 126 | H849 | 160 | J532 | 194 | O47 |
| | 93 | G31 | 127 | H920 | 161 | J546 | 195 | O67 |
| | 94 | G40 | 128 | H978 | 162 | J598 | 196 | O75 |
| 15 | 95 | G46 | 129 | H999 | 163 | J635 | 197 | O99 |
| | 96 | G53 | 130 | H1004 | 164 | J638 | 198 | O135 |
| | 97 | G55 | 131 | H1010 | 165 | J708 | 199 | O139 |
| | 98 | G58 | 132 | H1045 | 166 | J731 | 200 | O268 |
| | 99 | G68 | 133 | H1052 | 167 | M4 | 201 | O276 |
| 20 | 100 | G85 | 134 | H1075 | 168 | M6 | 202 | O289 |
| | 101 | G86 | 135 | H1096 | 169 | M43 | 203 | O338 |
| | 102 | G99 | 136 | H1116 | 170 | M60 | 204 | O349 |
| | 103 | G103 | 137 | H1165 | 171 | M68 | 205 | O351 |
| | 104 | G107 | 138 | H1301 | 172 | M71 | 206 | O372 |
| 25 | 105 | G108 | 139 | H1408 | 173 | M88 | 207 | O386 |
| | 106 | G112 | 140 | H1413 | 174 | M97 | 208 | O417 |
| | 107 | G114 | 141 | H1456 | 175 | M100 | 209 | O418 |
| | 108 | H45 | 142 | I5 | 176 | M114 | 210 | O463 |
| | 109 | H162 | 143 | I28 | 177 | M120 | 211 | S10 |
| 30 | 110 | H165 | 144 | I32 | 178 | M121 | 212 | S34 |
| | 111 | H171 | 145 | J5 | 179 | M125 | 213 | S70 |
| | 112 | H174 | 146 | J54 | 180 | M126 | 214 | S169 |
| | 113 | H225 | 147 | J66 | 181 | M128 | 215 | S185 |
| | 114 | H236 | 148 | J135 | 182 | M137 | 216 | S195 |

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|----|-----|-------|-----|-------|-----|-------|-----|-------|
| | 217 | AA20 | 251 | AJ6 | 285 | AM72 | 319 | AP137 |
| | 218 | AA35 | 252 | AJ8 | 286 | AM93 | 320 | AP76 |
| | 219 | AB10 | 253 | AJ52 | 287 | AK679 | 321 | AP87 |
| | 220 | AA240 | 254 | AJ53 | 288 | AK684 | 322 | AP90 |
| 5 | 221 | AA244 | 255 | AJ54 | 289 | AK699 | 323 | AP150 |
| | 222 | AA246 | 256 | AJ78 | 290 | AM155 | 324 | AP159 |
| | 223 | AA287 | 257 | AJ80 | 291 | AM167 | 325 | AP160 |
| | 224 | AA299 | 258 | AK368 | 292 | AM207 | 326 | AP162 |
| | 225 | AA318 | 259 | AJ127 | 293 | AM217 | 327 | AP168 |
| 10 | 226 | AB45 | 260 | AJ142 | 294 | AM224 | 328 | AP179 |
| | 227 | AA36 | 261 | AJ143 | 295 | AM226 | 329 | AP197 |
| | 228 | AA363 | 262 | AC339 | 296 | AM235 | 330 | AP215 |
| | 229 | AA365 | 263 | AC370 | 297 | AM259 | 331 | AP224 |
| | 230 | AA351 | 264 | AL14 | 298 | AM266 | 332 | AP226 |
| 15 | 231 | AB290 | 265 | AK401 | 299 | AM267 | 333 | AP242 |
| | 232 | AC41 | 266 | AK438 | 300 | AM277 | 334 | AP250 |
| | 233 | AC18 | 267 | AK583 | 301 | AM279 | 335 | AQ11 |
| | 234 | AC175 | 268 | AK585 | 302 | AC387 | 336 | AQ2 |
| | 235 | AC114 | 269 | AK598 | 303 | AC395 | 337 | AQ21 |
| 20 | 236 | AC111 | 270 | AK604 | 304 | AC410 | 338 | AQ23 |
| | 237 | AC100 | 271 | AK609 | 305 | AC412 | 339 | AQ3 |
| | 238 | AC222 | 272 | AK620 | 306 | AC423 | 340 | AQ34 |
| | 239 | AC325 | 273 | AM10 | 307 | AJ146 | 341 | AQ5 |
| | 240 | AI44 | 274 | AM104 | 308 | AJ147 | 342 | AR15 |
| 25 | 241 | AI6 | 275 | AM123 | 309 | AJ156 | 343 | AR22 |
| | 242 | AI86 | 276 | AM137 | 310 | AJ168 | 344 | AR28 |
| | 243 | AJ1 | 277 | AM15 | 311 | AJ169 | 345 | AR3 |
| | 244 | AJ10 | 278 | AM16 | 312 | AJ172 | 346 | AR34 |
| | 245 | AJ13 | 279 | AM30 | 313 | AJ173 | 347 | AR42 |
| 30 | 246 | AJ15 | 280 | AM38 | 314 | AJ174 | 348 | AR54 |
| | 247 | AJ20 | 281 | AM39 | 315 | AK528 | 349 | AR61 |
| | 248 | AJ21 | 282 | AM42 | 316 | AP116 | 350 | AM282 |
| | 249 | AJ26 | 283 | AM46 | 317 | AP120 | 351 | AM307 |
| | 250 | AJ27 | 284 | AM66 | 318 | AP135 | 352 | AM349 |

| | | | | | | | | |
|----|-----|--------|-----|-------|-----|--------|-----|-------|
| | 353 | AM372 | 387 | AR310 | 421 | AM616 | 455 | AM921 |
| | 354 | AM392 | 388 | AR323 | 422 | AM622 | 456 | AM931 |
| | 355 | AM400 | 389 | AR324 | 423 | AM625 | 457 | AM973 |
| | 356 | AM430 | 390 | AR325 | 424 | AM666 | 458 | AM996 |
| 5 | 357 | AP11 | 391 | AR349 | 425 | AM686 | 459 | AS56 |
| | 358 | AP2 | 392 | AR360 | 426 | AM704 | 460 | AS61 |
| | 359 | AP56 | 393 | AR364 | 427 | AM726 | 461 | AS63 |
| | 360 | AP57 | 394 | AR400 | 428 | AM728 | 462 | AS65 |
| | 361 | AP58 | 395 | AR415 | 429 | AM735 | 463 | AS83 |
| 10 | 362 | AP60 | 396 | AR417 | 430 | AM741 | 464 | AS85 |
| | 363 | AP67 | 397 | AM558 | 431 | AM742 | 465 | AS86 |
| | 364 | AP7 | 398 | AM566 | 432 | AM754 | 466 | AS88 |
| | 365 | AQ53 | 399 | AM600 | 433 | AM781 | 467 | AT107 |
| | 366 | AQ54 | 400 | AR420 | 434 | AM795 | 468 | AT111 |
| 15 | 367 | AQ61 | 401 | AR437 | 435 | AM814 | 469 | AT138 |
| | 368 | AQ64 | 402 | AR440 | 436 | AM833 | 470 | AT140 |
| | 369 | AQ71 | 403 | AR446 | 437 | AM838 | 471 | AT142 |
| | 370 | AQ73 | 404 | AR450 | 438 | AT16 | 472 | AT146 |
| | 371 | AQ83 | 405 | AR452 | 439 | AT19 | 473 | AT151 |
| 20 | 372 | AM1075 | 406 | AR455 | 440 | AT20 | 474 | AT157 |
| | 373 | AM1076 | 407 | AR463 | 441 | AT4 | 475 | AT181 |
| | 374 | AM1083 | 408 | AR464 | 442 | AT53 | 476 | AT97 |
| | 375 | AR100 | 409 | AR467 | 443 | AT63 | 477 | AS239 |
| | 376 | AR69 | 410 | AR474 | 444 | AT64 | 478 | AT226 |
| 25 | 377 | AM1017 | 411 | AR475 | 445 | AT74 | 479 | AT259 |
| | 378 | AM1032 | 412 | AS15 | 446 | AT94 | 480 | AT260 |
| | 379 | AM1036 | 413 | AS20 | 447 | AT95 | 481 | AT265 |
| | 380 | AM1045 | 414 | AS23 | 448 | AM1000 | 482 | AT280 |
| | 381 | AM1060 | 415 | AS31 | 449 | AM856 | 483 | AT340 |
| 30 | 382 | AM1067 | 416 | AS47 | 450 | AM885 | 484 | AT351 |
| | 383 | AR253 | 417 | AS48 | 451 | AM889 | 485 | AT352 |
| | 384 | AK642 | 418 | AS7 | 452 | AM892 | 486 | AT356 |
| | 385 | AK647 | 419 | AM610 | 453 | AM910 | 487 | AT359 |
| | 386 | AK650 | 420 | AM614 | 454 | AM918 | 488 | AT361 |

| | | | | | | | | |
|----|-----|-------|-----|--------|-----|-------|-----|-------|
| | 489 | AS252 | 523 | AU161 | 557 | AW106 | 591 | BE28 |
| | 490 | AS263 | 524 | AU164 | 558 | AW107 | 592 | BE3 |
| | 491 | AS264 | 525 | AZ285 | 559 | AW109 | 593 | BE34 |
| | 492 | AS268 | 526 | AZ286 | 560 | AW133 | 594 | BE9 |
| 5 | 493 | AS271 | 527 | AZ287 | 561 | AW140 | 595 | AZ12 |
| | 494 | AS294 | 528 | AZ290 | 562 | AW92 | 596 | AZ22 |
| | 495 | AS301 | 529 | AZ188 | 563 | AW95 | 597 | AZ32 |
| | 496 | AS330 | 530 | AZ191 | 564 | AW98 | 598 | AZ45 |
| | 497 | AS144 | 531 | AZ204 | 565 | BA185 | 599 | AZ46 |
| 10 | 498 | AS152 | 532 | AZ219 | 566 | BA204 | 600 | BF143 |
| | 499 | AS157 | 533 | AW170 | 567 | BA210 | 601 | BF146 |
| | 500 | AS162 | 534 | AW176 | 568 | BA226 | 602 | BF157 |
| | 501 | AS164 | 535 | AW178 | 569 | BG1 | 603 | BF160 |
| | 502 | AS167 | 536 | AW179 | 570 | BG13 | 604 | BF169 |
| 15 | 503 | AS180 | 537 | AW182 | 571 | BG3 | 605 | BF171 |
| | 504 | AS186 | 538 | AW185 | 572 | BG33 | 606 | BF176 |
| | 505 | AS187 | 539 | AW189 | 573 | BG36 | 607 | BF178 |
| | 506 | AU36 | 540 | AW192 | 574 | BG37 | 608 | AS196 |
| | 507 | AU39 | 541 | AW194 | 575 | BG40 | 609 | AS202 |
| 20 | 508 | AU43 | 542 | AW199 | 576 | BG43 | 610 | AS209 |
| | 509 | AU47 | 543 | AW222 | 577 | BG48 | 611 | AS216 |
| | 510 | AU50 | 544 | AW231 | 578 | BG58 | 612 | AS230 |
| | 511 | AU59 | 545 | AZ261 | 579 | BG72 | 613 | AS232 |
| | 512 | AU71 | 546 | AZ264 | 580 | BG73 | 614 | AX101 |
| 25 | 513 | AU101 | 547 | AZ302 | 581 | BF101 | 615 | AX104 |
| | 514 | AU102 | 548 | AZ303 | 582 | BF132 | 616 | AX107 |
| | 515 | AU105 | 549 | AK649 | 583 | AZ69 | 617 | AX109 |
| | 516 | AU106 | 550 | AK663 | 584 | BD51 | 618 | AX122 |
| | 517 | AU107 | 551 | AR336 | 585 | BD53 | 619 | AX124 |
| 30 | 518 | AU115 | 552 | AR356 | 586 | BD65 | 620 | AX127 |
| | 519 | AU118 | 553 | AR398 | 587 | BD66 | 621 | AX128 |
| | 520 | AU122 | 554 | AR399 | 588 | BD73 | 622 | AX130 |
| | 521 | AU138 | 555 | AM1016 | 589 | BD77 | 623 | AX132 |
| | 522 | AU139 | 556 | AW105 | 590 | BD80 | 624 | AX136 |

| | | | | | | | | |
|----|-----|-------|-----|-------|-----|-------|-----|-------|
| | 625 | AX137 | 659 | BG274 | 693 | AW33 | 727 | BG504 |
| | 626 | AX143 | 660 | BG276 | 694 | AW36 | 728 | BG510 |
| | 627 | AX146 | 661 | AX12 | 695 | AW47 | 729 | BG511 |
| | 628 | AX51 | 662 | AX17 | 696 | AW49 | 730 | BG513 |
| 5 | 629 | AX55 | 663 | AX256 | 697 | AW52 | 731 | BG516 |
| | 630 | AX56 | 664 | AX30 | 698 | AW60 | 732 | BG518 |
| | 631 | AX60 | 665 | AX32 | 699 | AW66 | 733 | BG526 |
| | 632 | AX65 | 666 | AX34 | 700 | AW76 | 734 | BG528 |
| | 633 | AX78 | 667 | AX49 | 701 | AY241 | 735 | BG552 |
| 10 | 634 | AX80 | 668 | AX6 | 702 | AY259 | 736 | BG553 |
| | 635 | AX81 | 669 | AX8 | 703 | AY268 | 737 | BG556 |
| | 636 | AX92 | 670 | AZ180 | 704 | BA123 | 738 | AX309 |
| | 637 | AX97 | 671 | BG191 | 705 | BA134 | 739 | AX315 |
| | 638 | AX98 | 672 | BG193 | 706 | BA170 | 740 | AX318 |
| 15 | 639 | AX99 | 673 | BG199 | 707 | BA176 | 741 | AY186 |
| | 640 | AZ109 | 674 | BG201 | 708 | BA178 | 742 | AY190 |
| | 641 | AZ114 | 675 | BG219 | 709 | BA179 | 743 | AY200 |
| | 642 | BF286 | 676 | BG220 | 710 | BA216 | 744 | AY208 |
| | 643 | BF290 | 677 | BG221 | 711 | BA233 | 745 | AY211 |
| 20 | 644 | BF314 | 678 | BG225 | 712 | BD372 | 746 | AY283 |
| | 645 | BG236 | 679 | BG228 | 713 | BD375 | 747 | AY289 |
| | 646 | BG237 | 680 | BG442 | 714 | BD379 | 748 | AY304 |
| | 647 | BG240 | 681 | BG449 | 715 | BD380 | 749 | AY307 |
| | 648 | BG241 | 682 | BG457 | 716 | BD403 | 750 | AY318 |
| 25 | 649 | BG248 | 683 | BG458 | 717 | BD407 | 751 | AY333 |
| | 650 | BG249 | 684 | BG461 | 718 | BD409 | 752 | AY334 |
| | 651 | BG250 | 685 | BG465 | 719 | BD413 | 753 | AY342 |
| | 652 | BG251 | 686 | BG467 | 720 | BD414 | 754 | AY358 |
| | 653 | BG255 | 687 | BG471 | 721 | BG481 | 755 | AY362 |
| 30 | 654 | BG260 | 688 | BG59 | 722 | BG482 | 756 | BF190 |
| | 655 | BG267 | 689 | AW12 | 723 | BG492 | 757 | BF191 |
| | 656 | BG271 | 690 | AW22 | 724 | BG494 | 758 | BF193 |
| | 657 | BG272 | 691 | AW24 | 725 | BG495 | 759 | BF197 |
| | 658 | BG273 | 692 | AW32 | 726 | BG503 | 760 | BF208 |

| | | | | | | | | |
|----|-----|-------|-----|-------|-----|-------|-----|-------|
| | 761 | BF211 | 795 | BG373 | 829 | BD174 | 863 | BI17 |
| | 762 | BF216 | 796 | BG374 | 830 | BD176 | 864 | BI2 |
| | 763 | BF221 | 797 | BG379 | 831 | BD177 | 865 | BI24 |
| | 764 | BF227 | 798 | BG386 | 832 | BD178 | 866 | BI25 |
| 5 | 765 | BF228 | 799 | BG388 | 833 | BD183 | 867 | BI3 |
| | 766 | BF245 | 800 | BG389 | 834 | BE50 | 868 | BI36 |
| | 767 | BF250 | 801 | BG391 | 835 | BE64 | 869 | BI37 |
| | 768 | BF258 | 802 | BG393 | 836 | BE89 | 870 | BI39 |
| | 769 | BF259 | 803 | BG396 | 837 | BG490 | 871 | BI40 |
| 10 | 770 | BF263 | 804 | BG409 | 838 | BG491 | 872 | BI41 |
| | 771 | BF270 | 805 | BG411 | 839 | BG501 | 873 | BI46 |
| | 772 | BF273 | 806 | BG414 | 840 | BG502 | 874 | BM1 |
| | 773 | BG280 | 807 | BG420 | 841 | BG512 | 875 | BM17 |
| | 774 | BG283 | 808 | HW105 | 842 | BG532 | 876 | BM4 |
| 15 | 775 | BG284 | 809 | BB54 | 843 | BK162 | 877 | BM41 |
| | 776 | BG288 | 810 | BD101 | 844 | BK165 | 878 | BM46 |
| | 777 | BG296 | 811 | BD104 | 845 | BK167 | 879 | BM69 |
| | 778 | BG305 | 812 | BD107 | 846 | BK171 | 880 | BM88 |
| | 779 | BG306 | 813 | BD109 | 847 | BK179 | 881 | BM90 |
| 20 | 780 | BG309 | 814 | BD119 | 848 | BK180 | 882 | BA106 |
| | 781 | BG324 | 815 | BD121 | 849 | BK183 | 883 | BA12 |
| | 782 | BG327 | 816 | BD127 | 850 | BK186 | 884 | BA32 |
| | 783 | BG329 | 817 | BD128 | 851 | BK194 | 885 | BA38 |
| | 784 | BG332 | 818 | BD132 | 852 | BK200 | 886 | BA40 |
| 25 | 785 | BG334 | 819 | BD136 | 853 | BK206 | 887 | BA71 |
| | 786 | BG335 | 820 | BD137 | 854 | BK216 | 888 | BA79 |
| | 787 | BG350 | 821 | BD140 | 855 | BK231 | 889 | BA8 |
| | 788 | BG356 | 822 | BD144 | 856 | BK232 | 890 | BA88 |
| | 789 | BG357 | 823 | BD151 | 857 | BK236 | 891 | BA90 |
| 30 | 790 | BG363 | 824 | BD154 | 858 | BK237 | 892 | BA91 |
| | 791 | BG365 | 825 | BD164 | 859 | BK241 | 893 | BA98 |
| | 792 | BG366 | 826 | BD165 | 860 | BK243 | 894 | BK15 |
| | 793 | BG368 | 827 | BD169 | 861 | BK246 | 895 | BK17 |
| | 794 | BG372 | 828 | BD170 | 862 | BK253 | 896 | BK24 |

| | | | | | | | | |
|----|-----|-------|-----|-------|-----|-------|------|-------|
| | 897 | BK257 | 931 | AY428 | 965 | BK146 | 999 | BG139 |
| | 898 | BK26 | 932 | AY437 | 966 | BK155 | 1000 | BG140 |
| | 899 | BK260 | 933 | AY440 | 967 | BK158 | 1001 | BG141 |
| | 900 | BK265 | 934 | AY442 | 968 | BK75 | 1002 | BG142 |
| 5 | 901 | BK270 | 935 | AY449 | 969 | BK78 | 1003 | BG145 |
| | 902 | BK271 | 936 | AY457 | 970 | BK92 | 1004 | BG148 |
| | 903 | BK280 | 937 | AY470 | 971 | BK93 | 1005 | BG151 |
| | 904 | BK284 | 938 | AY487 | 972 | BK95 | 1006 | BG156 |
| | 905 | BK286 | 939 | AY489 | 973 | BK96 | 1007 | BG158 |
| 10 | 906 | BK29 | 940 | AY511 | 974 | BM101 | 1008 | BG160 |
| | 907 | BK291 | 941 | BE153 | 975 | BM117 | 1009 | BG168 |
| | 908 | BK295 | 942 | BF327 | 976 | BM124 | 1010 | BG170 |
| | 909 | BK296 | 943 | BI64 | 977 | BM139 | 1011 | BG171 |
| | 910 | BK299 | 944 | BI66 | 978 | BM154 | 1012 | BG172 |
| 15 | 911 | BK304 | 945 | BI75 | 979 | BM155 | 1013 | BG173 |
| | 912 | BK307 | 946 | BI80 | 980 | BM158 | 1014 | BG93 |
| | 913 | BK308 | 947 | BI81 | 981 | BM94 | 1015 | BG95 |
| | 914 | BK339 | 948 | BI82 | 982 | AY102 | 1016 | BI102 |
| | 915 | BK34 | 949 | BI86 | 983 | AY107 | 1017 | BI103 |
| 20 | 916 | BK343 | 950 | BI87 | 984 | AY122 | 1018 | BI107 |
| | 917 | BK40 | 951 | BI88 | 985 | AY131 | 1019 | BI110 |
| | 918 | BK41 | 952 | BI91 | 986 | AY137 | 1020 | BI114 |
| | 919 | BK48 | 953 | BI92 | 987 | AY140 | 1021 | BI117 |
| | 920 | BK49 | 954 | BK102 | 988 | AY147 | 1022 | BI120 |
| 25 | 921 | BK57 | 955 | BK105 | 989 | AY157 | 1023 | BI122 |
| | 922 | BK59 | 956 | BK107 | 990 | AY160 | 1024 | BI124 |
| | 923 | BK61 | 957 | BK112 | 991 | AY183 | 1025 | BI126 |
| | 924 | BK68 | 958 | BK114 | 992 | AY93 | 1026 | BI127 |
| | 925 | BL341 | 959 | BK115 | 993 | BG102 | 1027 | BI129 |
| 30 | 926 | AY398 | 960 | BK117 | 994 | BG104 | 1028 | BI133 |
| | 927 | AY406 | 961 | BK120 | 995 | BG112 | 1029 | BI139 |
| | 928 | AY407 | 962 | BK130 | 996 | BG125 | 1030 | BI150 |
| | 929 | AY408 | 963 | BK134 | 997 | BG132 | 1031 | BI164 |
| | 930 | AY421 | 964 | BK142 | 998 | BG137 | 1032 | BI97 |

| | | | | | | | | |
|----|------|-------|------|-------|------|-------|------|-------|
| | 1033 | BI98 | 1067 | BQ58 | 1101 | BO71 | 1135 | BL209 |
| | 1034 | BI99 | 1068 | BD189 | 1102 | BO87 | 1136 | BL210 |
| | 1035 | BS1 | 1069 | BD194 | 1103 | BO9 | 1137 | BL211 |
| | 1036 | BS54 | 1070 | BD199 | 1104 | BD235 | 1138 | BL219 |
| 5 | 1037 | BS58 | 1071 | BD200 | 1105 | BD240 | 1139 | BL220 |
| | 1038 | BS81 | 1072 | BD201 | 1106 | BD241 | 1140 | BL229 |
| | 1039 | BS89 | 1073 | BD208 | 1107 | BD244 | 1141 | BL230 |
| | 1040 | BH100 | 1074 | BD209 | 1108 | BD247 | 1142 | BL243 |
| | 1041 | BH106 | 1075 | BD213 | 1109 | BD251 | 1143 | BL247 |
| 10 | 1042 | BH111 | 1076 | BD214 | 1110 | BD257 | 1144 | BL249 |
| | 1043 | BH123 | 1077 | BD222 | 1111 | BD260 | 1145 | BL255 |
| | 1044 | BH131 | 1078 | BH19 | 1112 | BD262 | 1146 | BL257 |
| | 1045 | BH157 | 1079 | BH195 | 1113 | BD265 | 1147 | BL271 |
| | 1046 | BH297 | 1080 | BH2 | 1114 | BD268 | 1148 | BL274 |
| 15 | 1047 | BH306 | 1081 | BH227 | 1115 | BD522 | 1149 | BL30 |
| | 1048 | BH309 | 1082 | BH272 | 1116 | BD538 | 1150 | BL67 |
| | 1049 | BH316 | 1083 | BH276 | 1117 | BD544 | 1151 | BL73 |
| | 1050 | BH323 | 1084 | BH281 | 1118 | BD548 | 1152 | BL89 |
| | 1051 | BH339 | 1085 | BH41 | 1119 | BD561 | 1153 | BD420 |
| 20 | 1052 | BH365 | 1086 | BH51 | 1120 | BL147 | 1154 | BD423 |
| | 1053 | BH389 | 1087 | BH66 | 1121 | BL15 | 1155 | BD426 |
| | 1054 | BH392 | 1088 | BH7 | 1122 | BL152 | 1156 | BD427 |
| | 1055 | BJ54 | 1089 | BH87 | 1123 | BL156 | 1157 | BD428 |
| | 1056 | BJ62 | 1090 | BH90 | 1124 | BL160 | 1158 | BD438 |
| 25 | 1057 | BJ66 | 1091 | BJ20 | 1125 | BL178 | 1159 | BD441 |
| | 1058 | BJ67 | 1092 | BJ27 | 1126 | BL179 | 1160 | BD445 |
| | 1059 | BJ69 | 1093 | BJ29 | 1127 | BL183 | 1161 | BD473 |
| | 1060 | BJ70 | 1094 | BJ38 | 1128 | BL185 | 1162 | BD486 |
| | 1061 | BJ75 | 1095 | BJ39 | 1129 | BL186 | 1163 | BD489 |
| 30 | 1062 | BJ76 | 1096 | BJ9 | 1130 | BL187 | 1164 | BD492 |
| | 1063 | BJ78 | 1097 | BO11 | 1131 | BL194 | 1165 | BD512 |
| | 1064 | BJ87 | 1098 | BO20 | 1132 | BL196 | 1166 | BL106 |
| | 1065 | BQ20 | 1099 | BO4 | 1133 | BL201 | 1167 | BL310 |
| | 1066 | BQ3 | 1100 | BO52 | 1134 | BL205 | 1168 | BN1 |

| | | | | | | | | |
|----|------|-------|------|-------|------|-------|------|-------|
| | 1169 | BN107 | 1203 | BD351 | 1237 | BN351 | 1271 | BP22 |
| | 1170 | BN12 | 1204 | BN189 | 1238 | BN354 | 1272 | BP24 |
| | 1171 | BN130 | 1205 | BN201 | 1239 | BN365 | 1273 | BP25 |
| | 1172 | BN132 | 1206 | BN212 | 1240 | BN422 | 1274 | BT99 |
| 5 | 1173 | BN133 | 1207 | BN280 | 1241 | BN425 | 1275 | BP28 |
| | 1174 | BN139 | 1208 | BN284 | 1242 | BN439 | 1276 | BP3 |
| | 1175 | BN141 | 1209 | BN329 | 1243 | BN460 | 1277 | BP4 |
| | 1176 | BN153 | 1210 | BN331 | 1244 | BN461 | 1278 | BP43 |
| | 1177 | BN156 | 1211 | BN591 | 1245 | BN463 | 1279 | BP47 |
| 10 | 1178 | BN171 | 1212 | BO153 | 1246 | BN472 | 1280 | BP504 |
| | 1179 | BN174 | 1213 | BO157 | 1247 | BN473 | 1281 | BP506 |
| | 1180 | BN180 | 1214 | BO159 | 1248 | BO100 | 1282 | BP508 |
| | 1181 | BN246 | 1215 | BO166 | 1249 | BO107 | 1283 | BP521 |
| | 1182 | BN267 | 1216 | BO178 | 1250 | BO114 | 1284 | BP528 |
| 15 | 1183 | BN268 | 1217 | BO189 | 1251 | BO121 | 1285 | BP530 |
| | 1184 | BN33 | 1218 | BO194 | 1252 | BO126 | 1286 | BP532 |
| | 1185 | BN40 | 1219 | BO210 | 1253 | BO133 | 1287 | BP537 |
| | 1186 | BN48 | 1220 | BO212 | 1254 | BO137 | 1288 | BP544 |
| | 1187 | BN5 | 1221 | BO213 | 1255 | BO398 | 1289 | BP545 |
| 20 | 1188 | BN563 | 1222 | BO218 | 1256 | BO399 | 1290 | BP55 |
| | 1189 | BN65 | 1223 | BO226 | 1257 | BO401 | 1291 | BP567 |
| | 1190 | BN69 | 1224 | BO279 | 1258 | BO432 | 1292 | BP569 |
| | 1191 | BN81 | 1225 | BO301 | 1259 | BO528 | 1293 | BP57 |
| | 1192 | BN97 | 1226 | BO323 | 1260 | BO535 | 1294 | BP590 |
| 25 | 1193 | BN99 | 1227 | BO358 | 1261 | BO538 | 1295 | BP61 |
| | 1194 | BD286 | 1228 | BO365 | 1262 | BO549 | 1296 | BP70 |
| | 1195 | BD288 | 1229 | BO385 | 1263 | BO551 | 1297 | BP71 |
| | 1196 | BD297 | 1230 | BO250 | 1264 | BO93 | 1298 | BP780 |
| | 1197 | BD316 | 1231 | BO254 | 1265 | BP101 | 1299 | BP783 |
| 30 | 1198 | BD317 | 1232 | BO256 | 1266 | BP118 | 1300 | BP784 |
| | 1199 | BD321 | 1233 | BO260 | 1267 | BP121 | 1301 | BP791 |
| | 1200 | BD327 | 1234 | BO261 | 1268 | BP15 | 1302 | BP797 |
| | 1201 | BD335 | 1235 | BO273 | 1269 | BP19 | 1303 | BP806 |
| | 1202 | BD339 | 1236 | BN342 | 1270 | BP21 | 1304 | BP809 |

| | | | | | | | | |
|----|------|-------|------|-------|------|-------|------|--------|
| | 1305 | BP810 | 1339 | BV243 | 1373 | CC71 | 1407 | BR572 |
| | 1306 | BP813 | 1340 | BV248 | 1374 | CC76 | 1408 | BR559 |
| | 1307 | BP814 | 1341 | BV250 | 1375 | CC78 | 1409 | BR538 |
| | 1308 | BP815 | 1342 | BV259 | 1376 | CC81 | 1410 | BR537 |
| 5 | 1309 | BP820 | 1343 | BV273 | 1377 | CC89 | 1411 | BR533 |
| | 1310 | BP84 | 1344 | BV275 | 1378 | CD124 | 1412 | BR500 |
| | 1311 | BP919 | 1345 | BV49 | 1379 | CD128 | 1413 | BR48 |
| | 1312 | BP925 | 1346 | BV51 | 1380 | CD140 | 1414 | BR475 |
| | 1313 | BQ115 | 1347 | BV66 | 1381 | CD145 | 1415 | BR436 |
| 10 | 1314 | BQ129 | 1348 | BV70 | 1382 | CD146 | 1416 | BR434 |
| | 1315 | BS116 | 1349 | BV71 | 1383 | CD173 | 1417 | BR4 |
| | 1316 | BT101 | 1350 | BV72 | 1384 | CD194 | 1418 | BR346 |
| | 1317 | BT133 | 1351 | BV73 | 1385 | CD31 | 1419 | BR342 |
| | 1318 | BT139 | 1352 | BV88 | 1386 | CD50 | 1420 | BR338 |
| 15 | 1319 | BT33 | 1353 | BW345 | 1387 | CF50 | 1421 | BR333 |
| | 1320 | BT4 | 1354 | CB25 | 1388 | CF62 | 1422 | BR332 |
| | 1321 | BW13 | 1355 | CB3 | 1389 | CF78 | 1423 | BR212 |
| | 1322 | BW18 | 1356 | CB30 | 1390 | CF85 | 1424 | BR195 |
| | 1323 | BW2 | 1357 | CB37 | 1391 | CF89 | 1425 | BR194 |
| 20 | 1324 | BW51 | 1358 | CC144 | 1392 | BR814 | 1426 | BR19 |
| | 1325 | BW61 | 1359 | CC145 | 1393 | BR782 | 1427 | BR141 |
| | 1326 | BW83 | 1360 | CC149 | 1394 | BR778 | 1428 | BR122 |
| | 1327 | BV185 | 1361 | CC153 | 1395 | BR77 | 1429 | BR107 |
| | 1328 | BV195 | 1362 | CC162 | 1396 | BR767 | 1430 | BR1010 |
| 25 | 1329 | BV200 | 1363 | CC25 | 1397 | BR758 | 1431 | BR101 |
| | 1330 | BV202 | 1364 | CC31 | 1398 | BR733 | 1432 | BR1008 |
| | 1331 | BV204 | 1365 | CC322 | 1399 | BR719 | 1433 | BQ135 |
| | 1332 | BV206 | 1366 | CC39 | 1400 | BR711 | 1434 | BP913 |
| | 1333 | BV210 | 1367 | CC397 | 1401 | BR71 | 1435 | BP911 |
| 30 | 1334 | BV212 | 1368 | CC403 | 1402 | BR63 | 1436 | BP897 |
| | 1335 | BV227 | 1369 | CC46 | 1403 | BR616 | 1437 | BP895 |
| | 1336 | BV238 | 1370 | CC50 | 1404 | BR610 | 1438 | BP894 |
| | 1337 | BV239 | 1371 | CC59 | 1405 | BR607 | 1439 | BP893 |
| | 1338 | BV241 | 1372 | CC69 | 1406 | BR595 | 1440 | BP884 |

| | | | | |
|----|------|-------|------|-------|
| | 1441 | BP883 | 1475 | BU65 |
| | 1442 | BP875 | 1476 | BU68 |
| | 1443 | BP870 | 1477 | BU76 |
| | 1444 | BP859 | 1478 | BV106 |
| 5 | 1445 | BP837 | 1479 | BV112 |
| | 1446 | BP833 | 1480 | BV123 |
| | 1447 | BP499 | 1481 | BV124 |
| | 1448 | BP492 | 1482 | BV126 |
| | 1449 | BP488 | 1483 | BV128 |
| 10 | 1450 | BP484 | 1484 | BV131 |
| | 1451 | BP483 | 1485 | BV133 |
| | 1452 | BP481 | 1486 | BV134 |
| | 1453 | BP475 | 1487 | BV135 |
| | 1454 | BN418 | 1488 | BV138 |
| 15 | 1455 | BN415 | 1489 | BV139 |
| | 1456 | BN405 | 1490 | BV140 |
| | 1457 | BN394 | 1491 | BV141 |
| | 1458 | BN390 | 1492 | BV145 |
| | 1459 | BN387 | 1493 | BV15 |
| 20 | 1460 | BN379 | 1494 | BV158 |
| | 1461 | BN377 | 1495 | BV160 |
| | 1462 | BR84 | 1496 | BV172 |
| | 1463 | BR853 | 1497 | BV180 |
| | 1464 | BR854 | 1498 | BV21 |
| 25 | 1465 | BR884 | 1499 | BV27 |
| | 1466 | BT160 | 1500 | BV29 |
| | 1467 | BU165 | | |
| | 1468 | BU29 | | |
| | 1469 | BU44 | | |
| 30 | 1470 | BU45 | | |
| | 1471 | BU53 | | |
| | 1472 | BU57 | | |
| | 1473 | BU6 | | |
| | 1474 | BU60 | | |

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selectin "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,
25 most preferably under highly stringent conditions; to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

| Stringency Condition | Polynucleotide Hybrid | Hybrid Length (bp) ² | Hybridization Temperature and Buffer ¹ | Wash Temperature and Buffer ¹ |
|----------------------|-----------------------|---------------------------------|---|--|
| 5 A | DNA:DNA | ≥ 50 | 65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide | 65°C; 0.3xSSC |
| B | DNA:DNA | < 50 | T _B *; 1xSSC | T _B *; 1xSSC |
| C | DNA:RNA | ≥ 50 | 67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide | 67°C; 0.3xSSC |
| D | DNA:RNA | < 50 | T _D *; 1xSSC | T _D *; 1xSSC |
| E | RNA:RNA | ≥ 50 | 70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide | 70°C; 0.3xSSC |
| 10 F | RNA:RNA | < 50 | T _F *; 1xSSC | T _F *; 1xSSC |
| G | DNA:DNA | ≥ 50 | 65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide | 65°C; 1xSSC |
| H | DNA:DNA | < 50 | T _H *; 4xSSC | T _H *; 4xSSC |
| I | DNA:RNA | ≥ 50 | 67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide | 67°C; 1xSSC |
| J | DNA:RNA | < 50 | T _J *; 4xSSC | T _J *; 4xSSC |
| 15 K | RNA:RNA | ≥ 50 | 70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide | 67°C; 1xSSC |
| L | RNA:RNA | < 50 | T _L *; 2xSSC | T _L *; 2xSSC |
| M | DNA:DNA | ≥ 50 | 50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide | 50°C; 2xSSC |
| N | DNA:DNA | < 50 | T _N *; 6xSSC | T _N *; 6xSSC |
| O | DNA:RNA | ≥ 50 | 55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide | 55°C; 2xSSC |
| 20 P | DNA:RNA | < 50 | T _P *; 6xSSC | T _P *; 6xSSC |
| Q | RNA:RNA | ≥ 50 | 60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide | 60°C; 2xSSC |
| R | RNA:RNA | < 50 | T _R *; 4xSSC | T _R *; 4xSSC |

The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_h - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log [Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sephacrose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

20 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

30 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune
- 20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may
- 25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,
- 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection
5 or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci
10 USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating
15 autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents
- which block costimulation of T cells by disrupting receptor:ligand interactions of B
20 lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of
25 well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

30 Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected
 5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured
 10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-
 15 3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa
 20 et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching
 25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto, 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 154:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162. Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma
15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of
20 progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the
25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein
30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or
5 progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural
10 cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized
15 neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from
20 chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

25 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of
30 fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,
20 alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can
15 stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one
25 cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et
30 al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A
5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors
20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.
25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those
30 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober. Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltzenberger et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

30 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides,
10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient,
20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

 In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a
25 mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either
30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous
5 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an
10 adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain
15 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

20 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical
25 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers,
30 antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix
= components. Other potential matrices are nonbiodegradable and chemically defined, such
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

| Sel. | Species | Tissue | Cell Type |
|------|---------|--------------|--------------------------------|
| AA | Human | Kidney | 19-23wks., M/F pool of 5 |
| AB | Human | Fetal Lung | Fetal Lung |
| AC | Human | Placenta | 26yrs., 1 specimen |
| AD | Murine | Embryo | Fetal ES cells |
| AE | Murine | Spleen | Adult spleen |
| AF | Murine | Fetal Brain | Fetal Brain |
| AG | Murine | Fetal Brain | Fetal Brain |
| AH | Murine | Fetal Thymus | Fetal Thymus |
| AI | Human | Blood | Adult PBMC/TH1or2 |
| AJ | Human | Testes | 10-61yrs., pool of 11 |
| AK | Human | Kidney | 19-23wks., M/F pool of 5 |
| AL | Human | Neural | Adult Glioblastoma line TG-1 |
| AM | Human | Kidney | 19-23wks., M/F pool of 5 |
| AN | Murine | Bone Marrow | Adult Stromal cell line FCM-4 |
| AO | Murine | Thymus | Adult Subtr. Adult Thymus |
| AP | Human | Placenta | 26yrs., 1 specimen |
| AQ | Human | Ovary | PA-1 Teratocarcinoma |
| AR | Human | Retina | 16-75yrs., pool of 76 |
| AS | Human | Brain | 19-23wks., M/F pool of 5 |
| AT | Human | Blood | Adult lymphocytes+dend. cells |
| AU | Human | Testes | 10-61yrs., pool of 11 |
| AV | Murine | Spleen | Adult spleen |
| AW | Human | Ovary | PA-1 Teratocarcinoma |
| AX | Human | Testes | 10-61yrs., pool of 11 |
| AY | Human | Retina | 16-75yrs., pool of 76 |
| AZ | Human | Colon | Caco-2 Adenocarcinoma |
| B | Human | Blood | PeripheralBloodMononuclearCell |
| BA | Human | Placenta | 26yrs., 1 specimen |
| BB | Human | Blood | Adult PBMC/TH1or2 |
| BC | Murine | Embryo | Fetal ES cells |
| BD | Human | Kidney | 19-23wks., M/F pool of 5 |
| BE | Human | Blood | Adult PBMC/TH1or2 |
| BF | Human | Brain | 19-23wks., M/F pool of 5 |
| BG | Human | Brain | N/A |
| BH | Human | Ovary | PA-1 Teratocarcinoma |
| BI | Human | Kidney | 19-23wks., M/F pool of 5 |
| BJ | Human | Ovary | PA-1 Teratocarcinoma |
| BK | Human | Retina | 16-75yrs., pool of 76 |
| BL | Human | Testes | 10-61yrs., pool of 11 |
| BM | Human | Muscle | N/A |
| BN | Human | Placenta | 26yrs., 1 specimen |
| BO | Human | Retina | 16-75yrs., pool of 76 |
| BP | Human | Kidney | 19-23wks., M/F pool of 5 |
| BQ | Human | Colon | Caco-2 Adenocarcinoma Caco2 |

| | | | |
|----|--------|----------------|-----------------------------------|
| BR | Human | Kidney | 19-23wks., M/F pool of 5 |
| BS | Human | Pituitary | Adult Pituitary |
| BT | Human | Blood | Adult PBMC |
| BU | Human | Placenta | 26yrs., 1 specimen |
| BV | Human | Brain | N/A |
| BW | Human | Blood | Adult PBMC |
| BX | Human | Ovary | PA-1 Teratocarcinoma |
| BY | Human | Blood | Adult PBMC/TH1 or 2 |
| BZ | Human | Kidney | 19-23wks., M/F pool of 5 |
| C | Human | Blood | Peripheral Blood Mononuclear Cell |
| CA | Murine | Embryo | Fetal ES cell embryoid bodies |
| CB | Human | Brain | 19-23wks., M/F pool of 5 |
| CC | Human | Brain | N/A |
| CD | Human | Brain | 19-23wks., M/F pool of 5 |
| CE | Human | Blood | Adult lymphocytes+dend. cells |
| CF | Human | Placenta | 26yrs., 1 specimen |
| CG | Human | Testes | 10-61yrs., pool of 11 |
| CH | Human | Kidney | 19-23wks., M/F pool of 5 |
| CI | Human | Brain | N/A |
| CJ | Human | Brain | 19-23wks., M/F pool of 5 |
| CK | Human | Testes | 10-61yrs., pool of 11 |
| CL | Human | Retina | 16-75yrs., pool of 76 |
| CM | Human | Adult Lung | Adult Lung |
| CN | Human | Brain | 19-23wks., M/F pool of 5 |
| CO | Human | Brain | N/A |
| CP | Human | Salivary Gland | N/A |
| CQ | Human | Heart | 13-73yrs., pool of 3 |
| CR | Human | Testes | 10-61yrs., pool of 11 |
| CS | Human | Brain | 19-23wks., M/F pool of 5 |
| CT | Human | Brain | N/A |
| CU | Human | Pineal Gland | N/A |
| CV | Human | Mammary | Adult Human Mammary |
| CW | Human | Brain | 19-23wks., M/F pool of 5 |
| CY | Human | Pineal Gland | N/A |
| CZ | Human | Testes | 10-61yrs., pool of 11 |
| D | Human | Blood | Peripheral Blood Mononuclear Cell |
| DA | Human | Placenta | 26yrs., 1 specimen |
| DB | Human | Prostate | Adult Prostate |
| DC | Human | Pineal Gland | Adult Pineal Gland |
| DD | Human | Testes | 10-61yrs., pool of 11 |
| DE | Human | Testes | Adult NCCIT TeratoCA |
| DF | Human | Brain | N/A |
| DG | Human | Placenta | 26yrs., 1 specimen |
| DH | Human | Brain | 19-23wks., M/F pool of 5 |
| DI | Human | Testes | 10-61yrs., pool of 11 |
| DJ | Human | Placenta | 26yrs., 1 specimen |
| DK | Human | Fetal Kidney2 | Fetal Kidney |

| | | | |
|----|--------|---------------|--------------------------------|
| DL | Human | Brain | N/A |
| DM | Human | Brain | N/A |
| DN | Human | Brain | 19-23wks., M/F pool of 5 |
| DO | Human | Testes | 10-61yrs., pool of 11 |
| DP | Murine | Embryo | Fetal ES cell embryoid bodies |
| DQ | Human | Placenta | 26yrs., 1 specimen |
| DR | Human | SalivaryGland | N/A |
| DT | Human | Brain | N/A |
| DU | Human | Brain | 19-23wks., M/F pool of 5 |
| DV | Human | Pineal Gland | Adult Pineal Gland |
| DW | Human | Brain | N/A |
| DX | Human | Testes | 10-61yrs., pool of 11 |
| DY | Human | Brain | N/A |
| DZ | Human | Testes | Adult NCCIT TeratoCA |
| E | Human | Blood | PeripheralBloodMononuclearCell |
| EA | Human | Brain | 19-23wks., M/F pool of 5 |
| EB | Human | Melanoma | Adult Melanoma |
| EC | Human | Brain | N/A |
| ED | Human | Placenta | 26yrs., 1 specimen |
| EE | Human | Testes | 10-61yrs., pool of 11 |
| EF | Human | Liver | Adult Liver |
| EG | Human | Pancreas | Adult HPC-3 Ductal AdenoCA |
| EH | Human | Blood | PeripheralBloodMononuclearCell |
| EI | Human | Brain | 19-23wks., M/F pool of 5 |
| EJ | Human | Placenta | 26yrs., 1 specimen |
| EK | Human | Brain | 19-23wks., M/F pool of 5 |
| EL | Human | Testes | 10-61yrs., pool of 11 |
| EM | Human | Fetal Kidney2 | Fetal Kidney |
| EN | Human | Brain | 19-23wks., M/F pool of 5 |
| EO | Human | Adrenal Gland | Adult Adrenal Gland |
| EP | Human | Placenta | 26yrs., 1 specimen |
| EQ | Human | Testes | 10-61yrs., pool of 11 |
| ER | Human | Brain | 19-23wks., M/F pool of 5 |
| ES | Human | Placenta | 26yrs., 1 specimen |
| ET | Human | Testes | 10-61yrs., pool of 11 |
| EU | Human | Kidney | Adult Kidney |
| EV | Human | Stomach | Adult Stomach |
| EW | Human | Placenta | 26yrs., 1 specimen |
| EX | Human | Testes | 10-61yrs., pool of 11 |
| EY | Human | Brain | 19-23wks., M/F pool of 5 |
| EZ | Human | Fetal Kidney2 | Fetal Kidney |
| FA | Human | Brain | 19-23wks., M/F pool of 5 |
| FB | Human | Placenta | 26yrs., 1 specimen |
| FC | Human | Testes | 10-61yrs., pool of 11 |
| FD | Human | SalivaryGland | N/A |
| FE | Human | Brain | N/A |
| FF | Human | Testes | Adult NCCIT TeratoCA |

| | | | |
|----|---------|----------------|--------------------------------|
| FG | Human | Brain | N/A |
| FH | Human | Brain | 19-23wks., M/F pool of 5 |
| FI | Human | Small Intest | Adult Small Intestine |
| FJ | Human | Lung CA | Adult Lung CA |
| FK | Human | Kidney | Adult Kidney |
| FM | Human | Brain | N/A |
| FN | Human | Brain | 19-23wks., M/F pool of 5 |
| FO | Human | Brain | N/A |
| FP | Human | Placenta | 26yrs., 1 specimen |
| FQ | Human | Testes | 10-61yrs., pool of 11 |
| FR | Human | Placenta | 26yrs., 1 specimen |
| FS | Human | Testes | 10-61yrs., pool of 11 |
| FT | Chicken | Fetal Lung | Fetal Lung |
| FU | Chicken | Limb Bud | Fetal St. 23 Limb Bud |
| FV | Human | Testes | Adult NCCIT TeratoCA |
| FW | Human | Testes | Adult NCCIT TeratoCA |
| FX | Human | Brain | 19-23wks., M/F pool of 5 |
| FY | Human | Placenta | 26yrs., 1 specimen |
| FZ | Human | Placenta | 26yrs., 1 specimen |
| G | Human | Blood | PeripheralBloodMononuclearCell |
| GA | Human | Testes | 10-61yrs., pool of 11 |
| GB | Human | Placenta | 26yrs., 1 specimen |
| GC | Human | Testes | 10-61yrs., pool of 11 |
| GD | Human | Placenta | 26yrs., 1 specimen |
| GE | Human | Brain | N/A |
| GF | Human | Brain | 19-23wks., M/F pool of 5 |
| GG | Human | Fetal Kidney2 | Fetal Kidney |
| GH | Human | Placenta | 26yrs., 1 specimen |
| GI | Human | Retinoblastoma | Adult Retinoblastoma Y79 |
| GJ | Murine | Spleen | Adult Spleen |
| GK | Human | Fetal Kidney2 | Fetal Kidney |
| GL | Murine | Lymph Node | Adult Lymph Node |
| GM | Human | Uterus | N/A |
| GN | Human | Blood | PeripheralBloodMononuclearCell |
| GO | Human | Adrenal Gland | Adult Adrenal Gland |
| GP | Human | Ovary | PA-1 Teratocarcinoma |
| GQ | Human | Pineal Gland | N/A |
| GR | Human | Pancreas | Adult HPC-3 Ductal AdenoCA |
| GS | Human | Retina | 16-75yrs., pool of 76 |
| GT | Human | Brain | N/A |
| GU | Human | Fetal Kidney2 | Fetal Kidney |
| GV | Rat | Retina | Newborn Retina |
| GW | Chicken | Limb Bud | Fetal St.26 Limb Bud |
| GX | Human | Brain | N/A |
| GY | Human | Testes | 10-61yrs., pool of 11 |
| GZ | Human | Brain | 19-23wks., M/F pool of 5 |
| H | Human | Blood | PeripheralBloodMononuclearCell |

| | | | |
|----|-------|----------------|--------------------------------|
| HA | Human | Testes | Adult NCCIT TeratoCA |
| HB | Human | Fetal Kidney2 | Fetal Kidney |
| HC | Human | Brain | 19-23wks.. M/F pool of 5 |
| HD | Human | Brain | N/A |
| HE | Human | Testes | 10-61yrs., pool of 11 |
| HF | Human | Brain | 19-23wks., M/F pool of 5 |
| HG | Human | Fetal Kidney2 | Fetal Kidney |
| HH | Human | Brain | N/A |
| HI | Human | Testes | 10-61yrs., pool of 11 |
| HJ | Human | Brain | N/A |
| HK | Human | Brain | 19-23wks., M/F pool of 5 |
| HL | Human | Fetal Kidney2 | Fetal Kidney |
| HM | Human | Testes | Adult NCCIT TeratoCA |
| HN | Human | Fetal Kidney2 | Fetal Kidney |
| HO | Human | Brain | N/A |
| HP | Human | Brain | 19-23wks., M/F pool of 5 |
| HQ | Human | Testes | 10-61yrs., pool of 11 |
| HR | Human | Brain | N/A |
| HS | Human | Brain | N/A |
| HT | Human | Brain | 19-23wks., M/F pool of 5 |
| HU | Human | Fetal Kidney2 | Fetal Kidney |
| HV | Human | Testes | 10-61yrs., pool of 11 |
| HW | Human | Brain | N/A |
| HX | Human | Brain Hippoca | Adult Brain Hippocampus |
| HY | Human | Trachea | Adult Trachea |
| HZ | Human | Brain Thalamus | Adult Brain Thalamus |
| I | Human | Blood | PeripheralBloodMononuclearCell |
| IA | Human | Thyroid | Adult Thyroid |
| IB | Human | Embryonal CA | Fetal NT2-D1 |
| IC | Human | WER1-Rb1 line | Adult Retinoblastoma |
| ID | Human | Muscle | N/A |
| IE | Human | Brain | 19-23wks., M/F pool of 5 |
| IF | Human | Uterus | N/A |
| IG | Human | Testes | 10-61yrs., pool of 11 |
| IH | Human | Muscle | N/A |
| II | Human | Brain | N/A |
| IJ | Human | Blood | PeripheralBloodMononuclearCell |
| IK | Human | Retinoblastoma | Adult Retinoblastoma Y79 |
| IL | Human | Retina | 16-75yrs., pool of 76 |
| IM | Human | Various | Various |
| IN | Human | Prostate | Adult Prostate |
| IO | Human | Brain | 19-23wks.. M/F pool of 5 |
| IP | Human | Fetal Kidney2 | Fetal Kidney |
| IQ | Human | Prostate | Adult Prostate |
| IR | Human | Brain Hippoca | Adult Brain Hippocampus |
| IS | Human | Trachea | Adult Trachea |
| IT | Human | Brain Thalamu | Adult Brain Thalamus |

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| GTGACCCCCA TCCCATCCAA TAGTCCCCAT CTCTTCTCAG CTCTCTCTGT AGTTTCTCTT | 60 |
| CCTCCGCCTG CCTTTTAACT TAGTGTTTCC CAGGACAGAG GTGACTCAGT TGTATCCAGA | 120 |
| CCGCTCTGTG ACTGAACACC CACTTTCTTT TCCTTTTCCA ATAAATATAT GTAACATACA | 180 |
| TGTCAACTAG GAACAAACA GTATCTCAGG AATCCACCAT CCAGTTAAAA ATGGACCCCTT | 240 |

ACCTTACCG TGCCCCTGCA GAGACCCCAA TACAGCGCAT TTCCCTCATT CTTTGGCTTT 300
TCTCAAGTTT TACCACGGCC TCTTTGGCCC TCGAG 335

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC AAAGAGGCCG TTGACCATTG ATAGAACACA GGCATACACA GGAAGATACA 60
 TTCACAGAAG AGCTTCCTGC ACAAAGTAAG CCACCAGCGC AACATGACAG TGAAGACCCT 120
 GCATGGCCCA GCCATGGTCA AGTACTTGCT GCTGTCGATA TTGGGGCTTG CTTTCTGAG 180
 TGAGGCGGCA GCTCGGAAAA TCCCCAAAGT AGGACATACT TTTTCCAAA AGCCTGAGAG 240
 TTGCCCCGCT GTGCCAGGAG GTAGTATGAA GCTTGACATT GGCATCATCA ATGAAAACCA 300
 GCGCGTTTCC ATGTCACGTA ACATCGAGAG CCGCTCCACC TCCCCCTGGA ATTACACTGT 360
 CACTTGGGAC CCCAACCGGT ACCCCTCGGA AGTTGTACAG GCCCAGTGTA GGAACCTGGG 420
 CTGCATCAAT GCTCAAGGAA AGGAAGACAT CTCCATGAAT TCCGTTCCCA TCCAGCAAGA 480
 GACCCTGTCTG ACGGCCTCTT TGGCCCTCGA GACA 514

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACCCTC CACCTGCAAA TCCACTGTCC ATACCCTTGG ATTGGTTGAA GAGCCTTTGG 60
 TCATACTGAA CTTCAATTGA AGTCCGAGGA TTAGGAACAC CGAGAGCAAT AACTTCACTG 120
 ATATCCCGAT TTTCATTCTC CTGAAGTTTC GACCTCTTAT CAGGAGCTGC CCTGGAAAGA 180
 TTCCGGTCAT GCTGTCTCTC TTTTCGCTG TCATGCCGGA TTTCATCCCT CTCACGTGCC 240
 TCCCCATCCT CTTTTTCCAC ATGAGTTTTC ATCCAGCTC TTCTCTCCCT GGCTTTCTGG 300
 GCCATTTCTC TAAGTTTCTC TNCANGTNTN NCCTTTTCTT TCTGAGCCAT TTTTCTCTCT 360
 ACTTGGGCGT CGACGGCCTC TGGGGCCCTC GAG 393

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGACCAGG CATACACAGG AAGATACATT CACAGAAAGA GCTTCCTGCA CAAAGTAAGC 60
 CACCAGCGCA ACATGACAGT GAAGACCCTG CATGGCCAG CCATGGTCAA GTACTTGCTG 120

| | |
|---|-----|
| CTGTCGATAT TGGGGCTTGC CTTTCTGAGT GAGGCGGCAG CTCGGAAAAT CCCCAAAGTA | 180 |
| GGACATACTT TTTTCCAAAA GCCTGAGAGT TGCCCGCCTG TGCCAGGAGG TAGTATGAAG | 240 |
| CTTGACATTG GCATCATCAA TGAAAACCAG CGCGTTTCCA TGTCACGTAA CATCGAGAGC | 300 |
| CGCTCCACCT CCCCTGGAA TTACACTGTC ACTTGGGACC CCAACCGTA CCCCTCGGAA | 360 |
| GTTGTACAGG CCCAGTGTAG GAACTTGGGC TGCATCAATG CTCAAGGAAA GGAAGACATC | 420 |
| TCCATGAATT CCGTTCCCAT CCAGCAAGAG ACCCTGGTCG TCCGGAGGAA GCACCAAGGC | 480 |
| TGCTCTGTTT CTTTCCAGTT GGAGAAGGTG CTGGTGAAGT TTGGCTGCAC CTGCGTCACG | 540 |
| TCAACGGCCT CTTTGGCCCT CGAG | 564 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| GTCGACCTTC AGTTGCCTCA GACCCCAGTA ATACAACGGT CACCACCATG AAACCTACAG | 60 |
| CGGCATCTAA TACAACAACA CCAGGGATGG TCTCAACAAA TATGACTTCT ACCACCTTAA | 120 |
| AGTCTACACC CAAAACAACA AGTGTTCAC AGAACACATC TCAGATATCA ACATCCACAA | 180 |
| TGACCGTAAC CCACAATAGT TCAGTGACAT CTGCTGCTTC ATCAGTAACA ATCACAACAA | 240 |
| CTATGCATTG TGAAGCAAAG AAAGGATCAA AATTTGATAC TGGGAGCTTT GTTGGTGGTA | 300 |
| TTGTATTAAC GCTGGGAGTT TTATCTATTC TGTCAACGGC CTCTTTGGCC CTCGAG | 356 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|--|-----|
| GTA CTGCTGC ACGGACTCTG GAACCATGAA CATATTTGAT CGAAAGATCA ACTTTGATGC | 60 |
| GCTTTTAAAA TTTTCTCATA TAACCCCGTC AACGCAGCAG CACCTGAAGA AGGTCTATGC | 120 |
| AAGTTTGGCC CTTTGTATGT TTGCGGCGGC TGCAGGGGCC TATGTCCATA TGGTCACTCA | 180 |
| TTTCATTGAG GCTGGCCTGC TGTCTGCCTT GGGCTCCCTG ATATTGATGA TTTGGCTGAT | 240 |
| GGCAACACCT CATAGCCATG AACTGAACA GAAAAGACTG GGACTTCTTG CTGGATTGTC | 300 |
| ATTCCTTACA GGAGTTGGCC TGGGCCCTGC CCTGGAGTTT TGTATTGCTG TCAACCCAG | 360 |
| CATCCTTCCC ACTGCTTTCA TGGGCACGGC AATGATCTTT ACCTGCTTCA CCCTCAGTGC | 420 |
| ACTCTATGCC AGGCGCCGCG GCTACCTCTT TCTGGGAGGT ATCTTGATGT CAGCCCTGAG | 480 |
| CTTGTGCTT TTGTCGACGG CCTCTTGGC CCTCGAGACA | 520 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GTCGACGTAC | CACCAGCAAC | CATCAATCCC | GTCTCCTCCT | GCCTCCTCTC | CTGCAATCCA | 60 |
| CCCCGCCACG | ACTATCGCCA | TGGCAGCCCT | GATCGCAGAG | AACTTCCGCT | TCCTGTCACT | 120 |
| TTTCTTCAAG | AGCAAGGATG | TGATGATTTT | CAACGGCCTG | GTGGCACTGG | GCACGGTGGG | 180 |
| CAGCCAGGAG | CTGTCTCTG | TGGTGGCCTT | CCACTGCCCC | TGCTCGCCGG | CCCGGAACATA | 240 |
| CCTGTACGGG | CTGGCGGCCA | TCGGCGTGCC | CGCCCTGGTG | CTCTTCATCA | TTGGCATCAT | 300 |
| CCTCAACAAC | CACACCTGGA | ACCTCGTGGG | CGAGTGCCAG | CACCGGAGGA | CCAAGAACTG | 360 |
| CTCCGCCGCC | CCCACCTTCC | TCCTTCTAAG | CTCCATCCTG | GGACGTGCGG | CTGTGGCCCC | 420 |
| TGTCACCTGG | TCTGTCTCT | CCCTGCTGCG | TGGTGAGGCT | TATGTCTGTG | CTCTCAGTGA | 480 |
| GTCGTGGAC | CCTTCCTCAC | TCACGGCCTC | TTTGGCCCTC | GAGACA | | 526 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCAMCTGTG | CAGCGGAGTT | TGACTTTATG | GAAAAAGAGA | CTCCACTGAG | ATACACAAAG | 60 |
| ACATTATTGC | TTCCAGTTGT | TCTTGTAGTG | TTTGTGCTA | TTGTTAGAAA | GATTATTAGT | 120 |
| GATATGTGGG | GTGTCTTAGC | TAAACAACAG | ACACATGTAA | GAAAACACCA | GTTTGATCAT | 180 |
| GGAGAGCTGG | TTTACCATGC | ATTGCAATTG | TTAGCATATA | CAGCCCTTGG | TATTTTAATT | 240 |
| ATGAGACTAA | AACTCTTCTT | GACACCATAC | ATGTGTGTTA | TGGCATCACT | GATCTGCTCA | 300 |
| AGACAGCTAT | TTGGATGGCT | CTTTTGCAAA | GTACATCCTG | GTGCTATTGT | GTTTGTATA | 360 |
| TTAGCAGCAA | TGTCAATACA | AGGTTCAGCA | AATCTGCAAA | CCCAGTGGA | GTCCACGGCC | 420 |
| TCTTTGGCCC | TCGAGACA | | | | | 438 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACCCTA | CACCATGTTT | TTCTCCACGT | TCTACCACGC | CTGCGACCAG | CCCGGGGAGG | 60 |
| CGGTGCTGTG | CATCCTCAGC | TACGACACGC | TGCAGTACTG | CGACTTCTTG | GGCTCCGGGG | 120 |
| CGGCCATCTG | GGTCACCATC | CTGTGCATGG | CACGGCTCAA | GACAGCCCTG | AAATACGTGC | 180 |
| TGTTTCTTCT | GGGTACACTG | GTCATCGCCA | TGTCCTTGCA | GCTGGACCGC | AGGGGCATGT | 240 |
| GGAACATGCT | GGGGCCCTGC | CTCTTTGCCT | TCGTGATCAT | GGCCTCCATG | TGGGCTTACC | 300 |
| GCTGCGGGCA | CCGGCGCCAG | TGCTACCCCA | CCTCGTGGCA | GCGCTGGGCC | TTCTACCTCC | 360 |
| TGCCCCGCGT | CTCTACGGCC | TCTTTGGCCC | TCGAG | | | 395 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|---|-----|
| GTCGACAGAM WNCAACCCTC AGACGCCACA TCCCCTKACA AGCTGMCAGG CAGGTTCTCT | 60 |
| TCCTCTCACA TACTGACCCA CGGKTCCACC CTCTCTCCCC TGGAAAGGAC ACCATGAGCA | 120 |
| CTGAAAGCAT GATCCGGRAC GTGGAGCTGK CCGAGGAGGN GYTCCCCAAG AAGACAGGGG | 180 |
| GGRCCCAGGG CTCCAGGCGG GGGTTTGTTC CTCAGWCTCT TCTCCTTCCT GATCGNGGGA | 240 |
| GGGGGCACCA CGCTCTTCTG TCTGCTGGAC TTTGGAGTGA TCGGNCCCCA GAGGGAAGGA | 300 |
| GTCCCCCAGG GGAACCTCTC T | 321 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|--|-----|
| GTCGACGGCC GAGAWGGACA TGAAGCAATA TCAAGGCTCC GGCGGCGTCG CCATGGATGT | 60 |
| GGNACGGAGT CGCTTCCCCT ACTGCGTGGT GTGGACGCCC ATCCCGGTGN TCACGTGGTT | 120 |
| TTTCCCCATC ATCGGGCCACA TGGGCATCTG CACATCCACA GGAGTCATTC GGGACTTCGC | 180 |
| GGGCCCCTAC TTTGTCTCAG AGGACAACAT GGCCTTTGGA AAGCCTGCCA AGTACTGGAA | 240 |
| GTGGACCCT GCTCAGGTCT ATGCTAGCGG GCCCAACGCA TGGGACACGG CTGTGCACGA | 300 |
| CGCCTCTGAG GAGWACAAGC ACCGCATGCA CAATCTCTGC TGTGACAACT GCCACTCGCA | 360 |
| CGTGGCATCG GCCCTGAATC TGATGCGCTA CAACAACAGC ACCAACTGGA ATATGGTGAC | 420 |
| GCTCTGCTTC TTCTGCCTGC TCTACGGGAA GTACGTCAGC GTTGGGGCCT TCGTGAAGAC | 480 |
| CTGGCTGCCC TTCATCCTTC TCCTGTCGAC GGCCTCTTTG GCCCTCGAGA CA | 532 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 580 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|---|-----|
| GTGTACACCA AGATGATGAC CAAGAAGCCG GGCATGTTCT TCAACCCCGA GGAGTCGGAG | 60 |
| CTGGACCTGA CCTACGGNAA CAGATACAA AACTGGAAGC TCCCTGACGN CTACGAGCGC | 120 |
| CTCATCCTGG ACGTCTTCTT TGGGAGGCAG ATGNACTTCG TGCGCAGGGA CGANCTCCNT | 180 |
| GAGGNTGGC GTATTTTCA CCCCCTGNT GTACCANATT GAGCTNGAGA AGGCCAAGCC | 240 |
| TCCAGGAACA CATGTGGGT CATTACCAA CAGGTCCAT CCACATGATG GTGAACATCA | 300 |
| ANCTTTGGGC GGACAANGAT TGCTGGGAAT GGAATCCTG TTTACTGGGG AGCTCTGGGA | 360 |
| GTTCTTGAGC TTTGCTGAAA GGTACCCTGC CATCATCTAT AACATCCTGC TCTTTGGGCT | 420 |
| GACCACTGCC CTGGGTCAGA GCWTCATCTT TATGACGATT GTGTATCTTG GTCCCCTGAC | 480 |
| CTGCTCCATC ATCACTACAA CTCGAAAGTT CTTCAAAAW KTGCCCGCTG TGATCCTCTT | 540 |
| CGCCAATCCC ATGTCGACGG CCTCTTTGGC CCTCGAGACA | 580 |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GTCGACACTA CTTATGCGGC TACTTTGTCC AGGGCACAAA ATGCCGTGGC AGTATCTAAC      60
TAAACCCCCA CAAAAGTCTT TAATAACAGT TTKGRATGTG AGAAATTTAG ATAATTTAAA      120
TATAAGGTGC AGGTTTAAAT TTCTGAGTTT CTTCTTTTCT ATTTTATTA AAAAGAAAAT      180
AATTTTCAGA TTTAATTGAA TTGGAAAAAA CAATACTTCC CACCAGAAAT ATATATCCTG      240
AAAATTGTAT TTTTGTATATA TAAACAACTT TTAAGAAAGA TCATTATCCT TTTCTCTACC      300
TAAATATGAG GAGTCTTAGC ATAATGACAA ATATTTATAA TTTTCAATT AATGGTACTT      360
GCTGGATCCA CACTAACATC TTTGCTAATA ATCTCATTGT TTCTTCGTCA ACGGCCTCTT      420
TGGCCCTCGA GACA                                     434
  
```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GTGGACGTTT TTTTTTCTT TTTCTTTTTT TTAAGAAAAA CCCATTTTTT TCCTTAAGGA      60
CTTACTAGCC AAAATTTCTT AAAGTTCGAG GACTCTACTA GCCATGGCCG AGCCATTCTT      120
GTCAGAATAT CAACACCAGC CTCAAACTAG CAACTGTACA GTGCTGCTG CTGTCCAGGA      180
AGAGCTGAAC CCTGAGCGCC CCCCAGGCGC GGAGGAGCGG GTGCCCGAGG AGGACAGTAG      240
GTGGCAATCG AGAGCGTTCC CCCAGTTGGG TGGCCGTCCG GGGCCGGAGG GGAAGGGAG      300
CCTGGAATCC CAACCACCTC CCTGCGAGC CCAGGCCTGT CCAGAATCTA GCTGCCTGAG      360
AGAGGGCGAG AAGGGCCAGA ATGGGGACGA CTCGTCCGCT GGCGGCGACT TYCCGCCGCC      420
GGCAGAAGTG GAACCGACGC CCGAGGCCGA GCTGCTCGCC CAGCCTTGTC ATGACTCCGA      480
GGCCAGTAAG ATGGGGTCGA CGGCCTCTTT GGCCCTCGAG ACA                          523
  
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GTCGACCCTC ANTGTCTGGA AACTGGTCTT GGAAGGGATN GTTTATNCTG AGTACACCTG      60
GGAAGTATTT GGGTACTGTC ANGAGCTGGA GTTGNCTNG NATTACCNTC TTCTGCCNA      120
TCTGGTGGTA GGGGTAAACC NG                                     142
  
```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTCCACCCGG GCCGCCCCCTC GCCGCCCCGGG CTCTTCGCGG GCTGCTCTTT GTCTCCCCGA      60
CCTCGATCCC TCGCTCTCCG GCGGCGTGCG GGCTCGTCTG AGGCTTCCCG CATCTCCCCG      120
CTGGAATCC TGCCTCCCCG GGGTTAGAGG AGGGTTCGTT CGAGGGCTGG AAGCGGGAAA      180
GCGGGGCGGA AGGACTGGGC TCATCGCCTC CTGATTAAC TGTGTCTTT ACTTAAATG      240
ACTTTTCCCC CACTTTGTCA AACTTGAGAA CTGTSTTGTG TGTGTGTGTT TCCTTGAGTC      300
TCTAGCTTCA AAATTAAGAG TAGGCGCTAC CGCTGCGATT GTGGGCAGTT GTGTGGTTGG      360
CGGTGCGTT TGGAGCTCTG AGTTGAAAAG ATGTACGTGA ATGTATGGTT TAGATTTTGT      420
TCTTTTTTTT GCGATTGTCi GATTGGGAGT ACTTTTCCTT TCGGAAATGG GCGAATTTGG      480
TTTTCTTTT GTTCATTGAG AACTGGGTCTG ACGGCCTCTT TGGCCCTCGA GACA      534
  
```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GTTCGCGAAG GGAAGAAGAA GATGAACAAG AACAATGCCA AGGCTCTGAG CACCTTGCGT      60
CAGAAGATCC GAAAATACAA CCGTGATTTC GAGTCCCATC TCACAAGCTA CAAGCAGAAC      120
CCCGAGCAGT CTGCGGATGA AGATGCTGAG AAAAGTGAGG AGGATTCAGA AGGCTCTTCA      180
GATGTGGATG AGGATGAGGA CGGAGTCAGT GCTGCAACTT TCTTGAAGAA GAAATCAGAA      240
GCTCCTTCTG GGGAGAGTCG CAAGTTCCTC MAAAAGATGG ATGATGAAGA TGAGGACTCA      300
GAAGATTCCG TAGATGATGA AGACTGGGAC WCAGGTTCCA CATCTCCGA CTCCGACTCA      360
GAGGAGGAAG AAGGGAAACA AACCGCGCTG GCCTCAAGAT TTCTTAAAAA GGCACCCACC      420
ACAGATGAGG ACAAGAAGGC AGCCGAGAAG AAACGGGAGG ACAAGCTAA GAAGAAGCAC      480
GACAGGAAAT CCAAGCGCCT GGATGAGGAG GAGGAGGACA ATGAAGGCGG GGTACCGGCC      540
TCTTTGGCCC TCGAGACA      558
  
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GTTGACGGCC AGCTTGCTGT CTAACCTTTC ACATCGGAGA AGCTCCTTGG CCTGGGAGGA      60
CTTCTCCGTG CTTTCCCCCT TCCAGAGAT GCCCCTGTCG AGGGAGTGGC AGAGACCATC      120
CTGGAGGGTG CCAGGAGCGG GGGCCCGTCT GAAGTCCCCG CCACCCTGGC GGTGCTCCGC      180
AGGCACCGGG CCATCCGACA TCGCACCTC GCTGGCGCGC ACGCTGGCCT GCTTGTGAAG      240
  
```

| | |
|---|-----|
| AGCATCCTTC AGCAGGCTGC CCAGCGGTGG CGCCTCCTGC ATAGACGCTT TGTTCCTCAA | 300 |
| AGTACTTGAC CTTTCCACAG CTTTCGGATA GACTTTCTTC TCTCTCTCTT CCAGCTTAAA | 360 |
| CAGAGCAAAG TTTTCCAAAT CACTCCCAGG TCCATGGGAT TTCTGGTGGG ATTCTGTGTT | 420 |
| CTCTGGGAAG CCGTCTGGTC GACGGCCTCT TTGGCCCTCG AGACA | 465 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|--|-----|
| GNNNTCGTTG TTCCAGAACT TGATGAGGGG ATCTCGGAAC AACACNGAAA CTTTTCCCTC | 60 |
| CCTCANTNAC GCACCNCGAC TCTCTATTGA GCCAACGGNA ANNCGGCCCT TCCCTCCAAG | 120 |
| TAACTTTGNA TTTGAAAATA AAAAAAAAAAG NTTGCTGTCC TTGCTATCCA AGAATAAATA | 180 |
| GACCTNCAAN TATTAATCTT TTGTTCCCT CGTCATTGTT CTCGTTCCCT TTCTNCCTTG | 240 |
| TTTCTTTTTT TGCACAATAT ATCAAGCNAT ACCAAGCATA CAATCAAACCT CCAAGCTCGG | 300 |
| AATTCGGCCA NAGAGACCGT CGACGGAAGA AATTGNCTGG AAACCTTGTT ATGGTGATAT | 360 |
| ATACCGTCCN CCAAGAAAAG GGATGCTGCT ATCAGTCTTT CTAGGATCCG GGACACAGAT | 420 |
| ATTAATTATG ACCTTTGTGA CTCTATTTTT CGCTTGCCTG GGAGTTTTGT CACCTGCCAN | 480 |
| CCGAGGAGCG CTGATGACGT GTGCTGTGGT CCTGTGGGTG CTGCTGGGCA CCCCTGCAGG | 540 |
| CTATGTTGCT GCCAGATTCT ATAAGTCCTT TGGAGGTGAG AAGTGGAAAA CAAATGTTTT | 600 |
| ATTAACATCA TTTCTTTGTC CTGGGATTGT ATTTGCTGAC TTCTTTATAA TGAATCTGAT | 660 |
| CCTCTGGTCA ACGGCCTCTT TGGCCCTCGA GACA | 694 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | |
|---|-----|
| AGACTCGTCT CAGACCAATT GCAGCCTTCT CAACCCAAAC GCCGACCAAG GAAAACTCA | 60 |
| CTACCATGAG AATTGCAGTG ANTTGCTTTT GCCTCCTAGG CATCACCTGT GCATACCAG | 120 |
| NTAAACAGGC TGATTCTGGA AGTTCTGAGG AAAAGCAGCT TTACAACAAA TACCCAGATG | 180 |
| CTGTGNCCAC ATGGCTAAAC CCTGACCCAT CTCAGAAACA GAATCTCCTA GCCCCACAGA | 240 |
| CCCTTCCAAG TAAGTCCANC GAAAGCCATG ACCACATGGA TGATATGGAT GATGAAGATG | 300 |
| ATGATGACCA TGTGGACAGC CAGGACTCCA TTGACTCGAG CGACTCTGAT GATGTAGATG | 360 |
| ACACTGATGA TTCTACCAG TCTGATGAGC CTCACCATC TGATGAATCT GATGAAGTGG | 420 |
| TCACTGATTT TCCCACGGAC CTGCCGTCGA CGGCCTCTTT GGCCCTCGAG ACA | 473 |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | |
|---|-----|
| AGAAGCTGTG ATCTTCAAGA CCATTGTGTC CAAGGAGATC TGTCTGATCC CAAGCAGAAG | 60 |
| TGGGTTTCAGG ATTCCATGGA CCACCTGGAC AAGCAACCCA AAACCTCCGAA GACGTGAACA | 120 |
| CTCACTCCAC AACCCAAGAA TCTGCAGCTA ACTTATTTTC CCCTAGCTTT CCCCAGACGT | 180 |
| CGACGCCTCT TTGCCCTCGA GACA | 204 |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS: --
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | |
|--|-----|
| GTCCACACAC GCCGACCACG GAAAACCTCAC TACCATGAGA ATTGCAGTGA TTTGCTTTTG | 60 |
| CCTCCTAGGC ATCACCTGTG CCATACCACT TAAACAGGCT GATTCTGGAA GTTCTGAGGA | 120 |
| AAAGCAGCTT TACAACAAAT ACCCAGATGC TGTGGCCACA TGGCTAAACC CTGACCCATC | 180 |
| TCAGAAGCAG AATCTCCTAG CCCCACAGAA TGCTGTGTCC TCTGAAGAAA CCAATGACTT | 240 |
| TAAACAAGAG ACCCTTCCAA GTAAGTCCAA CGAAAGCCAT GACCACATGG ATGATATGGA | 300 |
| TGATGAAGAT GATGACGACC ATGTGGACAG CCAGGACTCC ATTGACTCGA ACGACTCTGA | 360 |
| TGATGTAGAT GACACTGATG ATTCTCACCA GTCTGATGAG TCTCACCATT CTGATGAATC | 420 |
| TGATGAACTG GTCCTGATT TTCCGTCGAC GGCCTCTTG GCCCTCGAGA CA | 472 |

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | |
|---|-----|
| GTCGACTGAA AATTAACCCT CAGACGCCAC ATCCCTGAC AAGATGCCAG GCAGGTTCTC | 60 |
| TTCCTCTCAC ATACTGACCC ACGGGTCCAC CCTCTCTCCC CTGGAAAGGA CACCATGAGC | 120 |
| ACTGAAAGCA TGATCCGGGA CGTGGAGCTG GCCGAGGAGG NNTTNCCAA GAAGACAGGG | 180 |
| GGGGCCCAGG GGTCCAGNG GNGCTTGTTT CTCAGACTCT TCTCCTTCCT GATCGTGGGA | 240 |
| GGNGNACCA CGCTCTTCTG NCTGNTGNAC TTTGGAGTGG ATCCGGGCCC CAGAGGGAAG | 300 |
| AGTTCCCCCA GGGGACTCTT CTCTAATCNA GNCCTCTTGG | 340 |

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | |
|---|-----|
| GTGACGCGC GCCGGTAAAA ATGGCGAAAT GGGGGTAGGC GGCCTGGAC CTGAAGAGAT | 60 |
| GGGGCGCGCA GGTGGGGCGG TTGTCAGAGC CCCCTGACGT GGGCGCCGGG CTTTATCGG | 120 |
| CGATTGATC TGGCGACCTC GGGCCGGCGC CTAAGAGGTC AGACTGCCGA GCCTCCGGGT | 180 |
| CGCCAGCGGC CCCGCCGAGT GCCGGAGGCA ATGGATGAAC AGAGCGTGA GCGCTGKCTG | 240 |
| WCAGAGCAGA GAGCTCAATG TCCTCATTCC CGTGCTCCAC TCCAGCTACG AGAACTAGTA | 300 |
| AATTGTCGTT GGGCAGAAGA AGTAACACAA CAGCTTGATA CTCTTCAACT CTGCAGTCTC | 360 |
| ACCAAACATG AAGAAAATGA AAAGGACAAA TGTGAAAATC ACCATGAAAA ACTTAGTGTA | 420 |
| TTTTGCTGGA CTTGTAAGAA GTGTATCTAC CATCAGTGTG CACTTTGGGT CGACGGCCTC | 480 |
| TTTGGCCCTC GAGACA | 496 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | |
|--|-----|
| AGACACATAG ACCAACCGGG GAGATATGTT TGAATNTGAT GAAGATGAGA TGTCTATGT | 60 |
| GGATCTGNAC AAGAAGGAGA CCTCTGTCAT CTGGAGGAGA NTGNCCAACC CTTTTCCTTT | 120 |
| GAGNCTCAGG GNGGGCTGTC TAACATTGCT ATANTGAACA ACAACNTGAA TACCTTGATC | 180 |
| CAGCGTTCCA ACCACACTCA GNCCACCAAC GATCCCCCTG AGGTGACCGT GTTTCCTCAAG | 240 |
| GTCACGGCCT CTTTGGCCCT CGAGACA | 267 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|---|-----|
| GTGACCTTG AAGATGTTTT CTAAGAATC AAAAATGCTA CAAAGAAGTA TATCATTTTC | 60 |
| AAATATGGCT TTATCGTCTT GTTACTTTT ACCAGGAGAT GCCACTGTCA TAACTTCTTC | 120 |
| ATGGGATAAT AATGTCTATT TTTATTCCAT AGCATTGGA AGACGCCAGG ACACGTTAAT | 180 |
| GGGACATGAT GATGCTGTTA GTAAGATCTG TTGGCATGAC AACAGGCTAT ATTCTGCATC | 240 |
| GTGGGACTCT ACAGTGAAGG TGTGGTCTGG TGTTCTGCA GAGATGCCAG GCACCAAAAG | 300 |
| ACACCACTTT GACTTGCTGG CCGAGCTGGA ACATGATGTC AGTGTAGATA CAATCAGTTT | 360 |
| AAATGCTGCA AGCACACTGT TAGTTTCCGG CACCAAAGAA GGCACAGTGA ATATTTGGGA | 420 |
| CCTCACAACG GCCTCTTTGG CCCTCGAGAC A | 451 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|-----|
| GTTCACGCAA GTTGCTGGGC TGGTGGGGC CTGTCAAGTG AGGCCTGGTG GAGAAAGGTT | 50 |
| GAATTTGGAG GGCCAGGAAC AAGCTGGGAT GCAGGGGAGG CTTTCTAAAC TCTACAGTGC | 120 |
| TTCTAGAGAT GACGAGGAGG TAGGGAGTAG AAGAGAGCCG GACAGATTAG GGAGCTCCCA | 180 |
| GGGTGAGCTT GTGGGCAGSC CTSCAGAGGA GAAGAGGCTC TTCCCTAGGA GCTCAGAGGG | 240 |
| ACTTGTCTG GAAGACTGAT GGGAGATGTA TGCAGCTGTT TAGAGGCTGC TTTGGAGAAC | 300 |
| AAATGAACAT GGTTCGTGTT GTGCAAGCAG TTAAGTGGT TCTTTTGGCT CATATATCTT | 360 |
| CCAATAAAGA CATTGAGCGA GGAGAGTTGA TACCGTCATG TTTTGGAGC TTAAGCACAG | 420 |
| ACTGGCAGGT CGACGGCCTC TTTGGCCCTC GAGACA | 456 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|-----|
| GTCGACAGAA TTCACAACAT CCAAGATTC CACCTCNCA GATGTTTTCT AAAGNAATCA | 60 |
| AAAATGCTAC AAAGAAGTAT ATCATTTTCA AATATGGCTT TATCGTCTTG TTTACTTTTA | 120 |
| CCAGGAGATG CCACTGTCAT AACTTCTTCA TGGGATAATA ATGCTATT TTATTCCATA | 180 |
| GCAATTTGGA GACGCCAGGA CACGTTAATG GGACATGATG ATGCTGTTAG TAAGGATCTG | 240 |
| TTGGCATGAC AACAGGCTAT ATTCTGCATC GTGGGACTCT ACAGTGAAGG TGCGGTCTGG | 300 |
| TGTTCCCTGC AGAGATGCCA GGCACCAAAA GACACCACTT TGGCTTGNTG GCCGAGCTGG | 360 |
| ACATGATGTC AGNGTNGGTA CAATCAAGNT TANNA | 395 |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|-----|
| GTGGNCCGAG ATAGAGGAGG CTTCCCTCCA AGAGGACCCC GNGTTCCTCG AGGGAACCCC | 60 |
| TCTNGAGGAG GAAACGTCCA GCACCGAGCT GGAGACTGGC AGTGTCCCAA TCCGGGTGTT | 120 |
| GGAAACCAGA ACTTCCCCTG GAGAACAGAG TGCAACCACT GTAAGGCCCC AAAGMCTGAA | 180 |
| GGCTTCTCTC CGCCACCCTT TCCGCCCTCG GGTGGTGATC GTGRCAGAGR TGGCCCTGST | 240 |
| GGCATACGGG GAGGAAGAGR TGGCCTCATG GATCGTGGTG GTCCCGGTGG AATGTTTCAA | 300 |
| GRTGGYCGTK GTGGAGACAG AGRTGKCTTC CGTKGTGGCC GGGGCATGGA CCGAGGTGKC | 360 |
| TTTGGTGGAG GAAGACNAGG TGTCCCTGGG GGCCCCCTG NTCCTTTGAT GGAACAGATG | 420 |
| GGAGGAAGAA GAGGAGGACG TGGGTCGACG NCCTCTTTGT CCCTCGAGAC A | 471 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GTCGACCGTC TACGCCTACA CCATGTTCTT CTCCACGTTT TACCACGCCT GCGACCAGCC      60
CGGGGAGGCG GTGCTGTGCA TCCTCAGCTA CGACACGCTG CAGTACTGCG ACTTCTTGGG      120
TCCCGGGGCG GCCATCTGGG TCACCATCCT GTGCATGGCA CGGCTCAAGA CAGTCCTGAA      180
ATACGTGCTG TTTCTTCTGG GTACACTGGT CATCGCCATG TCCTTGCAGC TGGACCGCAG      240
GGGCATGTGG AACATGCTGG GGCCCTGCCT CTTTGCCTTC GTGATCATGG CCTCCATGTG      300
GGCTTACCGC TCGGGGCACC GCGGCCAGTG CTACCCACC TCGTGGCAGC GCTGGGCCTT      360
CTACCTCCTG CCCGGCGTCT CTACGGCCTC TTTGGCCCTC GAGACA                      406

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

GTCGCCCCAGC AAGTGAGCAG ATCCTCCGAG GCACCAGGNN ACTCCAGCCC ATGCCATGGC      60
GGATTCTGAG CGCTCTCGG CTCCTGGCTG CTGGGCCGCC TGCACCAACT TCTCGCGCAC      120
TCGAAAGGGA ATCCTCCTGT TTGNTGAGAT TATATTATGC CTGGTGATCC TGATCTGCTT      180
CAGTGNCTCC ACACCAGGCT ACTCCTCCCT GTCGGTGAYT GAGATGATCC YTSCTCSCTA      240
TCTTTCTCTT GTTGTCTACA TGTGTGACCT GCACCACCAA GATACCATTC ATCAACTGSS      300
CCTGGAGTGA TTCTTCCGA ACCCTCATAG GGGSAATCCT CTACCTGATC AMCTCCATTG      360
*KGTCCTKGT TGAGAGAGGA AACCACCCCN TNAATCGTTC GTAGGGGTAC TGGGCCTAAT      420
CGCTACGGCC TCTTTGGCCC TCGAGACA                      448

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

TTNCAATCNC CGATCCCCAT CACGAATGGG GGGCACC GGG TTACCCCCC CCTCCCGCCG      60
TAGGGTAGGC ACACNCTGAG CCAGTCAGTG TATCGCGCGT GCATCCCCCG ACATCTAAGG      120
GCATCACAGA CCTGTINTTG NTCAATCTCG GGTGGNTGMN CGCCAATTGT CNCTCTAAGA      180
ANATGGGGGA CGCCGNCCGC TCGGGGGTNG CGTAACTAGN TAGNATNCCA GAGTCTCGTT      240
CGTTATCGGA AGTAACCAGA CANATCGCTC CNCCAACTAA GANNGGCCAT NCACCACCAC      300
CCACGGAATC GAGANAGAGC TATCAATCTG TTGTAGGACA TAACCCGGCT TCTTGGTCAT      360
CATCNTGGTG TACNCGNCCT CTTTGNCCCT CGAGACA                      397

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCCTGCCTGC | TGGGCCGCCT | TNCACCCAAC | TTCTCGCGCA | CTCGAAAGGG | AATCCTCCTG | 60 |
| TTTGCTGAGA | TAAATANTAT | NCCTGGTGAT | CCTGATCTGC | TTCAGTGCCT | CCACACCAGA | 120 |
| CNACTCCTCC | CTGTCCGTGA | TTGAGATGAT | CCTTGCTGCT | ATTTTCTTTG | TTGTCTACAT | 180 |
| GTGTGACCTG | CACACCAAGA | TACCATTGAT | CAACTGGCCC | TGGAGTGATT | TCTTCCGAAC | 240 |
| CCTCATAGCG | GCAATCCTCT | ACCTGATCAC | CNCCGTTGTT | GTCCTTGTTG | AGAGAGGAAA | 300 |
| CCACTCCTAC | AATCGTCGCA | GGGGTACTGG | GCCTAATCGC | TACGGCCTCT | TTGGCCCTCG | 360 |
| AGACA | | | | | | 365 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACGACA | CGCTGTCTTC | ACTACCTGAT | TGCCCAGAAG | ATCCACACTG | TCTACACTAC | 60 |
| CTGCCTGGCC | AGTAGATCCA | CGGTATCTAC | ACTACCTCCC | TGGCCAGCAG | ATTCACCCAG | 120 |
| TCTACACTAA | CCGCTTGTC | AGCAGGTCCA | CCCTGTCTAC | ACTACGTGCC | TGCCAGCAGA | 180 |
| TCCAAGCTGT | CTACACTCCC | TGCCTGGCCA | GATGATCCAT | GCTATCTCCA | CTACCTGCCT | 240 |
| ATCCAAGTGA | TCCACCCTCT | CTTTACTACC | TTCTGTCCG | GCAGATTGAC | CCTCTCTACT | 300 |
| CTACCTGCCT | GGCCAGCAGA | TCCACGCTAT | CTACACTACC | TGACTTACCA | GATCCACCCT | 360 |
| GTCTACACTA | CATGCTTGTC | CAGCAGGTCC | ACCCTGTCTA | CACTACCTGC | CTCTCCAGAA | 420 |
| GATCCACGTC | AACGGCCTCT | TTGGCCCTCG | AGACA | | | 455 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGGANTTNGG | CCCAAAGAGC | CCGTTTGAGT | NAACCNAAGA | AGTCAAGATT | GGCCCNAAGT | 60 |
| TCCAGANATG | TTTGAAGAC | CTGGAGAACT | GTTACAGTGN | AAATGAAGAA | GACAGTTCCT | 120 |
| CCATTGATCA | TCTGTCTCTG | AATCAGAAAT | CCTTCTATCA | TGTAAGCTAT | GGCCCACTCC | 180 |
| ATGAAGGCTG | CATGGATCAA | TCTGTGTCTC | TGAGNATCTC | TGAAACCTCT | AAAACATCCA | 240 |
| AGCTTACCTT | CAAGGAGAGC | ATGGTGGTAG | TANCANCCAA | CGGGAAGGTT | CTGAAGAAGA | 300 |
| GACGGTTGAG | TTTAANCCAA | TCCATCACTG | ATGATGACCT | GGAGGCCATC | GCCAATGACT | 360 |
| CAGAGGAAGA | AATCATCAAG | CCTAGGTCAT | CACCTTTTAG | CTCCCCGAGC | AATGTGAAAT | 420 |
| ACAACTTTAT | GAGGATCATC | AAATACGAAT | TCATCCTGAA | TGACGCCCTC | AATCAAAGGT | 480 |
| CGACGGCCTC | TTTGGCCCTC | GAGACA | | | | 506 |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CGGTAACGCN | GTTNTCTNA | GGCGAGCTCA | GGGAGNACAA | GAAACCCCTCC | CGTGGAGCAA | 60 |
| GAANGCCACA | AGCTCNCTTG | ATCTTGATTA | TCAGGACGAA | AACAGACCGT | GAAAGCGGGG | 120 |
| CCTCACGATC | CTTCTGACCT | NNTGGGTNTT | AAGCAGGAGG | TGTCAGAAAA | GTTNCCACAG | 180 |
| GGATAACTGN | CTTGTGNCGN | CCAAGCGNTC | ATAGCGACGT | CGCTTTTGA | TCCTTCGATG | 240 |
| TCGGCTCTTC | CTATCATTGT | GAAGCAGAAT | TCACCAAGCG | TTGGATTGTT | CACCCACTAA | 300 |
| TAGGGAACGT | GAGCTGGGTT | TAGACCGTCG | TGAGACAGGT | TAGTTTTACC | CTACTGATGA | 360 |
| TGTGTTGTTG | CCATGGTAAT | CCTGCTCAGT | ACGAGAGGAA | CCGCAGGTTT | AGACATTTGG | 420 |
| TGTATGTGCT | TGGCTGAGGA | GCCAATGGTC | GACGGCCTCT | TTGGCCCTCG | AGACA | 475 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 460 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GTTGACCCGA | TGGAGGAGGA | GGAGGTTGAG | ACGTTCCGCT | TTCAGGCAGA | AATTGCCCCAG | 60 |
| TTGATGTCAT | TGATNCATCA | ATACTTTCTA | CTCGANCAAA | GAGATCTTTC | TGAGAGAGCT | 120 |
| CATTTCAAAT | TCATCAGATG | CATTGGACNC | AATCCGGTAT | GAAAGCTTGA | CAGATCCCAG | 180 |
| TAAATTAGAC | TCTGGGAAAG | AGCTGCATAT | TAACCTTATA | CAGAACAAAN | AAGANCGAAC | 240 |
| TCTCACTATT | GTGGATACTG | GAATTGGAAT | GACCAAGGCT | GACTTGATCA | ATAACCTTGG | 300 |
| TACTATCGCC | AAGTCTGGAC | CAAAGCGTTC | ATGGAAGCTT | TGCAGGCTGG | TGCAGATATC | 360 |
| TCTATGATTG | GCCAGTTCGG | TGTTGGTTTT | TATTCTGCTT | ATTTGGGTGC | TGAGAAAGTA | 420 |
| ACTGTGATCA | CCGTCGACGG | CCTCTTGGC | CNGCGAGACA | | | 460 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCAAGCAATA | CCCAAGCAAA | CAATCNACTC | CAANCTCGGA | ANTCGNCCNA | AGAGACCGTC | 60 |
| GACCCCGTGT | TCACNATGGT | AGNNACGCCG | NCTACCATCG | ANAGTTGATA | GGGCAGACGT | 120 |
| TCNGTGGGT | CGTCTCCCCC | CCGGGGGGCG | TGCGATCGCC | CCGAGGTTAT | CTAGAGTCAC | 180 |
| CACACCCGCC | GGCGCCCNCC | CCCCGNCCGN | NAAAAAAGA | GGGGCTGTCN | GGGNTGGTTT | 240 |
| TGNTNTGATA | AATANACGCA | TCCCCCCCCC | GNNGGGGGNN | AGCGCCCGTC | GGCATGTATT | 300 |
| ANCTCTAGAA | TTACCACAGT | TATCCAAGTA | GGAGAGGAGC | GAGCGNCCAN | AGGANCCATA | 360 |
| NCTGATTTAA | TGAGCCATTC | NCAGTTTCNC | TGTTCCGNCC | GTGCGTACGN | AACGACCTCT | 420 |
| TTGTNCNTAA | AGNCG | | | | | 435 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GTCGACCACA CTGCTGCTCA CGCTCAGCAA CCTCATGTTC CTGGCCCCCA TCGCCGTCTC      60
AGTGCGGCGA TTCTTCCTGG TGGAGGCCTC CGTCTACGCC TACACCATGT TCTTCTCCAC      120
GTTCTACCAC GCCTGCGACC AGCCCGGGGA GCGGGTGTCTG TGCATCCTCA GCTACGACAC      180
GCTGCAGTAC TCGCACTTCT TGGGCTCCGG GCGGGCCATC TGGGTCACCA TCCTGTGCAT      240
GGCAGGCTC AAGACAGTCC TGAAATACGT GCTGTTTCTT CTGGGTACAC TGGTCATCGC      300
CATGTCCTTG CAGCTGGAC GCAGGGGCAT GTGGAAGTTG CTGGGGCCCT GCCTCTTTGC      360
CTTCGTGATG ATGGCCTCCA TGTGGGCTTA CCGCTGCGGG CACCGGCGCC AGTGCTACCC      420
CACCTCGTGG CAGCGCTGGG CTTTCTACCT CCTGCCCCGC GTCTCTACGG CCTCTTTGGC      480
CCTCGAGACA                                     490

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

CGTCTCAGGC CAGTTNCANC CTTCTCANN CAGAACGGCGN CCCAAGGAAA ANCTCACTAC      60
CATGAAGAAT TGCAGTGATT TGCNTTTGCC TCCTAGGCAT CACCTGTGCC ATACCAGNTA      120
AANCAGGCTG ATTCTGGAAG TTNCTGAGGG AAAAAGCAGC TTTACAACAA ATACCCAGAT      180
GCTGTGGCCA CATGGCTAAA CCCTGANCCA TCTCAGAAGC AGAATCTCCT AGCCCCACAG      240
AATGCTGTGT CCTCTGAAGA AACCAATGAC TTAAACAAG AGACCCAAAC AAGTNAGTCC      300
NACGAAAGCC ATGACCACAT GGATGATATG GATGATGAAG ATGATGATGA CCATGTGGAC      360
AGCCAGGACT CCATTGACTC GNNCGACTCT GATGATGTAG ATGACACTGA TGATTCTCAC      420
CAGTCTGACG AGTCTACCA TTCTGATGAA TCTGATGAAC TGGTCACTGA TTTTCCCACG      480
GACCTGCCGT CGACGGCCTC TTTGACCCTC GAGACA                                     516

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GCCAAGACTC GTCTCAGNCC AGTTGCAGCC TTCTCANCCA AACNCCGACC CAAGGANAAC      60
TCCCCTACCA TGAGAATTGC AGTGATTGTC TTTTGCCCTC TAGGCATCAC CTGTGCCATA      120
CCAGTTAAAC AGGCTGATT C TGGAAGTTC CTGAGGAAAA GCAGCTTTAC AACAAATACC      180

```

```

CAGATGCTGT GTCCACATGG CTAAACCCTG ACCCATCTCA GAAGCAGAAT CTCCTAGCCC      240
CACAGAATGC TGTGTCCTCT GAAGAAACCA ATGACTTTAA ACAAGAGANN CANCCAAGTA      300
AGTCCANCGA AAGCCATGAC CACATGGATG ATATGGATGA TGAAGATGAT GATGACCATG      360
TGGACAGCCA GGA CTCCATT GACTCGANCG ACTCTGATGA TGTAGATGAC ACTGATGATT      420
CTCACCAGTC TGACGAGTCT CACCATTCTG ATGAATCTGA TGAAGTGGTC ACTGATTTTC      480
CCACGGACCT GCCGTCGACG GCCTCAATGN CCCTCGAGAC G                          521

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

GCAAGCAANC AATCCAACCC AAGNTNGGGA NTCGNCCNAA GAGNCCGTTG ANCAGAAGCC      60
ANTNATGGAT GANCAGCGCG ACCTTATCTC CAACAATGAG CAACTGNCCA TNCTGGGNCC      120
GGNCGCCCTG GGCNCCGGA GAGCAAGTGC ANCCGCGGAG CCCTGTACAC AGGCTTTTCC      180
ATCCTGGTGA CTCTGCTCCT CGCTGGCCAG GCCACCACCG CCTACTTCCT GTACCAGCAG      240
CAGGNCCGGC TGGACAAACT GACAGTCACC TCCCAGAACC TGCAGCTGGA GAACCTGCGC      300
ATGAAGCTTC CCAAGCCTCC CAAGCCTGTG AGCAAGATGC GCATGNCCAC CCCGCTGCTG      360
ATGCAAGCGC TGCCCATGGG AGCCCTGCCC CAGGGGCCCA TGCAGAATGC CACCAAGTAT      420
GGCAACATGA CAGAGGACCA TGTGATGCAC CTGCTCCAGA ATGCTGACCC CCTGAAGGTG      480
TACCCGCCGT CGACGGCCTC TTTGGCCCTC GAGACA                          516

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

TGCTATCCNA GNATAAAATA AGACCCTGCA ANTATTAATC TTNTTTGTTT CCTCGTCATT      60
GTTCTCGTTC CCTNTCTTCG TTGTTTCTNN TTCTGCACAA TATNTTCAAG CTATACCGAG      120
CATACAATCA AACTCCAAGC TCGGAATTCG NCCAAAGAGG CCGTCGAGCC GAATTCTCCA      180
CNAGAATAGC ATTTCTGCTC ATCTGCATGG TCGCAGTCAC GAGCCAGATG NCCTGNTTTN      240
CCACAGTTGT AGCAGCATTG CTCTCGCTCT CTCTTGGGCT CCTTGCAGTC CTTGGCAATG      300
TGGCCGCCTC TACCGCAGTT ATAGCAGGCA TCCTCCTGAA GATCACAATC CTTGGCAAGA      360
TGACCAGACT CACCACAGCG ATAACAATA TCTGGAAGAG ACGAGGAAAC AAAGTGGAAA      420
CCTCTATCCG AGGTAAACC ACCTCTGCCA CGGCTTCTCA TTCCACGACC ACGGCCTCTT      480
TGGCCCTCGA GACA                          494

```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCTCCANATN | ANCTTTNTTC | CTCTCATTGT | NTCGTCCCTC | CTCCTTGTTT | TTTNTGCCC | 60 |
| AAAATCCANC | AAANCCAACA | ACCATCCNCN | CCACCTGGAA | GTNGCCCAAA | GAGGCCGNAC | 120 |
| CAAGAAGTGT | CGATTCCCTT | GTNTGNAGGA | GCGACCAGGA | ACATCTACGG | TTGAGAAGAA | 180 |
| AGAAAGANTG | CCTTCGTCGA | TGTCTTCCTG | TGTGAANTTT | CCAGACATAG | CCCAGTCGAC | 240 |
| CAGCCTTCCC | CACNAGACTG | GAGCGTCTCT | ATTGTATNTG | GGTCCCTGTA | AGAGTAGAAG | 300 |
| GGTGAAAATC | CCANTGTGTC | TGAGTNTTGC | GCCNCCACCA | TAAACACCGC | CTTTTCTCG | 360 |
| AATTTCTGTA | TNCAAGAAAN | TGTCAGTCAT | CACACGTGCA | AGGATNTTAA | GACTGNCATG | 420 |
| ATCTGGGNCC | GTGTAGGGGN | CAGNTCGGAT | NCATTACCCC | ACGTAATTCA | CCGGGANGGG | 480 |
| CATCAGGAAG | TGAGTCTTCA | TCTCCAGGG | CGTGNAGGTG | GGTNCCATGA | CCAGCTTCCT | 540 |
| AATGACCTGG | GAGCCATGGG | GAACGTGGGC | ATCTCCACCA | GAGCTACTGG | GCACAGGTTT | 600 |
| CTCGACCGTG | TGTGGNCGCA | CAGACCGTCG | ACGGCCTCTT | TGNCCCTCGA | GACA | 654 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GTCCGACCTGA | GAATCTGGAA | AAATTGGAGA | AGTTGGGTAT | GAGCTCAGAC | CTGGTGAGCA | 60 |
| GGCTGCCTAC | CATTTATAGA | AATGCACATG | ACATCAAGAA | TAAGAGCTCT | GCCCCCAGCA | 120 |
| GAGTGCCTCC | TCTTTTGTG | CCACAGGGGA | CTTCTGAAAG | AAAAGACAGT | TCAGGTTCTG | 180 |
| TGTCCCCAMA | CACTCTTAGC | CAGGAGGAGG | GTGATCAGAT | CTGTTTGTTC | CATATCCGGA | 240 |
| AAAGTTGTAG | CTTTCAAGAT | AAGTGCCATA | GAGTTCATTT | CCATTTGCCG | YATCGATGGC | 300 |
| AATTCTTGGA | TAGAGGCAAA | TGGGAGGATT | TGGACNACAT | GGAACNTATT | GTAGAGNCAT | 360 |
| ATTGCAATCC | CCCCATAGAA | AGGATCCTGT | GCTCTGAGTC | AGCCAGTACC | TTTCACTCTC | 420 |
| ATTGTCTGAA | CTNTAACGCC | ATGACTTACG | GTGCTACCCA | GGCTCGCCGC | CTCTCCACGG | 480 |
| CCTCTTTGGC | CCTCGAGACA | | | | | 500 |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| GTCCGACACAA | ATGTTTCCTT | GGATAATCCA | GCTTTACATG | GTGAGAACCA | TGCTAGAGTC | 60 |
| CCTCATTGCA | GACAAAAGTG | GTTCCAAGAA | AACCTTGAGA | AGTAGCCTTG | AGGGGCCCCAC | 120 |
| CATATTGGAC | ATAGAAAAAT | TTCATCGAGA | GTCATTCTTC | TACACTCACT | TGATAAATTT | 180 |
| CAGTGAAACG | CTGCAGCAGT | GCTGTGACCT | TTCGCAGCTG | TGGTTCCGAG | AGTTCCTCCT | 240 |
| GGAGCTGACC | ATGGGCAGGA | GGATCCAGTT | CCCCATTGAG | ATGTCGATGC | CCTGGATCCT | 300 |
| GACGGACCAC | ATCCTGGAGA | CCAAGGAGGC | ATCGATGATG | GAGTACGTGC | TCTACTCCCT | 360 |
| GGACCTGTAC | AATGACAGCG | CCCACTACGC | GCTCACCAGG | TTCAACAAGC | AGTTCCTCTA | 420 |
| CGACGAAATT | GAGGCCGAGG | TCACGGCCTC | TTTGGCCCTC | GAGACA | | 466 |

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

GTCGACGGAA GTTGATTTT AATGATAAAG TACAATGAAG GGAGGGCAGA GGGGCTAAGC      60
CTAGCTGTCT GGGGTGCTGT GGTGGTGGTA GACTGGCTAC ACAAAGTGTG GCTGCTGCTG      120
CTGCTTCTTG GTGGCCGCCT TGCTGGCGAG GTCCTTGCC TTCTCTGTAG CTGCCAGTGC      180
CGTCTCCTTT GCCTTCTCCT TGGCTTCCTT GGCTGTCTCA ACAAGTGTTT TGGAAGGGGC      240
CTCGCCTTGC AGCTTAGCCA AGATATATTC AAAACCCCTC ATAGTCTTGG TCACGTTGCT      300
TTTGAACCGG GCAAGACCAA ATTCCTGGAC AGCTCTGGCT ACACAACTG TTGCTGGTCA      360
ACGGCCTCTT TGGCCCTCGA GACA                                     384
  
```

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GTGACGGGAC AAAATCTAG GGAGGCACCA ATCCTGAAAG AGTTTAAGGA AGAAGGGGAA      60
GAGATACCTA GAGTAAACC AGAGGAGATG ATGGATGAGA GACCCAAAAC AAGATCCCAG      120
GAACAGGAGG TGTTAGAGAG AGGAGGGAGA TTTACAAGAT CCCAGGAAGA GGCTAGAAAA      180
AGTCATCTGG CCAGACAGCA GCAGGAGAAG GAAATGAAAA CAACATCTCC CCTTGAGGAG      240
GAAGAAAGAG AAATAAAATC TTCACAAGGC TTAAGGAAA AATCGAAGTC TCCTTCCCCT      300
CCTCGACTGA CTGAAGATCG AAAGAAGGCC CCACTTGTAG CGCTGCCAGA GCAAAGTGC      360
AGCGAGGAGG AGACTCCTCC ACCTTTACTA ACAAAGGAAG CATCTTCTCC ACCACCTCAT      420
CCACAGCTCC ATAGCGAAGA AGAAATAGAG CCCATGGAAG GCCCAGCCCC CCCTGTCTCTC      480
ATTCAGTTAT CTCCTCCTAA TACAGATGCT GACACCAGGT CGACGGCCTC TTTGGCCCTC      540
GAGACA                                     546
  
```

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

GTCGACGTCG GTGGTGCAG CGGCGGCGGC GGCGGTTCCA GCATGAAGAG GAGAGCTGGC      60
CTGGGGGGCA GCATGAGGTC AGTGGTGGGC TTCTTGTCCT AGCGGGGCTC GCATGGGGAC      120
CCCCTGCTCA CTCAGGACTT TCAGAGGAGA CRCCTGCGGG GCTGCAGAAA CCTCTACAAG      180
AAGGACCTCC TCGGCCACTT CGGCTGTGTC AATGCCATTG AATCTCTCAA CAATGGAGGC      240
CAGTGGCTGG TCTCAGGAGG AGATGACCGC CGGGTTCTGC TATGGCACAT GGAACAAGCC      300
ATCCACTCCA GGGTCAAGCC CATACAGCTG AAAGGAGAGC ACCATTCCAA CATTTTGTG      360
  
```

| | |
|---|-----|
| CTGGCTTTCA ACAGTGGGTA CACTAAAGTG TTCTCTGGAG GCAATGATGA GCAAGTTATC | 420 |
| CTCCATGATG TTGNAAGCAG TGAGACATTG GACGTGTTTG CTCATGAAGA TGCAGTATAT | 480 |
| GACTTGCTG TGGTCNGCGC CCTCTTTGGC CCTCGAGACA | 520 |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

| | |
|--|-----|
| GTCGACTCCA GACACACCCC CCAGTCGAGC CCTGCAGCCA AACAGAGCCT TCACAACCAG | 60 |
| CCACACAGAG CCTGCCTCAG CTGCTCGCAC AGATTACTTC AGGGCTGGAA AAGTCACACA | 120 |
| GACACACAAA ATGTCACAAT CCTGTCCCTC ACTCAACACA AACCCCAAAG CACAGAGAGC | 180 |
| CTGCCCTCAGT ACACTCAAAC AACCTCAAAG CTGCATCATC ACACAATCAC ACACAAGCAC | 240 |
| AGCCCTGACA ACCCACACAC CCCAAGGCAC GCACCCACAG CCAGCCTCAG GGCCACAGG | 300 |
| GGCACTGTCA ACACAGGGGT GTGCCAGAG GCCTACACAG AAGCAGCGTC AGTACCCTCA | 360 |
| GGATCTGAGG TCCCAACACG TGCTCGCTCA CACACACGGC CTGTTAGAAT TCACCTGTGT | 420 |
| ATCTACGCA TATGCACAG CACAGCCCTC AACGGCCTCT TTGGCCCTCG AGACA | 475 |

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|---|-----|
| CCTGCCACAA TAATNTCCNA AGCCTAAAAC CCGAGCAATA CAANCNAACC CAAGCTCGGA | 60 |
| AATCGGGCCA AAGAGACCGT TCTTAGNTGG TGGAGCGATT TGTCTGGTTN ATTCCGATAA | 120 |
| ACGAACGAGA CTCTGGCATG CTAAGTAGTT ACGCGACCCC CGAGCGGTG GCGTCCCCCA | 180 |
| ACTTCTTAGA GGGACAAGTG NCGTTCANCC CACCCGAGAT TGAGCAATAA CAGGTCTGTG | 240 |
| ATGCCCTTAG ATGTCCGGGG CTGCACGGC GCTACACTGA CTGGCTCAGC GTGTGCCTAC | 300 |
| CCTACGCCGG CAGGCGCGGG TAACCCGTTG AACCCATTG GTGATGGGGA TCGGGGATTG | 360 |
| CAATTATTCC CCATGAACGA GGAATTCCCA GTAAGTGCGG GTCATAAGCT TCGGTTGATT | 420 |
| AAGTCCCTGT CGACGGCCTC TTTGGCCCTC GAGACA | 456 |

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|---|----|
| GTCGCRRCAA SMTYTYTMMA CTGTGGNGGG GCTCTACCCN TGAGGGCCTG GCCGCARCNT | 60 |
|---|----|

| | |
|---|-----|
| GGCTGSGGGC TGWCGACTAT GAACAGRTCG AGAAMGTGKN CGATTACTAC CCGGAGTACA | 120 |
| AGCTRCTCTY CGAGGGTGCA GGTAGGCAAC CCTGGAGACA TGACKCTGGA GGGMCGATTA | 180 |
| CTTTGAGYAC GAGGTAAARC TGAACAAGTT GTSCTTCCTG ANACAGTWCC ACCTTGGTGT | 240 |
| CTTCTATRCC TTCGTGAAGC TCAAGGAGCA GGAGTGTCKC AACATCGTGT GGATCGCTGA | 300 |
| ATGTATCTRC CAACGCMSS GCRMMYCSMA MSWCAWCCWY ATTCTSTRTC CTKSYAASGT | 360 |
| CWCAMTGAAN CWAGCCCTCT CAATTGCACT GCACTGTGTG TGTGTGTGTG TGTGTGTGC | 420 |
| GTGTGTGTG CGTGTGTGTG TATGTGTCT GTGACAAGCC TGTGGCTCAC CTGGTCGAGC | 480 |
| GCCTCTTTGG CCCTCGAGAC A | 501 |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|---|-----|
| CCNCCGTTTG TTGTNNTGCA CCAAANANCC NCNAATTGNC CANANAAAAT TGATGGGAAG | 60 |
| ACCACTTAAA GGGGGGGNAN TTAGGCGGGN CAAAGACAAG GCACCCNACA AGATGTCGTT | 120 |
| TGTTCCAGAG CTGATTGAGG GGTATCTCGG AAGNAACACN GAAACTTTTT TCCTTCCTTC | 180 |
| AATTCAACGC ACACTACTCT CTAATGACCN NCGGAATACG GCCTTCCTTC CAGTTACTTG | 240 |
| AATNTGAAAT AAAAAAAGT TTGCTGTCTT GCTATCCAAG TATAAATAGA CCTGCAATTA | 300 |
| TTAATCTTTT GTTTCCTCGT CATTGTTCTC GTTCCCTTTC TTCCTTGTTT CTTTTCTGC | 360 |
| ACAATATTTT AAGCTATACC AAGCATACAA TCAACTCCAA GCTCGGAATT CGGCCAAGA | 420 |
| GGCCGTCGAC GAACCACCGG CTGAAAATTG GCTTCTTCAA CCAGCAGTAT GCAGAGCAGC | 480 |
| TGCGCATGGA GGAGACGCC ACTGAGTACC TGCAGCGGG CTCAACCTG CCCTACCAGG | 540 |
| ATGCCCGCAA GTGCCTGGGC CGCTTGGCC CTCGAGACA | 579 |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | |
|--|-----|
| CCTGCNCCAA NANTTCNAA CCNAATAACC CAANAANACC AATCCNNCT CCANCTGGGG | 60 |
| AATTCGGNCC NAAGAGACCG TTGTNTTGAT GACAAGTCGA AGCCAANAAT ACCCATNCAAC | 120 |
| CTGCTCCCAA TCATGCAGGN TNCNGCCACT GCTGCCCTTG CCGTCCCTCC TCTGCACCAT | 180 |
| GGCTNCTCCT GCAACCAGGT CCTCTCTGCA CCACTTGCTG CTGANACGCC GACCGCCTGC | 240 |
| TGCTTCAGCT ACACCTCCCG ACAGATTCCA CAGAATTTCA TAGCTGACTA CTTTGAGACG | 300 |
| AGCAGCCAGT ACTCCAAGCC CAGTGTATC TTCCTAACCA AGAGAGGCCG GCAGGTCTGT | 360 |
| NNTGACCCCA GTGAGGAGTG GGTCCAGAAA TACGTCAAGT ACCTGGAGCT GAGTGCCAGA | 420 |
| GGGGTCCAGA AGCTTCGAGG CCCAGCGACC TCACTGGGCC CAGTGGGGAG GAGCAGGAGC | 480 |
| CTGANCTTG GGAACATGCG TGTGACCTCT ACAGCTACCT CGTCGACGGC CTCTTTGGCC | 540 |
| CTCGAGACA | 549 |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACCTCC | CAGGTCATTA | GGAAGCTGGT | CATGGAACCC | ACCTTCAAGC | CCTGGCAGAT | 60 |
| GAAGACTCAC | TTCCTGATGC | CCTTCCCGGT | GAATTACGTG | GGTGAATGCA | TCCGAAGTGT | 120 |
| CCCCTACACG | GACCCAGATC | ATGCCAGTCT | TAAATCCTT | GCACGTTTGA | TGACTGCCAA | 180 |
| ATTCTTGCAT | ACAGAAATTC | GTGAAAAAGG | CGGTGCTTAT | GGTGGAGGCG | CAAAACTCAG | 240 |
| CCACAATGGG | ATTTTCACCC | TTTACTCTTA | CAGGGACCCA | AATACAATAG | AGACGCTCCA | 300 |
| GTCTTTTGGG | AAGGCTGTCG | ACTGGGCTAA | GTCTGGAAAA | TTCACACAGC | AAGACATCGA | 360 |
| CGAAGCCAAA | CTTTCTGTCT | TCTCAACCGT | AGATGCTCCT | GTCGCTCCTT | CAGACAAAGG | 420 |
| AATGGACCAC | TTCTTGACG | GCCTCTTTGG | CCCTCGAGAC | A | | 461 |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GTCGACAATA | ATTCCACCTC | ACCAGGATAA | TACCCATCCT | TCAGCACCAA | TGCCTCCACC | 60 |
| TTCTGTTGTG | ATACTGAATT | CAACTCTAAT | ACACAGCAAC | AGAAAAATCAA | AACCTGAGTG | 120 |
| GTCACGTGAT | AGTCATAACC | CTAGCACTGT | ACTGGCAAGC | CAGGCCAGTG | GTGAGCCAAA | 180 |
| CAAGATGCAG | ACTTTGACAC | AGGACCAGTC | TCAAGCCAAA | CTGGAAGACT | TCTTTGTCTA | 240 |
| CCCAGCTGAA | CAGCCCCAGA | TTGGAGAAGT | TGAAGAGTCA | AACCCATCTG | CAAAGGAAGA | 300 |
| CAGTAACCTT | AATTCTAGTG | GAGAAGATGC | TTTCAAAGAA | ATCTTTCAAT | CCAATTCACC | 360 |
| GGAAGAATCT | GAATTCGCCG | TGCAAGCGCC | TGGGTCTCCC | CTAGTGGCTT | CCTCTTTATT | 420 |
| AGCTCCTAGC | AGTGGCCTTT | CAGTTCAAAC | TTCCACCAG | GGCTTTACTG | CAAAACAAGC | 480 |
| ACGGTCAACG | GCCTCTTTGG | CCCTCGAGAC | A | | | 511 |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACAGTC | CAAAGTCTCA | AGACAGTTAT | CCTGTTAGTC | CTCGACCTTT | TAGTAGTCCA | 60 |
| AGTATGAGCC | CCAGCCATGG | AATGAATATC | CACAATTTAG | CATCAGGCAA | AGGAAGCACC | 120 |
| GCACATTTT | CAGGTTTTGA | AAGTTGTAGT | AATGGTGTA | TATCAAATAA | AGCACATCAA | 180 |
| TCATATTGCC | ATAGTAATAA | ACACCAGTCA | TCCAACCTGA | ATGTACCAGA | ACTAAACAGT | 240 |
| ATAAATATGT | CAAGATCACA | GCAAGTTAAT | AACTTCACCA | GTAATGATGT | AGACATGGAA | 300 |
| ACAGATCACT | ACTCCAATGG | AGTTGGAGAA | ACTTCATCCA | ATGGTTTCCT | AAATGGTAGC | 360 |
| TCTAAACATG | ACCACGAAAT | GGAAGATTGT | GACACCGAAA | TGGAAGTTGA | TTCAAGTCAG | 420 |
| TTGAGACGCC | AGTTGTGTGG | AGGAAGTCAG | GCCGCGTCTA | CGGCCTCTTT | GGCCCTCGAG | 480 |
| ACA | | | | | | 483 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

GTCGACGAGG TGGTGATCAT GGAAGACGCC CCTGACTATT ATGCAGTGGA AGACATTTTC      60
AGCGAGATCT CAGACATGTA TGAGACAATT CATGACATCA AGATCTCTGA CTTTCATGGAG      120
ACCACCGACT ACTTCGAGAC CACTGACAAT GAGATAACTG ACATCAATGA GAACATCTGC      180
GACAGCGAGA ATCCTGACCA CAATGAGGTC CCCAACAAACG AGACCACTGA TAACAACGAG      240
AGTGCTGATG ACCACGAAAC CACTGACAAC AATGAGAGTG CAGATGACAA CAACGAGAAT      300
CCTGAAGACA ATAACAAGAA CACTGATGAC AACGAAGAGA ACCCTAACAA CAACGAGAAC      360
ACTTACGGCA ACAACTTCTT CAAAGGTGGC TTCTGGGGCA GCCATGGCAA CAACCAGGAC      420
AGCAGCGACA GTGACAATGA AGCAGATGAG GCCAGTGATG ATGAAGATAA TGATGGCAAC      480
GAAGGTGACA ATGAGGTCAC GGCCTCTTTG GCCCTCGAGA CA                          522

```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GTCGACAGAT CATGTTGGAA GAGCCCCCAG TAGCAAAAGT GTTAGAGCCT TCAGAAACCC      60
TTGTGGTATC ATCAGAGACA CCTACTGAGG TGTACCCTGA GCCAAGCACA TCAACAACAA      120
TGGATTTTCC AGAGTCATCT GCAATTGAAG CGCTAAGATT GCCAGAGCAG CCTGTAGACG      180
TACCATCGGA GATTGCAGAT TCATCCATGA CAAGACCGCA GGAGTTGCCG GAGCTGCCTA      240
AGACCAACAGC GTTGGAGCTG CAGGAGTCGT CGGTGGCCTC AGCGATGGAG TTGCCGGGGC      300
CACCTGCGAC CTCCATGCCG GAGTTGCAGG GGCCCCCTGT GACTCCAGTG CTGGAGTTAC      360
CTGGGCCCTC TGCTACCCCG GTGCCAGAGT TGCCAGGGCC CCTTTCTACC CCAGTGCCTG      420
AGTTGCCAGG GCCCCCTGCG ACAGCAGTGC CTGAGTTGCC AGGGCCCTCT GTGACACCAG      480
TGCCACAGTT GTCGCAGGAA TTGCCGTCAA CGGCCTCTTT GGCCCTCGAG ACA                          533

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

CCACCAGACA TAAAGTACTG ACATGATCAG AGGAATCATC AGCAACTGCA TNTCCATTGC      60
TAAGCCAGTA ATCAGGATGC AAATCCAGTT AAAGAGGAGC ATGAATAAAT AGTCTGCTGG      120
CCTCCCATCA AAAGCTCCTG TTTCAAGTCG CGTAGAATAC TGATATAAGA AATATANATT      180

```

| | |
|---|-----|
| GACCAAATAA AGAAATCCAG TTCCTGGACC CACAGGGAAA TAAAAGGTGG CAGTGATTGN | 240 |
| CCTCCAAATC TGAAAGCGAT ANAGGAAGGC TTCGGGCCAG AGGAAGAGGT AGGCCGGGCT | 300 |
| GATGAGGCCG AGTTTGCCGA CCAAGGGCAC GGNGACGGTG GCGGCGAACC AATAGCGCGT | 360 |
| GATCGCCGGG ATGCTCCTGA ACCAGTCTCC GATGTCCGAC ATCTTCGACC CACAGGTAGC | 420 |
| CAAGATGCAC AAGACGCCC GACTCCCCGC GCCGACCCC TCACGACGCG GCCGGCTCCG | 480 |
| CGACTGTTAG GTGTCTAGGT GGAAGCCGCG TCGAC | 515 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | |
|---|-----|
| ATNCNGGAGN CCCAGATGCT GTGGGCCATG ATCGCANNTT GNNTGAGAGA ATTGGCAGAA | 60 |
| NCAGANTACT CCTAGCNAGA NCAGTATTNT GTGTNACTCT GGAGAATTNC AGTGATGNAA | 120 |
| AAAAANAGAC CNGTNCAAGT AAGTCCAGCG AAAAGCATGC CCACATGGAT GAANTGGATG | 180 |
| ATGAAGATGA TGCCNNCCNT GNGGNCAGCA GGAACCTCTN TNNTGCGNG NCNACTCNTG | 240 |
| NTGNTGTAGA TGANGCTGGT NAAGCNNANC AGTCTGNTGA GNCTCCTCGA GTCTGATGGA | 300 |
| TCTNATGAGC AGANCGNTGA TTCGTCNGCC GCCGTNCTCC TTNGAGCCCN CNAGACA | 357 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

| | |
|---|-----|
| CTTGTAGATG GAGCGGGGAG NCAGACTNCT GGGNGCTGCG TGANTGCTGA CGTGAGATGG | 60 |
| ATTAATTAAT GGCNAGCAAG NATGGNGNCT NCGAGCCCCT CCCTGNNGCT NCCTNCCAGN | 120 |
| NGTGGCAATN GCGTACGTGG NCAGACTTCA GGNAGAAAAA AAAAAAANGG GNCNCGTAAG | 180 |
| CTGCTGCGGG NNCAGCAGCT TGAGACTGNC AAGTGACTCA GATGCAGAGT CAGACTNTCC | 240 |
| GGCTAGCTCT AACAACTCCN CCGTCTCCAA CACCAGCACC GAGGGCTTCG GGGACATCAT | 300 |
| GTCTTTGACC AGCAGCCTCT ATCGGAACCA CAGTACCAGC TTCAGTCTTT CAAACCTCAC | 360 |
| ACTNCCGTCG NCGGCCTCNT TGGCCTTTNG AGGCGA | 396 |

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | |
|--|----|
| GTCGACCCCA GATGAAATGT CATGGCAAAT TTGATAAAAA CCAAGAGGGA GTGAACTGA | 60 |
|--|----|

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGCTGGGGGA | GGGAAGGGTC | AAGTCGAGGG | AAGGTGAAAC | CAAAGGCAC | TGAGCATGCG | 120 |
| TGGTGGGGCA | GGGAAGGACA | CCATCACTCC | AGAGACAGTA | TGGTAACAAA | GGGACAGGAA | 180 |
| TGGTCCAGGC | CAGCTTCAGG | CTCTTCAGAA | GCCAGAGAGA | TGTCCAAGTC | TACCAAACCG | 240 |
| AGTTCTCCAA | GGCTTTTCAA | GAAATGGGAT | TTGCTTGCAA | GATGAATGAG | GGAGGAGGTC | 300 |
| CCATGGCTTC | TAAGAGATCA | ACCCAAGTCT | TCCAATACTC | ACTGCTAAGT | CCCACCTGGG | 360 |
| TCCCCAGAG | CCAGGAAGCT | CCCTGGTGGC | AGGTCCCCCT | CTTGCCCTCA | CGGCTCTTT | 420 |
| GGCCCTCGAG | ACA | | | | | 433 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS: --

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGCACAAA | TAGTTCTGTT | AAAGAATACC | GAATGGAAGT | TCCATCTTCG | TTTTCAGAAG | 60 |
| ACATGTCAA | TATCAGGTCA | CAGCATGCAG | AAGAACAGTC | CAACAATGGT | AGATATGACG | 120 |
| ATTGTAAAG | ATTTAAAGAC | CTCCACTGTT | CCAAGGATTC | TACCCTAGCT | GAGGAAGAAT | 180 |
| CTGGGTTCCC | TTCTACTTCT | ATCTCTGCAG | TTCTGTCTGA | CTTAGCTGAC | TTGAGAAGCT | 240 |
| GTGATGGCCA | AGCTTTGCCC | TCCCAGGACC | CTGAGGTTGC | TTTATCTCTC | AGTTGTGGCC | 300 |
| GTTCCAGAG | ACTCTTTAGT | CATATGCAGC | AACATGACAT | TTTAGATACC | CTGTGTAGGA | 360 |
| CCATTGAATC | TACAATCCAT | GTGTCACAA | GGATATCTGG | CAAAGGAAAC | CAAGCTGCTT | 420 |
| CTTGGTCAAC | GGCCTCTTTG | GCCCTCGAGA | CA | | | 452 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTNAAANTTA | CCATCACAGT | TNCTACAATC | GGCTCTTTCC | AATTGGCNA | CAACNCTGGG | 60 |
| TCATCAATGC | TCCTGAGAAG | ATCATAAAGG | AATTTATCAA | TAAAACTTTG | TCCGACAAGG | 120 |
| GAAATNCCCC | ACCCTCTGAG | GTGCTGCTCA | CGTCTCTCTG | GTCCTTGCT | GTGACCATAT | 180 |
| TTTCCGTCGG | GGGNATGATC | GGCTCCTTTT | CCGTCGGACT | CTTCGTCAAC | CGCTTTGGCA | 240 |
| GGCGCAANNC | AATGCTGATT | GTCAACCTGT | TGGCTGTCAC | TGGTGGCTGC | TTTATGGGAC | 300 |
| TGTGTAAAGT | AGCTAAGTCG | GTTGAAATGC | TGATCCTGGG | TCGCTTGTT | ATTGGCCTCT | 360 |
| TCTGCGGACT | CTGGTCGACG | GCCTCTTTGG | CCCTCGAGAC | A | | 401 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTTGAGAGCA | GCATGTTTTN | NCCACTGAAA | CTCATCCTGC | TGCCAGTGTT | ACTGGATTAT | 60 |
| TCCTTGGGCC | TGAATGACTT | GAATGTTTCC | CCGCCTGAGC | TAACAGTCCA | TGTGGGTGAT | 120 |
| TCAACTCTGA | TGGGATGTGT | TTTCCAGAGC | ACAGAAGACA | AATGTATATT | CAAGATAGAC | 180 |
| TGGACTCTGT | CACCAGGAGA | GCACGCCAAG | GACGAATATG | TGCTATACTA | TTACTCCAAT | 240 |
| CTCAGTGTGC | CTATTGGGCG | CTTCCAGAAC | CGCGTACACT | TGATGGGGGA | CATCTTATGC | 300 |
| AATGATGGCT | CTCTCCTGCT | CCAAGATGTG | CAAGAGGCTG | ACCAGGGAAC | CTATATCTGT | 360 |
| GAAATCCGCC | TCAAAGGGGA | GAGCCAGGTG | TTCAAGAAGG | CGGTGGTACC | GCATGTGCTT | 420 |
| CCAGAGGAGC | CCAAAGAGCT | CATGGTCCAT | GTGGGTGGAT | TGATTTCAGT | GGGATGTGTT | 480 |
| TTCCAGAGCA | CAGAAGTGAA | ACACGTGACC | AAGGTAGAAT | GGATATTTTC | GTCGACGGCC | 540 |
| TCTTTGGCCC | TCGAGACA | | | | | 558 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGGAGAAAA | TTGCTGCTGA | GAAGGACATT | TTGAAGGTTT | TGTGGCTGA | AAAAGCTGTT | 60 |
| TCTGGAATCA | CCCCTAGATC | TTTCTTGAAG | ACTTGAATTA | GATTACAGCG | ATGGGGACAC | 120 |
| AGAAGGTCAC | CCCAGCTCTG | ATATTTGCCA | TCACAGTTGC | TACAATCGGC | TCTTTCCAAT | 180 |
| TTGGCTACAA | CACTGGGGTC | ATCAATGCTC | CTGAGAAGAT | CATAAAGGAA | TTTATCAATA | 240 |
| AAACTTTGAC | GGACAAGGGA | AATGCCCCAC | CCTCTGAGGT | GCTGCTCACG | TCTCTCTGGT | 300 |
| CCTTGTCTGT | GGCCATATTT | TCCGTCGGGG | GTATGATCGG | CTCCTTTTCC | GTCGGACTCT | 360 |
| TCGTCAACCG | CTTTGGCAGG | CGCAANTCAA | TGCTGATTGT | CAACCTGTTG | GCTGTCACTG | 420 |
| GTGACTGCTT | TATGGGACTG | TGTAAAGTAG | CTAAGTCGGT | TGAAATGCTG | ATCCTGGGTC | 480 |
| GCTTGGTTAT | TGGCCTCTTC | TGCGGACTCT | GGTCGACGGC | CTCTTTGGCC | CTCGAGACA | 539 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTTGACCCCA | TTTTCCACCA | CCAAGCAAGC | AGAGCCTGTT | GTTTTGTCCA | AAATCAAAAC | 60 |
| TGCACATCCA | CAGAGCAGAG | ATCTCAAAGA | TTATGCGAGA | ATGTCAGGAA | GAAAGTTTCT | 120 |
| GGAAGAGAGC | TCTGCCTTTT | TCTCTTGTA | GCATGCTTGT | CACCCAGGGA | CTAGTCTACC | 180 |
| AAGGTTATTT | GGCAGCTAAT | TCTAGATTG | GACCATTGCC | CAAAGTTGCA | CTTGCTGGTC | 240 |
| TCTTGGGATT | TGGCCTTGGA | AAGGTATCAT | ACATAGGAGT | ATGCCAGAGT | AAATTCCATT | 300 |
| TTTTTGAAGA | TCAGCTCCGT | GGGGCTGGTT | TTGGTCCGTC | GACGGCCTCT | TTGGCCCTCG | 360 |
| AGACA | | | | | | 365 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

GTCGACCTCG GTAAATGCCT CAGTTCCCCT CCCAGATGGA GGCATCGTTG TGAGAGTCTG      60
ATTGGGAGGG GAATATGAAA ATGTTTTTCG AAGATAAAAG TACTACACAG ATGTGAGGTG      120
GTTTTGCCTT GGAAGAAAGT GCTCCTTAGA TGTGTCGGA TGTATGCAG AGTGATCGTG      180
GCGTGTCAAT CTTTCTTTTG GGTGTTTTGC AGCCTGAGAC ATAAGGTAAT TGTGAGAAAA      240
GGGAGACGTA GAAGTGTTGA TCTGTGGAAG CTCACTCTTA ACAAGAATTC TAAGATGCAC      300
ATTTAAGTAC TTGCCATGAC GTGAGGTGTT GTCACACGTC AACCCTGAGA TGCTGTCAGT      360
GTCCCAGGGG ACTTGACATT TATGTTACCC AGGAATGACT GTGTAAATGT GCAGGTGCAG      420
GCCGGGCGCC GTGGCTCAGT GCCTGTAATC CCAGCACTTT GGGAGCCCCG TCGACGGCCT      480
CTTTGGCCCT CGAGACA

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

GTAGACANCA NTAGAAAAAC AAAAATCTCA TAATGCAAAA GCATCAAGTG TTTGACTCTG      60
AGAAGCGCCT TGTATGCCCA GTTACTCTCG TTCTCCCTCA GCTCTTGCTT GTGCTTCTCC      120
ACCTGCCATT CCACTTTGGC CTGGTACTGC CTGTAGTCTT CCTGGCAGGC CCCAGTCCA      180
GTTCTTTGGA GCAGCTGGGC ATCCAAGAAG AGGTCATTGC TGTGGAAGGA GCCCTCTCGC      240
TCCCTCCCCA GCCTCTCAAT CACAGCCAGG AGCTCTGCCT GCTGCTGCCT CTGCTCCTCC      300
ACAGAGCCCC AGTTGTTGAA GGCACAGTAC CTTCTCTCAC ACTCCCGCGC CAGGTCTTTC      360
AGGCTGCACT TGTCCGTGTT TGCTACATAG TCATCCAGGG CCTGGCCCCG TCGACGGCCT      420
CTTTGGCCCT CGAGACA

```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

CCTGCNCNAA ANNANTCCAA GCNAANNCCC AAACAATCCC AATNCCNACC CCAAGCTNGG      60
GAGTTCGGCC CAAAAGAGGC CCNCGAACG TAGATTNCAG TGAGCCAAGA TCGTNCCACT      120
GCACNCCAAG CCNNGGCANC CAAGAGCGAA ACTCCGTNCN CNCNNANAA AGAGAAAATT      180
AGCCGGGCGT GGTGGCGTTA ATCCCANCTA CTTGTGAGGN TAAGGGAGGA GAATTGCTTG      240
AACCCAGGAG GCAGAGGTTG CAGTGAGCTG AGATCACGCC ATTGCACTCC AGCCTGGGCC      300
ACAAGAGCAA GACTCCATCT CCAAAAAAAG AAAAAAATAG CGTCAGAAAA ATGTCCTTGT      360
ATGCCATTTT CTCCATTTTA TTGACATTTT GCCCGACTTT TGTCTTTGTT TCAGGGAAAT      420
CGTGGAACAC ATGGTCCAGC ACTTTAAAC ACAGATCTTT GGGGATCGGA AGCCCGTGT      480
TGACGGCAGG GTCAACGGCC TCTTTGNCCC TCGAGACA

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

AAACCAAAAC TCATGTTGCT TGNCCCCCA TCGTCGTCTC AAGTGNGGGC GANNACTTTC      60
CTGGTTGGAG CCCTCCGTCC NAACNNCTAA CACAATGTTC TTTCNCAAAC GTTCTACNAA      120
CGCCTGCGAC NAGNCCAGGG AGGGGGTGCT GTGNATCCTC AGCNACGACA CGCTGCAGTA      180
CTGCGACTTC TTGGGCTCCG GGGCGGCCAT CTGGGTCACC ATNCTGTGNA TGGCACGGCT      240
CAAGACAGTC CTGAAATACG TGCTGTTTCT TCTGGGTACA CTGGTCATCT CCATGTCCTT      300
GCAGCTGGAC CGCAGGGGCA TGTGGAACAT NCTGGGGCCC TCCCTCTTTG CCTTCGTGAT      360
CATGGCCTCC ATGTGGGCTT ACCGCTGCGG GCACCGGCGC CAGTGCTACC CCACCTCGTG      420
GCAGCGCTGG GCCTTCTACC TCCTGCCCCG CGTCTCTACG GCCTCTTTGN CCCTCGAGAC      480
A                                                                                   481

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

GACCCTCCAN TAATAANCCT TTTGTTTCCC TCGTCNNTGT TNGTCCGTTT CCCTTTCTCN      60
CCCTGTTTTC NNNTNCCTGC ACCAATATTT CCAANCTAAT ACCCAAGCAA NACAATCCNA      120
ACTCCAAGCT CGGGAATTCG GCCCAAAGAG ACCGTAGGCC GAAACCCACC GGANGGAACC      180
ATCTCACTGT GTGTAAACAT GACTNCCAAG CTGNCCGTGG CTCTCTTGGC AGCCTTCCTG      240
ATTCTGCAG CTCTGTGTGA AGGTGCAGTT TTNCCAAGGA GTGCTAAAGA ACTTAGATGT      300
CAGTGCATAA AGACATACTC CAAACCTTTC CACCCCAAAT TTATCAAAGA ACTGAGAGTG      360
ATTGAGAGTG GACCACACTG CGCCAACACA GAAATTATTG TAAAGCTTTC TGATGGAAGA      420
GAGCTCTGTC TGGACCCCAA GGAAGAACTGG GTGCAGAGGG TTGTGGAGAA GTTTNTGAAG      480
AGGGCGTCCA CGGCCTCTTT GGCCCTCGAG ACA                                     513

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

CAANTAATAA ANCTTTTGTT TCCCTCGNCA TTGTNNTCGT TCCCCTGTCC NGCCTTGTTT      60
CCNNNGTCTT GCACCAATAT TTCCAACCN AATACCCAAG CATACAATCC NNACTCCAAG      120
CTNGGAATTC GCCCANAGAG ACCGTGNGG GAAGAANTTG NCTGGAACT TGTTTCATGGT      180

```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GATATATACC | GTCCTCCAAG | AAANGGGATG | CTGCTATCAG | TCTTTCTAGG | AGCCGGGANA | 240 |
| CAGATATTAA | TTATGACCTT | TGTGACTCTA | TTTTTCGCTT | GCCTGGGAGT | TTTGTCACCT | 300 |
| CCCANCCGAG | GAGCGCTGAT | GACGTGTGCT | GTGGTCCTGT | GGGTGCTGCT | GGGCACCCCT | 360 |
| GCAGGCTATG | TTNCTGCCAG | ATTCTATAAG | TCCTTTGGAG | GTGAGAAGTG | GAAAACAAAT | 420 |
| GTTTTATTAA | CATCATTTCT | TTGTCTGGG | ATTGTATTG | CTGACTTCTT | TATAATGAAT | 480 |
| CTGATCCTCT | GGTCAACGGC | CTCTTTGGCC | CTCGAGACA | | | 519 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGGCCCAAA | GACANGCANN | CCNACAAGAT | GTCGTTGTTT | CAAGAAGCTG | ATNGAGGGGT | 60 |
| ATCTCGGAAG | CACACGGAAA | CTTTTCCTT | CCTTCAATTC | NACGCACACT | AACTCTCTAA | 120 |
| TGAGCAANCG | GTATACGGCC | TTCCTTCCAG | TTACTTGNAT | GTGAAATAAA | AAAAAGTTTG | 180 |
| CTGTCTTGCT | ATCAAGTATA | AATAGACCTN | CAATTATTAA | TCTTTTGTTT | CCTCGTCATT | 240 |
| GTCTCGTTC | CCTTCTTCC | TTGTTTCTTT | TTCTGCACAA | TATNTCAAGC | TATACCAAGC | 300 |
| ATACAATCAA | CTCCAAGCTC | GGAATTCGGC | CNAAGAGGCC | GTCGACCGTT | CGTTATCGGA | 360 |
| ATTAACCAGA | CAAATCGCTC | CACCAACTAA | GAGCGNCCAT | GCACCACCAC | CCACGGAATC | 420 |
| GAGAAAGAGC | TATCAATCTG | TTGAAGAACA | TGCCCGGCTT | CTTGTCATC | ATCATGGTGT | 480 |
| ACACGNCCTC | TTGNCCCTC | GAGACA | | | | 506 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|-----|
| TTCTTGTTT | CCTTTTCCT | NCCCCAATAT | TTCCAAGCTA | ATACCCAAGC | AATACAATCC | 60 |
| NACTCCAANC | TCGGGAATTC | GGCCCCACAGA | GACCGNTGAC | CNTGTAAATG | AGTGAGGCAG | 120 |
| GAGTCCCGNG | GAGGTTAGTT | GTGTCAATAA | AAATGATTAA | GGATACTAGT | ATAAGAGATC | 180 |
| AGGNTCGTCC | TNTAGTGTG | TGTATGGNTA | TCATTTGTTT | TGAGGNTAGT | TTGATTAGTC | 240 |
| ATTGTTGGGT | GGTGATTAGT | CGGTTGTTGA | TGAGATATNT | GGAGGTGGGG | ATCAATAGAG | 300 |
| GGGGANATAG | AATGATCAGT | ACTCCGNCAG | GTAGGCCTAG | GATTGTGGGG | GCAATGAATG | 360 |
| AAGCGAACAG | ATTTTCGTTT | ATTTTGGTTC | TCAGGGTTTG | TTATAATTTT | TTATTTTAT | 420 |
| GGNCTTTGGT | GAGGGAGGTA | GGTGGTAGTT | TGTGTTTAAAT | ACAAAAAGTT | GGGTCGACGN | 480 |
| CCTCTTTGNC | CCTCGAGACA | | | | | 500 |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACCGGATTG | GGNCCNAAAG | AGACCGGTTG | CCCAAACTT | TCTGCTGAGA | AGGACATTTT | 60 |
| GGAGGGGNTT | TGTTGGGCTG | AAAAAAGCT | GTTTCCTGGG | AATNNAACCC | CCNAGANCTT | 120 |
| TCTTGAAGAC | NTTGAATTAA | GATTACCAAN | CGATGGGGGA | CACAGGAAGG | TCCACCCCCA | 180 |
| NGCTCTGATA | TNTGCCATCA | CAGTTGCTAC | AATCAGCTCT | TTCCAATTG | GCTACCAACA | 240 |
| CTGGGGTCAT | CAATGCTCCT | GAGAAGATCA | TAAAGGAAT | TATCAATAAA | ACTTTGACGG | 300 |
| ACAAGGGAAA | TGCCCCACCC | TCTGAGGTGC | TGCTCACGTC | TCTCTGGTCC | TTGTCTGTGG | 360 |
| CCATATNTTC | CGTCGGGGGN | ATGATCGGCT | CCTTTTCCGT | CGGACTCTTC | GTCAACCGCT | 420 |
| TTGGCAGGCG | CAATTCAATG | CTGATTGTCA | ACCTGTTGGC | TGTCACTGGT | GGCTGCTTTA | 480 |
| TGGGACTGTG | TAAAGTAGCT | AAGTCGGTTG | AAATGCTGAT | CCTGGGTCCG | TTGGTTATTG | 540 |
| ACCTCTTCTG | CGGGTCGACG | ACCTCTTTGG | CCCTCGAGAC | A | | 581 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCAACCTGG | GAGGCTCTCC | CCCACCTTCT | TTCAATCTCT | TCTCAAATC | TGCATCCTCA | 60 |
| GAGGGGCTT | GCCTGATTGG | CCTTCTTAAA | ATGGATCTGC | CCCACCCAC | TTTGTACTTG | 120 |
| CTGTGCCCTC | TGCTTTCAGG | CGTGTCTCA | AACAGGATCT | CAACAAGGCC | TCCCCTGACC | 180 |
| ACACTTTAAA | ACTGCATGCC | CTATATATAC | CCCATCTCTC | TTATTTTAT | TTGTCTCCCT | 240 |
| AATGCTTATC | CCCAGTATAC | TCTGTTTATT | GTCTGTCTCT | CCTCACTACA | AAATAAACTC | 300 |
| CCCAAGGCTT | AGAGTTTTTT | CTGTCTTGTC | CCTGCTATAT | ACCAGTGCTT | AGAACAGCGC | 360 |
| CCTGCACAGA | ATAGAGGCC | AATTCAATAT | GGATTGCTA | CCACTACATC | CTATTTGTTT | 420 |
| CCTTCCCATC | ACTTTTCGAA | CACTCATCTA | TTCAGCTCTG | CTGACCTGTT | TCACATCTGG | 480 |
| ATCCTGTATA | GCAACGTGCA | CGGCCTCTTT | GGCCCTCGAG | ACA | | 523 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTNGACTGAT | ACTCGAGTAC | CTGGATCAGC | GGCTGAAAGC | TGCAGAGAAC | AAGTTTGCCA | 60 |
| AGTGCCTCAT | GACCTGTCTC | AAATGCTGCT | TCTGGTGCCT | GGAGAAGTTC | ATCAAATTCC | 120 |
| TTAATAGGAA | TGCCTACATC | ATGATTGCCA | TCTACGGCAC | CAATTTCTGC | ACCTCGGCCA | 180 |
| GGAATGCCTT | CTTCCTGCTC | ATGAGAAACA | TCATCAGAGT | GGCTGTCCTG | GATAAAGTTA | 240 |
| CTGACTTCTT | CTTCCTGTTG | GGCAAATTC | TGATCGTTGG | TAGTGTGGGG | ATCCTGGCTT | 300 |
| TCTTCTTCTT | CACCCACCGT | ATCAGGATCG | TGCAGGATAC | AGCACCACCC | CTCAATTATT | 360 |
| ACTGGGTTCC | TATACTGACG | GTGATCGTTG | GCTCTACTT | GATTGCGTCG | ACGGCCTCTT | 420 |
| TGGCCCTCGA | GACA | | | | | 434 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
GAGGCCCTC AANTTCTGCC ATTTTATTTT ATTTTGTGA NCTGGAGTNT TGCTCTGTAT      60
CCCAGGCTGG AGTGCAGTGG CGCAATCTCG GCTCACTGCA AGNTCCTCCT CCCGGGTCA      120
CGCACATTCT CCTGCTTCAG CCTCCCTAGT AGCTGGGACT ACAGGAGCCC GCCACCACGN      180
CTTGTTAATT TTTTTGTAT TTTAGTAGA GACAGGNTTT CACTNTNTTA GTCAGGATGG      240
TCTCATTNTT CTGANGTCAT GATCCGCCCA CCTCGGCCTC CCAAAGTGCT GGGAKTACAG      300
GMGCGARCCA CCGCGCCCGG CCTATTTTTT GKGGGTTTNA WWTCTGGGTG ACTTGTGAGC      360
AGGAAGTTTT TGTTKTTTTT TTTCCANTGA AAAGATCTGG CCANAATAGT GGGNNTGTCA      420
AAGTATCTCT TTGCAGNTTT AATTTGCATT TTCCANTGA CTAAGATGAT GTTGTGCAAT      480
TTTTTCAGAN ACTGTNTGCT ATCTGTATAT CATCTCTTTT TTTTTTTTC TTTTGAAGT      540
GGATCCGGTN CGNCCTCTTT GCCCTCGAG ACA                               573
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
GAANCCCCAT CCACTTCNCG GGAGGGGGGA GAGCGCGGNG ACGGGTCTCG CTCCCTCGGC      60
CCCGGGATTC GGCGGGTGCA GNTGCCGAT CCTTCAGCGT CTGNATCTCG GCGTCGCCCC      120
GCGTACCGTC GCCCGGCTCT CCGCCGCTCT CCCGGGGTT CGGGGCACTT GGGTCCACA      180
GTCTGGTCCT GCTTCACCTT CCCCTGACCT GAGTAGTCRC CATGGCACAG GTTCTCAGAG      240
GCACTGTGAC TGACTTCCCT GGATTTGATG AGCGGGCTGA TGCAGAACT CTTCGGAAGG      300
CTATGAAAGG CTGGGCACA GATGAGGAGA GCATCCTGAC TCTGTTGACA TCCCGAAGTA      360
ATGCTCAGCG CCAGGAAATC TCTGCAGCTT TTAAGACTCT GTTTGKCAGG GATCTTCTGG      420
ATGACCTGCG GAAGTGGATC CGGTTGGGCC TCTTTGGCCC TCGAGACA                468
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
GAACCGGATC CACTTCCGGG AAAACCTCGG ATTAGCAAGC AATAAAAACA TGACCTCACT      60
CTTCTCAAA GGAGCCCCTG GTCTCCCTG TGTGACTCAG TTCTTTCCAT CTGTTTGTC      120
CGCTGAAGC CTCTTCTGC GCTGACTGTG ACATCGGAAC GTGGCCTTCC TGTACCCCC      180
TCCGTGCCAC GCACTGAAGG CCACCCCCC CCACCTGGGA AACTAAGAAC TGGATATTT      240
GCCTCATTCA CTTGTACTGT AACAAATGTAT ATAATTGGT TGGTATTTCA CTATTTAATT      300
TTTAAAGAAGC CTATTTTACT AGTGTTTTAT ATGAACAAAG TACTGCAGAA GTTAAACCTG      360
```

TGTTGTATTT TTTCTGAGAT GTTTTCCTTT AAGAGATACT TTTTGCTCAG TTTTATATG 420
CCAGGAAGTG GATCCGGTTC GGCCTCTTTG GCCCTCGAGA CA 462

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCCCGATNC ACTTCCGTGG NAAGAGCCTG CAATCCCNCC TACTCAGGAG GCTGAGGCAG 60
GAGAATCGCC CGAACCCGAA AGGTGGAGGT TGCAGTGAGC TGAGAATGTG CCACCGCACT 120
CCAGCCTGGG TGACAGGGCG AGACTCTCTC AAAGTAAATA AATTAAAAAA ATTTAANAAG 180
ATCATCAAAG AACAAACGAA ATTTTGTTAT TTCAGTAAGT CAATTTAAAC AATAGAAGCC 240
AATTCTACCA CCAGAGGARC RMMATAAAAT CTCATTATTA ATTGAGGGTG GCTTCTCTMC 300
CAGGTGRRAA ATTCTATAGR CAGGTATTTT GKTTACTACT GACAGGTAAT AAGATTGTTT 360
CTWAGGTAAA GGTAAACCCA GCAACACAAC ATTCTTCACT TTTGTTTAAT GAACCTCNAN 420
ATTCATCATA TTACTTNTAT TTGCTAGCAT GCTTTTGTG GAAGTGGATC CGGTCGGCC 480
TCTTTGGCCC TCGAGACA 498

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CGASCCGGAT CCACTTCCCC CTTACGTATC ATTTGTCACA CAGGCCTCAG CCTGAAAAAA 60
AATTCCAGTT TTTGTGTATT GCAGTTCCCG TATGCTATTG TCAACCAACA GTTCCCGTGA 120
TCCTTGAGT CTAATGAGTT TGGATGCATC TATGTTCCCTA CTGGATCCAC TGTCCTGTCT 180
CGGCAGCTCT TCCTCACTGC TGCTACTCTT TTCTGGACAC TCCTTTTTTT CCATTGTGCA 240
AATGTGGTAT TTATGTCTTT ACTGTATCTT TTTTACCCAT GTGAGTTTCA GGAGCCCCAG 300
GGTGCAGGAA GGAGGAGCGG AGGCTTGTTG CTTGGACACT GCCAGGCTGC TCTGTGTCT 360
GTTCTCTTG GRAAGTGGAT CCGGTTCCGC CTCTTGGCC CTCGAGACA 409

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAACCGGATC CACTTCCGAA GAGAAGGTCA GAGCGCACTG CAGGCAGCGC GGCTCTGGGA 60
AGAACTTCAC GGAGCCCCCTT CTTAGAGCAG GGAGGGGGCT TTCTCAGTGA AATGTTTGGT 120

| | |
|---|-----|
| TTTCTGCTGC CTCCTCTGCC CCAGGCCCCC CTCGAGGGTA CTGCCTATCC CAGATAGGTC | 180 |
| AGTGCACCAG GGACCCGGCC GCCAGCACCG CCGACCCCTC CCAGAGTGAC GCCCTTGTTT | 240 |
| ACTGACAAAG AGACCTGTCC CAGGAGTGTC CTCACCCGAG CCGGTCAGCT GTGGGTGGTT | 300 |
| TTCCTGTTAC GACGCTCAGT AGCCTGTAGC AATAACAAAC TCGTGGCTAT GAATGCAGAT | 360 |
| GCAGTGTCT CATAGAATAA CTGTTCTGTC ACTTTTACAG ACAAATCTAC GACAAAAAAA | 420 |
| AAGATCAACT TTTTTTTTCC GAACAACAAA AAAAATGAAT GATTACAATA GGAAAGGGAA | 480 |
| AAATTAAATA GCTACATATC ATTAACAAAT TAATGTTCTT CAAAAATAC CTACAAATTT | 540 |
| CTCTGTACAT TCTTTACGCA CAGCGTAACG ATGGAAGTGG ATCCGGTTCG GCCTCTTTGG | 600 |
| CCCTCGAGAC A | 611 |

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | |
|--|-----|
| GAACCGGATN CACTTCCCCT CCACGTAGTT GGNAGGGGAA CCAGCCAACC CGGCCATAGA | 60 |
| TCTCCCCTCG CCACCAGCCT TGGTGTCCTT TCTTGTTAAG GATCTTGATG ATGTCACCCCT | 120 |
| CCTTGAGCGA CAGCTCTGAT CGGTCTCGGG CGCAGAAGTC ATAGCGGGCT TTGGGTGTGC | 180 |
| CAAAATACTT TGTGCTTCCC ACTGNTGGNC TGCTGATGGT TCTCTTTTCA NGCTCCTTGA | 240 |
| AGGGGAACTG CAANGTGGTG TCCAGAGACT TGAAGCAATC CNTTAGAGAG TTCTGNTGGT | 300 |
| AAAACCTCAC CAGNTCCGTA AGCCCCCNGA AAGNCTTTTT CTCTGTGATC CGGTACAGAA | 360 |
| CCTTCTTCTG TCA | 373 |

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | |
|---|-----|
| GTTGACCGCC CACGATGATC TTGCCGCCAC GCTTGCTGGT CTTCTCCACT GACAAGGCAG | 60 |
| TGCTCAGGCC CTGCTCATGC TTCCCAGAC CCTGGCCCTC CCGGAAGCCG NACTTCTGCA | 120 |
| TGATCTTGTG CGCCACCGTG CCCCCATGT TAGCGAGGAA GGAGTTGCTA GGTCCGGTTG | 180 |
| GAGATCTCGG TCTGTCTTGT TCCTCGTACA CTGGGGGAGG AATGGCTGCT TTGGAAGACT | 240 |
| GTGATCGAGG TCTTGAGTCC TCTTCATAAG GAAAATCTCG GGGTAACTCT TTGTCTTTCT | 300 |
| CTACCAGAGA AGTGGGTGGG GCAATGGCAG CTCCGCCCAT ACTTCTCTTC CTCCTCTCTC | 360 |
| GCTCATAATC TTCATCTTCA TCAGAATCTG GATCTGGTCT CCTTGCAAAC CCACTTGCTT | 420 |
| CATGTCTGTC TTTACGCCCTT TTTCCCTTT CTTCTATTTC CGTCGACGGC CTCTTTGGCC | 480 |
| CTCGAGACA | 489 |

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GACGACTTTG | TGGGTATTAA | TTTTTGTTTA | AGTTTAAAT | AAAAGTAAAG | ATTCATTTTG | 60 |
| GATATCAGTT | GAAACCCCTT | AGTAACTCAG | TTTCTGTTAT | TCTTGTCTC | ATTCCTTTA | 120 |
| AATACACTTG | TTCTTGGCTT | TGCCATTTT | GATTCTGTGA | AGTAGGCAGG | AGCAGGGATT | 180 |
| AATTTATACA | GTATTCCTGT | TCTGAACAAA | ACCAGAAAAG | TCACTGTATA | AACTTGACTT | 240 |
| AAAATAGTAT | CTTTCTCTTY | TCATGTATTT | TCATTTGGGG | GAAAAAAAT | CTCTTTAATT | 300 |
| GTAACCTGAA | TTCAAGCTGT | ACCCCTCCAT | GGTCCTACAC | TCTAGAGCTA | ATCTGGTTGG | 360 |
| GCAGAAAGGC | AGAAGGATGG | TATATTGTCC | CATTGTGCCT | ATAATGTATT | TTAAATTGGT | 420 |
| CATTCCACCT | TACCTAATGG | AAATCTTGC | AGCTTTCCTA | GTGCTCATCA | GCGGTTTTAG | 480 |
| GAATTCATA | ACGTCGACGG | CCTCTTGGC | CCTCGAGACA | | | 520 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTTGACGGCG | TGGTGGCGGG | TGCCTGTAAT | TCCAGCTACT | CAGGAGGCTG | AGGAAGGAGA | 60 |
| ATCATTTGAA | CCTGGGAAGT | GGGGTTGCA | GTGAGCCAAA | ATCGTGCCAT | TGCACTCCAG | 120 |
| CCTGGGCAAC | AAGAGTGAAA | CTCCATCTCA | GAAAAAATAA | AAAAAATAAG | | 180 |
| GAAGGAACCG | GTGGGGCAAG | CAGAGTTAAG | ATGCTTTGCT | AAGTTAAAAA | GTCTACTAAC | 240 |
| TACCAAATCT | TGCTGTGGYT | TATCCAGAGC | TCTCAAAATG | CTGCCAATCT | ATTTTAAAGA | 300 |
| AGACCTAAAT | CCTCATTTTG | GCTTTTAGGA | CACTAGGATT | TGCCTTCAAC | CCATGTCTCC | 360 |
| AGTCATATAT | TTTCTTACTA | TTCTTCAAAC | ATACCTTTTT | CTCTTTTCTT | CACTCTTCAT | 420 |
| TATGCTGTTT | AAATCGTCGA | CGGCCTCTTT | GGCCCTCGAG | ACA | | 463 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GTACAAGAAG | TGGTCCATTC | CTTTGTCTGA | AGGAGCGACA | GGAGCATCTA | CGGTTGAGAA | 60 |
| GACAGAAAGT | TTGGCTTCGT | CGATGTCTTG | CTGTGTGAAT | TTTCCAGACT | TAGCCCAGTC | 120 |
| GACAGCCTTC | CCAAAAGACT | GGAGCCTCTC | TATTGTATTT | GGGTCCCTGT | AAGAGTAAAC | 180 |
| GGTGAAAATC | CCATTGTGGC | TGAGTTTTGC | GCCTCCACCA | TAAGCACC GC | CTTTTCTCG | 240 |
| AATTTCTGTA | TGCAAGAATT | TGGCAGTCAT | CAAACGTGCA | AGGATTTTAA | GACTGGCATG | 300 |
| ATCTGGGTCC | GTGTAGGGGA | CAGTTCGGAT | GCATTACCC | ACGTTATTCA | CCGGGAAGGG | 360 |
| CATCAGGAAG | TGACTCTTCA | TCTGCCAGGG | CTTGAAGGTG | GGTTCCATGA | CCAGCTTCCT | 420 |
| AATGACCTGG | GAGCCATGGG | GAACGTGGGC | ATCTCCACCA | GAGCTGCTGG | GCACAGGTTT | 480 |
| CTCGACCGTG | TGTGGGCGCA | CAGGCCGTGC | ACGGCCTCTT | TGGCCCTCGA | GACA | 534 |

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

GTCGACCAGG ACTAGATTCT GTCTCTCCAA AGTGGCCCAA GCCCTGTTCT CTGTACTAGG      60
GAAGCCAGCT GTGTCTTTTC GAGGACAGTT GGTCCAGCCA GCAGGCTCAG TTCAGATACC      120
AGACAACCAT TCCAGCACGA GGGCTCAGCG CCCTGGCCCC GCGGCTCGCT CCAGTGCCTG      180
TGTGCCCACC AGCACATCCA TGAGGTAGTC CAATTTCGCC TCGTCCAGCT CCGGAGCTTC      240
CTCCTTGGCC GGCCATCCT CAGGGCCTGG TTTGAGGCCC TCAGAGGCTG GTGCCCAAAG      300
TTCATTGTCA TACATAGAGG TGTCATATC CTCAAACAGG CCCTCAAGCC CATCGTCCAG      360
TAGACAGCCA GTGGCTGGGC CCAGCAGGTC CAAGGCACCC AGGCTGGGCG CTGCTCCCCC      420
GATGCTACGG CCTCTTTGGC CCTCGAGACA                                     450
  
```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

GTCGACGGCG GYCATGGCAA AGCAGTACGA CTCGGTGGAG TGCCCCTTTT TTGTGATGAA      60
GTYTCCAAA ATACGAAGAA GCTCGCCAAG ATCGGCCAAG GCACCTTCGG GGAGGTGTTC      120
AAGGCCAGGC ACCGCAAGAC CGGCCAGAAG GTGGCTCTGA AGAAGGTGCT GATGGAAAAC      180
GAGAAGGAGG GGTTCCCAT TACASCCTTG CGGGAGATCA GGATCCTTCA GCTTCTAAAA      240
CACGAGAATG TGGTCAACTT GATTGAGATT TGTCGGAACC AAAGCTTCCC CTTTATAACC      300
GCTGCAAGGG TAGTATWTTA CCTGGTGTTC GACTTCTGCG AGCATGACCT TGCTGGGCTG      360
TTGAGCAATG TTTTGGTCAA GTTCACGCTG TCTGAGATNC AAGAGGGTGA TGCAGATGCT      420
GCTTAACGGC CTCTTTGGCC CTCGAGACA                                     449
  
```

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

GTCGACAAAA CATGGAGTTG TTCCTTTGGC CACATATATG CGAATCTATA AGAAAGGTGA      60
TATTGTAGAC ATCAAGGGAA TGGGTACTGT TCAAAAAGGA ATGCCCCACA AGTGTTACCA      120
TGGCAAAACT GGAAGAGTCT ACAATGTTAC CCAGCATGCT GTTGGCATTG TTGTAAACAA      180
ACAAGTTAAG GGCAAGATTG TTGCCAAGAG AATTAATGTG CGTATTGAGC ACATTAAGCA      240
CTCTAAGAGC CGAGATAGCT TCCTGAAACG TGTGAAGGAA AATGATCAGA AAAAGAAAGA      300
AGCCAAAGAG AAAGGTACCT GGGTTCAACT AAAGCGCCAG CCTGCTCCAC CCAGAGAAGC      360
ACACTTTGTG AGAACCAATG GGAAGGAGCC TGAGCTGCTG GAACCTATTC CCTATGAATT      420
  
```

CATGGCACAA TAGGTGTTAA AAAAAAAAAA TAAAGGACCT CTGGGGTCAA CGGCCTCTTT 480
GGCCCTCGAG ACA 493

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTCGACGAGG GGGTCATGGY AGGCAGGGGC AGGTGCGTCA GAGATGGAGC GCAGGTCCTG 60
 CATGGAGAAG CTCGCGAGCC TGCCGGCCAG CGCCCCCTGA CTCTTGGTGG CAGCCTGCAC 120
 AGCAGCGGAG GCGGCAATGT TGAGGCCCCG CTTCCCGAAG CTGAGCACGG TCTCGTAGCT 180
 GCGCTCCTTG GCCTGCACGA TGTACGCGTC GATCTCCTTC TCATGGCGGG ACAGGGACGG 240
 GTGGACAAAC TTGCGGTAAA GCAGGCTGGC GCCCTTGGTG TAGGGTGAGA GCAGCCACAG 300
 CACGAAGGCC ATCTTGATCT CATAGTAGAA AGGGAACCAG GAGATAAAAA TGTCTGTAAC 360
 GATCTCTGCT GCCATGAAGA GTGCARCAA CTATCCAGTA CATCATCCAG TGGACGGCCT 420
 CTTTGGCCCT CGAGACA 437

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTCNACCGCC CTTCTTGTCT CCTCCTCAGT NGTACACCTG TGTGGTCTCC ACCACCTCAG 60
 ACTTNCTCCG CCCCTTTCAG TNGGAAGAAG GNGCAGGCCC GTCTCGGGGT CCTCCACGCA 120
 CCGNTCCAGA AGTTGCCTGT ACGTGAGGTT CTCATGCGTG TTGGGGTNAA AGAAGCCCTT 180
 GGTGTCGTCG CTGGGGTCCG CCGGGACGCG GKTCACTCTC TCACTGAAGT AGCCCCGCTG 240
 GTAGRSCAG TCCACAGACA CGCGGTGGTT GTGYACGGGG TCGATGATRC CGCCCCGTGGC 300
 GATCTGGGCC TCCAGNAGGN GGATNCCGTG CTGCNNGAGA ACCAGNCCCT TCTNNATGTC 360
 CTGGAAGAGN GAGATGGTCC CCCCCGAGTA GGGGTCTCTG TANCCGGTGA CGNCCTTCTC 420
 GACAGACAGC ATCTGCTCGT GAAGCTCGGG GCCCACCACG CCCGCCTTCA CGGCCTCTTT 480
 GGCCCTCGAG ACA 493

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGACCCAC GTTAGTACGG TTGGATAGGA TATGCTCTCA TGGTAACGCG TCCAAGTTGG 60

| | |
|--|-----|
| AATGGTCTTC CAGTCTCCAT GGNATCCACA TGCTACTGGC GTTAGTTCCA GATCTTGAGG | 120 |
| AAGNTATCCC AGGACCCTGT CGCCACAGGC ATGNCATCGT CANTCACGCC CAGGCAGCTG | 180 |
| ACGCGGTTGT CATGNCCAGN CAAGACAAC TCCCGGTCGG GTTTGNGTGC ATCCAGACG | 240 |
| TTGCAGTTGA AGTCGTCGTA CCCAGCAAGG AGGAGGSGSC CGCTCTTGGW GAAGGAGACA | 300 |
| GAGKTGATCC CCCAGATGAT GTTGTCTATG GAGTAAGTCA TGAGCTCCYG GTCAGCACGA | 360 |
| AGGTCAAACA GCCTGCNGGT GCGTCGTCT GAGCCAGTGC CAAATGCATT GCCATTTGGA | 420 |
| AAGAANCAAA TGNCAATTGAT GTCAGACTCG TGCCCACTGA AGGTCTNCCG GCACATGCCT | 480 |
| TCTCGCATAT CCCAGAGTTT GTCTGAAGCA TCACAAGCAC CAGAGACGAA CAGTCTGGTG | 540 |
| TCAGTCGACG GCCTCTTTGG CCCTCGAGAC A | 571 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | |
|---|-----|
| GTCCAGGTAC CACCAGCAAC CATCAATCCC GTCTCCTCCT GCCTCCTCTC CTGCAATCCA | 60 |
| CCCCGCCACG ACTATCGCCA TGGCAGCCCT GATCGCAGAG AACTTCCGCT TCCTGTCACT | 120 |
| TTTCTTCAAG AGCAAGGATG TGATGATTTT CAACGGCCTG GTGGCACTGG GCACGGTGGG | 180 |
| CAGCCAGGAG CTGTTCTCTG TGGTGGCCTT CCACTGCCCTT TGCTCGCCGG CCCGGAATA | 240 |
| CCTGTACGGG CTGGCGGCCA TCGGCGTGCC CGCCCTGGTG CTCTTCATCA TTGGCATCAT | 300 |
| CCTCAACAAC CACACCTGGA ACCTCGTGCC CGAGTGCCAG CACCGGAGGA CCAAGAACTG | 360 |
| CTCCGCCGCC CCCACCTTCC TCCTTCTAAG CTCCATCCTG GGACGTGCGG CTGTGGCCCC | 420 |
| TGTACCTGG TCTGTCTCT CCCTGCTGCG TGGTGAGGCT TATGTCTGTG CTCTCAGTGA | 480 |
| GTTGCTGGAC CCTTCCTCAC TCACGGCCTC TTTGCCCTC GAGACA | 526 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | |
|---|-----|
| GTTGACTTTG TGGGTATTAA TTTTGTGTTA AGTTTAAAT AAAAGTAAAG ATTCATTTTG | 60 |
| GATATCAGTT GAAACCCCTT AGTAACTCAG TTTCTGTTAT TCTTGTTCTC ATTTCTTTA | 120 |
| AATACACTTG TTCTTGGCTT TTGCCATTTT GATTCTGTGA AGTAGGCAGG AGCAGGGATT | 180 |
| AATTTATACA GTATTCTGT TCTGAACAAA ACCAGAAAAG TCACTGTATA AACTTGACTT | 240 |
| AAAATAGTAT CTTTCTCTTT TCATGTATTT TCATTTGGGG GAAAAAAAT CTCTTTAATT | 300 |
| GTAACCTGAA TTCAAGCTGT ACCCTCCAT GGTCTACAC TCTAGAGCTA ATCTGGTTGG | 360 |
| GCAGAAAGGC AGAAGGATGG TATATTGTCC CATTGTGCCT ATAATGTATT TTAAATTGGT | 420 |
| CATTCACCT TACCTAATGG AAATTCTTGC AGCTTTCCTA GTGCTCATCA GCGGTTTTAG | 480 |
| GAATTCATA ACGTCGACGG CCTCTTTGGC CCTCGAGACA | 520 |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCG | TTGACGGGGC | TGGAGGAGGA | AGAAGAGGTG | GATCCCCCGA | 60 |
| TCCAGGGAGA | ACTGGAGAAG | TTAAATCAGT | CCACGGATGA | TATCAACAGA | CGGGAGACTG | 120 |
| AACTTGAGGA | TGCTCGTCAG | AAGTTCCGCT | CTGTTCTGGT | TGAAGCAACG | GTGAAACTGG | 180 |
| ATGAACTGGT | GAAGAAAATT | GGCAAAGCTG | TGGAAGACTC | CAAGCCCTAC | TGGGATGCAC | 240 |
| GGAGGTGGC | GAGGCAGGCT | CAGCTGGAAG | CTCAGAAAGC | CACGCAGGAC | CTCCAGAGGG | 300 |
| CCACAGAGGT | GCTCCGCGCC | GCCAAGGAGA | CCATCTCCCT | GGCCGAGCAG | CGGCTGCTGG | 360 |
| AGGATGACAA | GCGGCAGTTC | GACTCCGCCT | GGCAGGAGAT | GCTGAATCTC | GCCACTCAGA | 420 |
| GGGTCATGGA | GGCGGAGCAG | ACCAAGACCA | GGAGCGAGCT | GGTGCATAAG | GAGGTCGACG | 480 |
| GCCTCTTTGG | CCCTCGAGAC | A | | | | 501 |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACCGTG | TCCAGAGCCC | ACCTCCCTCA | CACCCACACA | GCGCTTCCTA | AAGGCAGGGA | 60 |
| CAGGAGCTGG | CCTCCCTCGC | CTGCTGGCAT | GGGGCTGGAC | ACAGGAGGAA | GTGGCGTGGG | 120 |
| GGTGCTCTGA | GGGGAGTGAG | GCGGCAGGAT | AGCTTCCCCA | GCAGGTCTCT | GGCTCAGGTC | 180 |
| CAGGTATCTC | CTCCTCCCCA | TACCTCTGCC | TCTCGCCTCC | GCTCAGAAAA | GCAGGTGCCC | 240 |
| TTAAGAGCCA | TCTCCACCCC | CATGTAAACT | GCACACAGGA | AGGGAGAGGC | CACTCCGACT | 300 |
| GCTCTGAGGT | CCAGGTAGGA | TGGTTTCCCC | CAGTGTCTGG | GTGGGGAGCA | AGGAACTCCA | 360 |
| GGGGCGACCT | TGTGCCACCG | CATCACCTTC | CTGCTCAGGG | AAGGGGCCCC | TGCTGCCGCT | 420 |
| TGGAGGGTGC | CATGCCCAGA | GCCTCTGCCC | CTAGCCTCAG | CCTCGCCTAC | TCACTGGGGG | 480 |
| CTCCAGCACC | CCCGGCCGTC | AACGGCCTCT | TTGGCCCTCG | AGACA | | 525 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACGCGA | GTGGAGACCT | GTGGTAGAGA | AGCTCCTTTT | GATGTCCTAC | AGGCTTTCCA | 60 |
| CTGTGGTGTG | TCCAGTCATT | CAGAGCTCAT | CCCCTGAAGG | CCTCATCCCA | ATGGACACTG | 120 |
| ATTCAGAGTC | AGCAASCCGC | TTACAGATGA | TTCTGAATGA | GATTCANCCT | CGAGATACTA | 180 |
| ATGATTATTT | TAACCAAGCC | AAAATATTGA | AAGAACATGA | TAGCTTTGAT | ATGAAGGACT | 240 |
| TGAATGCTAG | TGTGGTGAAT | ATTGATACTT | CTACAGAAAT | CAAAGGTAAA | GAAGTAAAAA | 300 |
| CATGTGATGT | AACTGCCGAG | ATGGTGCTGG | TATGTTGTTG | GAGAAGTATG | AAGGAAGTTG | 360 |
| CTTTACTTTT | AGGCATGTTG | TGCCAGCTTC | TGCCCATGTC | AACGGCCTCT | TTGGCCCTCG | 420 |
| AGACA | | | | | | 425 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

GGGACGTAAT CAACCCAAGC TTATGACCCG CACTTACTGG GAANTCNTCG TTCATGGGGA      60
AGAANTGCAA TCCCCGATCC GCCATCACGA ATGGGGGGCA CCGGGTTANC CGCGCCTCCC      120
GGCGTAGGGT AGNCACACNC TGANNCAGTC AGTGATATCG CCGTGATCN CCGGACATCT      180
AAGGGCATCA CAGACCTGTT NTTGNTCAAT CTCGGGTGGN TGNNGGCCAC TTGTCNCTCT      240
AAGAANATGG GGGACGCCGC CCNCTCGGGG GTNGCGTAAC TAGNTAGNAT NCCAGAGTCT      300
CGTTCGTAT CGGAAGTAAC CAGACANATC GTCCCCCAN CTAAGANNGG CCATNCACCA      360
CCACCCACGG AATCGAGANA GAGCTATCAA TCTGTTGTTA GGACATGCCC GGCTTGCTTG      420
GTCATCATCT TGGTGACNC GACCTCTTGG NCCCTCGAGA CA                          462

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

GTCGACAGAA ATCATTATTC TTTATTTGCA GNCATTCCAC CCCACCTATG TTTTCTTCTC      60
CTTCCTTCTT CTCTGTCAGG AGAGTTCTTG TCATGCTGAG CTTCTTCATT GTATGGCATT      120
TATATTTTAG CACTGTTTTA TTATTGCCTT CTGTATCAGC ATGTTCAACA TTTTCTTCAA      180
ATATAACACA GGTCCCTAGA GTGTCTTCAT ACTCCCCAGC AAAGACACAG CTGTCCACTT      240
GCAGAATGGG CCTCTCAGTG TCAATGCCCA AAACCTTGCA TTTATTTTCA CATTTTGAGA      300
GGAAGTCTGA ATCAATAATT CCTGATAATT CCACCAGAAC CAACTGCTCC TCCTCTTCTT      360
CGTCTTCTCC GTCCTCTGGA CTCGCTCGT CCGCCGCCGC CGCCATGGTC CCGCGGCGGT      420
TGACGGCCTC TTTGGCCCTC GAGACA                          446

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GANTTCCAGT GAAGTTGCCT TTTTGCCNMC CCTAGNCATC CAACCTNTCN AAAACCAAGT      60
ANACNAGGCT GATTCTGGAA GTTCTTGAGG AAAAAGCAAG CTTTACAACC AAAATACCCA      120
GATGCTGTGN CCACATGGCT AAACCTTGA CCCATCTCAG AAGCAGAATC TCCTANCCCC      180
ACAGAGTGCT GTGTCCTCTG AAGAAACCAA TGACTTTAAA CAAGAGACCC TNCCAAGTAA      240
GTCCANCGAA AGCCATGACC ACATGGATGA TATGGATGAT GAAGATGATG ATGACCATGT      300

```

| | |
|---|-----|
| GGACAGCCAG GACTCCATTG ACTCGANCGA CTCTGATGAT GTAGATGACA CTGATGATTC | 360 |
| TCACCAGTCT GATGAGTCTC ACCATTCTGA TGAATCTGAT GAACCGGTCA CTGATTTTCC | 420 |
| CACGGACCTG CCANCAACGT CGACGNCCTC TTTGNCCCTC GAGACA | 456 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| GTCGACAGCG ACCGCTCCTC CCTTCCTTCC TTGAATCAGA GCACGGTAGA AAGCTGCTGC | 60 |
| TCTATGCCGA AGTGTTCGGA AATTCTTGGC AGCTGCATAG ACCGCGGGGC TGTCCCCTAA | 120 |
| CCTTTGCTCT TGTGCGCTCC TCCACCAGGA GGGCCCCCCT CCCTGTACCC CAGCTTCCCA | 180 |
| CAGAGCTGCA GGCACAGCTT GGCTGCCTCC CGCTTCCAGA CCCCTATCTC CATCAGGTGG | 240 |
| GCCTGAGGCG GGGCTGACTC TTTCTTTAGG CCCCTCACAG GGAAGTGGCAC | 300 |
| TCAGTAAGCA GGGGTGACAA CTAGAGGAAT GGCAGGGTGT GTTCAGCTGG GAGAAGAGTT | 360 |
| ACCAGAGACG CTGTGATTCT TCAGGTGTGA GGGCAACTGT TACAAGACTT AAGTAGCAAC | 420 |
| AACAACCATG GTAGACGCTG CCTTCGATTG TGCCCTTGGG AGTCCCAGGC CTGGCACCAG | 480 |
| GCCCTACTCA TCCTTCATTT CTTTTTCTTT TCTTTTGTTC TTTGTTTTTT GGGTTTTTTT | 540 |
| GTCACGCGCC TCTTTGGCCC TCGAGACA | 568 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|---|-----|
| GATTCANTTT GGATATCAAG TTGNCNCCCC CNTAGTAACT CAGTTTCTGT TATTCTTGTT | 60 |
| CTCANCTTCC CNATAAAAC ACTTGTTTCGT GGCTNNTGCC ANNTTGATTC TGTGAAGTAG | 120 |
| GCAGGAGCAG GGATTAATTN ATANAGTATT CCTGTTCTGA NCGCAACCAG AAAAGTCACT | 180 |
| GTATAAACTT GACTTAAAT AGTATCTNTC TCTTTTCATG TATANTCAGG TGGGGGGGNA | 240 |
| AAAATCTCTT TAATTGTAAC CTGAANTCAA GCTGTACCCC NCCATGGTCC TACACTCTAG | 300 |
| AGCTAATCTG GNTGGGCAGA AAGGCAGAAG GATGGTATAT TGTCCCATTG TGCCTATAAT | 360 |
| GTATNTTAAA NTGGTCATTC CACCTTACCT AATGGAAATT CTTGCAGCTT TCCTAGTGCT | 420 |
| CATCAGCGGT TTTAGGAAGT CACTAACGTC GACGGCCTCT TTGGCCCTCG AGACA | 475 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCTGAGTTGT | GTCTAAGGNN | CNCAAGACAA | GTACCCAAGT | TTCTCTAGN | TNTTCTCTTT | 60 |
| AAGCTTCTCN | AGTCATACAT | TTNCAAGCGT | CCTTTTGTCA | ACCATNCCAG | TCNANATACA | 120 |
| TTATTTGTCC | TCCAATGGNT | GACTTGCCAG | CATCTACGTG | NCCAATGAAT | ACTACATTTA | 180 |
| CATGCTCTTT | CTTAGGAGCA | CCTGGCGGTG | CAACCACAGA | CTTAGGTNTT | GGGATTTCTT | 240 |
| CTTCTCTCTC | CATCATTTCA | TGGGCACTTT | TCTCTGGCGG | CCTTCCATCT | CCCAGGAAC | 300 |
| CACCCCTGG | CTCTGCTTCA | CTTATTTCTT | CTTTGTGCTC | CCATGATTCT | TCTGGAGACA | 360 |
| TTTCTGTCTC | TCCACTTTCT | ACAATAGGTT | CTGAAAGTTC | CATGCTAACA | GCTGAATTTG | 420 |
| AACCTTCACA | CAATGACTGT | TCGTCGACGG | CCTCTTTGGC | CCTCGAGACA | | 470 |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTCACAGTC | ATCAATTATA | GACCCACAA | CATGCGCCCT | 60 |
| GAAGACAGAA | TGTTCCATAT | CAGAGCTGTG | ATCTTGAGAG | CCCTCTCCTT | GGCTTTCCTG | 120 |
| CTGAGTCTCC | GAGGAGCTGG | GGCCATCAAG | GCGGACCATG | TGTCAACTTA | TGCCGCGTTT | 180 |
| GTACAGACCC | ATAGACCAAC | AGGGGAGTTT | ATGTTTGAAT | TTGATGAAGA | TGAGCAGTTC | 240 |
| TATGTGGATC | TGGATAAAAA | GGAGACCGTC | TGGCATCTGG | AGGAGTTTGG | CCGAGCCTTT | 300 |
| TCCTTTGAGG | CTCAGGCGGG | GCTGGCTAAC | ATTGCTATAT | TGAACAACAA | CTTGAATACC | 360 |
| TTGATCCAGC | GTTCCAACCA | CACTCAGGCC | GTCGAG | | | 396 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACCCGATTGC | TAAATGGATT | ATGAAAGCAA | ATTGCTACTG | 60 |
| GGAGGTGATG | GTCAAAAGCA | AACTTAGATG | GTTTTCACAC | CATCTGTCAT | CATGACTCAA | 120 |
| AGGGAAATGC | TAGCCACACC | ATTTTCCAGT | GAAGCCACTG | CTTTACACAG | TAGATACACA | 180 |
| TAGCTTCCTA | TTGTTATTTT | CTTTTCTAAT | TATGTACATT | TAGAAAAAAA | ATACAACACT | 240 |
| GTGTTAAACA | GCAGGACAGC | TAGCAATGGA | ACATACAACA | CTATGCTGAA | AAACCACAAC | 300 |
| AGCTTGGTTA | AGCGGAGGAG | AGAAAACAGAG | ATGGCCTTCA | TGGAGTGAAG | CTGTCAATGC | 360 |
| CTGCCATCTC | CTTAGTCTGT | GACGGATCTG | CACTCTGAGG | GCAGGCCTTC | TGAGCGCCGC | 420 |
| CACTTTGCCA | GGCGCTGCTT | AAACCATTTT | TGGGTCTCCT | CCTCGGAAAG | GCCTGCCTCG | 480 |
| GCCGCGATGA | GGCACAGCGT | GGTGAATCC | GGGTGCTTGT | CGAG | | 524 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTTTTTT TCTTTTTTTA GGCATATGTA GTAATATTAG | 60 |
| AAACATTATA TTTGGGAAAC TTGATTCTT GAAAGAGAAA ACAAAGCAT GTGAATAAAC | 120 |
| TTTGAAGTGT TCACCTCAGT TTGGGACCAA ACTGCTTGGA TCTTTGTAAA AACCGGTTTT | 180 |
| GTATGTCAAG GAGGAGTTTA AGGCCTTTCC GACCACCTTG TGTTCCCCTT TTCTGCGCAG | 240 |
| CCATGTATCA CGTGGAGTTG CTCCTTACCA CACCTCACGT GCCCCTGAGC CCTATTTCTT | 300 |
| GATTTCTTCT GGGCTGGACT TCCCCGTTCT CCACCAGCAG CTCCAGTATC CCTGTTGAAT | 360 |
| TCTAGACCTG CGTCGAG | 377 |

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGCGGACAAG TTTGAGAGAC CTGGCCTTGG CCAAAGCCCT | 60 |
| CGATTCGCTG TGTCAAAAA ACTGAGGTGA GAAGAGACCA CCACCCTCTC CACCACCCTC | 120 |
| TCAGTAGGAA AGCGGGATCA ACAGAGATCA GAAGGACAGC ACACTCACAC CTGCACATGA | 180 |
| ACACACCATC TATGTCAGGA AATCCAGGGG AAGGGGAAGA GGGGTGGAGT GGCTCCGCAG | 240 |
| GGCTGACCTG ACAGGGGACA GGAACACTCC CCTAGACCCA GGAAGTCGC CCCAAATCCA | 300 |
| AAGCTCTTGA AAGGAGGTAT GGCCTCGAAA CTCCAGAAGC CTCTTCTGCC AACGCACCGA | 360 |
| GGACCTGCAC CTCCATTCA GCACGCGTCG AG | 392 |

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | |
|---|-----|
| CAATTCGGCC AAAGAGGCCT ACAGCATTTT TACTCCTTCC AAGAAGAGCA GCAAAGCTGA | 60 |
| AGTAGCAGCA GCAGCACCAG CAGCAACAGC AAAAAACAAA CATGAGTGTG AAGGGCATGG | 120 |
| CTATAGCCTT GGCTGTGATA TTGTGTGCTA CAGTTGTTCA AGGCTTCCCC ATGTTCAAAA | 180 |
| GAGGACGCTG TCTTTGCATA GGCCCTGGGG TAAAAGCAGT GAAAGTGGCA GATATTGAGA | 240 |
| AAGCCTCCAT AATGTACCCA AGTAACAACT GTGACAAAAT AGAAGTGATT ATTACCCTGA | 300 |
| AAGAAAATAA AGGACAACGA TGCCTAAATC CCAAAGTCGA G | 341 |

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGCAGTAGCA TGTGCAGCAA CCAATCAAGA TGGAGAACTA | 60 |
| TACCTGCACT CATTGTGTG TTTGCATGTA TAGTTCTCTG CAGTAGCATG TGCAGCAACC | 120 |
| AATCAAGATG GAGAACTGTT CCATCGCAAA GCTCCCTCTT GCCACTTCTT TTTAGCCACC | 180 |
| CAATCTCTC TGCTCCCGTC GAG | 203 |

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC | 60 |
| TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTC AACTCTTTGG CTTAATTCTC | 120 |
| TCGGAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT | 180 |
| TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT | 240 |
| TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAATC TTTTCTTAGG CATTTTGAAG | 300 |
| AATTGGAAAG AGGAGAGTGA CAGAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTC | 360 |
| AAACTTTTAA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG | 420 |
| GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTTCGAAAAG | 480 |
| CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAATCATC | 540 |
| CAAGTGATGG CTGAAGTGC GCCAGCAGCT AAAACAGGGG TCGAG | 585 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTGGCGGCC GCGGAGACGC AGAGTCTTGA GCAGCGCGGC | 60 |
| AGGCACCATG TTCCTGACTG CGCTCCTCTG GCGCGGCCGC ATTCCCGGCC GTCAGTGGAT | 120 |
| CGGGAAGCAC CGGCGGCCGC GGTTCGTGTC GTTGCCCGCC AAGCAGAACA TGATCCGCCN | 180 |
| CCTGGAGATC GAGGCGGAGA ACCATTACTG GCTGAGCATG CCCTACATGA CCCGGGAGCA | 240 |
| GGAGCGCGGC CACGCGCGG TGCGCAGGAG GGAGGCCTC GAGGCCATAA AGGCGGCCGC | 300 |
| CACCTCCAAG TTCCCCCGC ATAGATTCAT TCGGACCAG CTCGACCATC TCAATGTCGA | 360 |
| G | 361 |

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AAACAAAATG | GTTATCAACC | ACTTGGAGAA | GTTGTTTGTG | 60 |
| ACAAACGATG | CAGCAACTAT | TTTAAGAGAA | CTAGAAGTAC | AGCATCCTGC | TGCAAAAATG | 120 |
| ATTGTAATGG | CTTCTCATAT | GCAAGAGCAA | GAAGTTGGAG | ATGGCACAAA | CTTTGTTCTG | 180 |
| GTATTGCTG | GAGCTCTCCT | GGAATTAGCT | GAAGAACTTC | TGAGGATTGG | CCTGTCAGTT | 240 |
| TCAGAGGTCA | TAGAAGGTGA | TGAAATAGCC | TGCAGAAAAG | CTCATGAGAT | TCTTCCTAAT | 300 |
| TTGGTATGTT | GTTCTGCAAA | AAACCTTCGA | GATATTGATG | AAGTCTCATC | TCTACTTCGT | 360 |
| ACCTCCATAA | TGAGTAAACA | ATATGGTAAT | GAAGTATTTT | TGGCCAAGCT | TATTGCTCAG | 420 |
| GCATGTCGAG | | | | | | 430 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGAAGAAGAT | GATCCTAAAC | AAAGCTCTGA | TGCTGGGGGC | 60 |
| CCTCGCCCTG | ACCACCGTGA | TGAGCCCTTG | TGGAGGTGAA | GACATTGTGG | CTGACCACGT | 120 |
| TGCCTCTTAC | GGTGTAAGT | TGTACCAGTC | TTACGGTCCC | TCTGGCCAGT | TCACCCATGA | 180 |
| ATTTGATGGA | GACGAGGAGT | TCTATGTGGA | CCTGGAGAGG | AAGGAGACTG | TCTGGAAGTT | 240 |
| GCCTCTGTTC | CACAGACTTA | GATTTGACCC | GCAATTTGCA | CTGACAAACA | TCGCTGTGCT | 300 |
| AAAACATAAC | TTGAACATCC | TGATTAAACG | CTCCAACCT | ACCGCTGCTA | CCAATGAGGT | 360 |
| TCCTGAGGTC | GAG | | | | | 373 |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTTAACCAG | AATGACAGTC | TTTCCCCTAT | CTTCCTTCTT | 60 |
| TATTCTTATC | TTCTATCTTT | CCCTCCCAAA | CTCTTTCCCC | GACATAACAG | AAAACATGAA | 120 |
| GGAATTAAG | GAGGCCAGGC | CGCGCAAAGA | TAACAGGCGT | CCAGATCTGG | AAATCTATAA | 180 |
| GCCTGGCCTT | TCTCGGCTAA | GGAACAAGCC | CAAAATCAAG | GAACCCCTG | GGAGTGAGGA | 240 |
| ATTCAAAGAT | GAAATTGTTA | ATGACCGAGA | TTGCTCTGCT | GTTGAAAATG | GTACACAGCC | 300 |
| CGTCGAG | | | | | | 307 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | |
|--|-----|
| GGAGCTGCAC ATGGTACTTT TGGAGAGCCT GGTGGAAATC ATTTTGGTTG CTGTTTCAGCA | 60 |
| TGTGGATTAT AGTCTTCGAT GTGAGCAGGA TCCAGAGAAG AAAGCTTTTA TCAGACAGAA | 120 |
| TGCATCCTTT TTATATGAAA CAGTCCTCCC TGTGGTGGAG AAAAGGTTTG AAGAAGGTGT | 180 |
| GGGGAAACCT GCCAAGCAAC TCCAAGATCT GAGGAATGCA TCTAGACTTA TTCGTGTGAA | 240 |
| TCCTGAAGTC GAG | 253 |

(2) INFORMATION FOR SEQ ID NO:120: ..

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACACATATTG GAAAAATGAT CTTTTTGGAG CACTGTTCTG | 60 |
| CTGCTTAGAC CCAGTACTCA CTATTGCTGC TAGTCTCAGT TTCAAAGATC CCATTTGTCA | 120 |
| TTCCACTGGG AAAAGAAAAAG ATTGCAGATG CAAGAAGAAA GGAATTGGCA AAGGATACTA | 180 |
| GAAGTGATCA CTTAACAGTT GTGAATGCGT TTGAGGGCTG GGAAGAGGCT AGGCGACGTG | 240 |
| GTTTCAGATA CGAAAAGGAC TATTGCTGGG AATATTTTCT GTCTTCAAAC AACTGCAGA | 300 |
| TGCTGCATAA CATGAAAGGA CAGTTTGCTG AGCATCTTCT TGGAGCTGGA TTTGTAAGCA | 360 |
| GTAGAAATCC TAAAGATCCA GAATCTAATA TAAATTCAGA TAATGAGAAG ATAATTAAAG | 420 |
| CTGTCGAG | 428 |

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACAAGACGTC ATTTCAAAA GTGCGCCATT CTGAGGATAT | 60 |
| GCAGTTTGCC TTCTCTTATT TTTATTATCT CATGAGTGCA GTGCAGCCAC TGAATATATC | 120 |
| TCAAGTCTTT GATGAAGTTG ATACAGATCA ATCTGGTGTC TTGTCTGACA GAGAAATCCG | 180 |
| AACACTGGCT ACCAGAATTC ACGAACTGCC GTTAAGTTTG CAGGATTTGA CAGGTCTGGA | 240 |
| ACACATGCTA ATAAATTGCT CAAAAATGCT TCCTGCTGAT ATCACGCAGC TAAATAATAT | 300 |
| TCCACCAACT CAGGAATCCT ACTATGATCC CAACCTGCCA CCGGTCACTA AAAGTCTAGT | 360 |
| AACAAACTGT AAACCAAGTAA CTGACAAAAT CCACAAAGCA TATAAGGACA AAAACAAATA | 420 |
| TAGGTTTGAA ATCATGGGAG AAGAAGAAAT CGCTTTTAAA ATGATTCTGTA CCAACGTTTC | 480 |
| TCATGTGGTT GGCCAGTTGG ATGACATAAG AAAAAACCTT GTCGAG | 526 |

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
GGGTGGCAAT ATGGA CTTC TCTTTCTGC CANCCANAC CCATACATCG GGATTCCTAT      60
AATACCTTCG TTGGTCTCCC TAACATGTAG GTGGNGGNGG GGAGATATAC AATAGAACAG      120
ATACCAGACA AGACATAATG GGCTAAACAA GACTACACCA ATTACACTGC CTCATTGATG      180
GTGGNACATA ACGAGCTAAT ACTGTAGCCC TAGACTTGAT AGCCATCATC ATATCGAAGT      240
TTCCTACCC  TTTTCCATT TGCCATCTAT TGAAGTAATA ATAGGCGCAT GCAACTTCTT      300
TTCTTTTTTT TTCTTTCTC TCTCCCCGT  TGTTGTCGAG      340
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
GAATTCGGCC AAAGAGGCCT ACGTCCTTTT AAATCTTAAT GAAATATCAT GGAATATTGT      60
ATGGTCTTCA TATCGTTCTA TATAATGCAA ATGGTGAAC TCTCTGTTCT TTGCTTTCTT      120
GAAAGCATCC ATCCGATCAG TAGCTTTCCC AATAGAAAAA CCTGCAGCTC CTTTTCGGTT      180
CCCCACAGCC ACCAAGACAC GGATCGATTT CTTTCTTCCC TCTTTCGCG TCATAGTGAA      240
AACGTTTCTT ACCTCAAGTA TCCTGGTATC AAAATCCTCA TATGTTTCTC CACAGTCGAG      300
```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
GAATTCGGCC AAAGAGGCCT ACCAGCTTTG AGGTTGACCT GTTCTCTTT GTCTGCCTTC      60
CCAAAACACC AGCCCCCAGG AAGACATTAA GCAGCCTTAA GCTTAAATTC CTA CTCCCTC      120
TTCCAAATTT GGCTCACTTG CCTTAGATCC AAGGCAGGGA AAGGAAAAGA AGGGGGGTCT      180
CTGGCTTTAT TACTCCCCTA AGTCTTTACT CTGACTTCCC CAAACCCAGA AAGATTTTCT      240
CCACAGTGTT CATTGAAAG AGGAGTATTT TGTCCCATTT TCCCCTTCCT CATTATCAAA      300
CAGCCCCAGT CTTCTTGTC TCTGCTAAGA AAGTAGAGGC ATGATGATCT GCCTCTCAAC      360
TGCCCTAGTC GAG      373
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACGCAGATAC | GGGCTTACAG | ATACTTTTTA | CACTCTTACA | 60 |
| AAATGTTGCA | CAAGAAGAAG | CTGCAGCTCA | GAGTTTTTAT | CAAACCTATT | TTTGTGATAT | 120 |
| TCTCCAGCAT | ATCTTTTCTG | TTGTGACAGA | CACTTCACAT | ACTGCTGGTT | TAACAATGCA | 180 |
| TGCATCAATT | CTTGCATATA | TGTTTAATTT | GTTTGAAGAA | GGAAAAATAA | GTACATCATT | 240 |
| AAATCCTGGA | AATCCAGTTA | ACAACCAAAT | CTTTCTTCAG | AAATATGTGG | CTAATCTCCT | 300 |
| TAAGTCGGCC | TTCCCTCACC | TACAAGATGC | TCAAGTAAAG | CTCTTTGTGA | CAGGGCTTTT | 360 |
| CAGCTTAAAT | CAAGATATTC | CTGCTTTCAA | GGAACATTTA | AGAGATTTC | TAGTTCAAAT | 420 |
| AAAGGAATTT | GCAGGTGAAG | ACACTTCTGA | TTTGTTTTGT | GAAGAGAGAG | AAATAGCCCT | 480 |
| ACGGCAGGCT | GATGAAGAGA | AACATAAACG | TCAAATGTCT | GTCCCTGGCA | TCTTTAATCC | 540 |
| ACATGAGATT | CCAGAAGAAA | TGTGTGATTA | AAATCCAAAT | TCATGCTGTT | TTTTTCTCT | 600 |
| GCAACTCGTT | AGCAGAGGAA | AACAGCATGT | GGGTATTTGT | CGAG | | 644 |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACGTTATACT | ATTAGATCCT | TTCATTATCA | ATCCCTTTTA | 60 |
| AAGGCAAGGA | AACAGGTTCA | GCAAGATCAG | CTGACTTCTC | TGTGTAAGTG | GGACCTGAGA | 120 |
| TTTGAAAGTT | GAGAGCAGCA | TGTTTTGCCC | ACTGAACTC | ATCCTGCTGC | CAGTGTTACT | 180 |
| GGATTATTCC | TTGGGCCTGA | ATGACTTGAA | TGTTTCCCCG | CCTGAGCTAA | CAGTCCATGT | 240 |
| GGGTGATTCA | GCTCTGATGG | GATGTGTTTT | CCAGAGCACA | GAAGACAAAT | GTATATTCAA | 300 |
| GATAGACTGG | ACTCTGTAC | CAGGAGAGCA | CGCCAAGGAC | GAATATGTGC | TATACTATTA | 360 |
| CTCCAATCTC | AGTGTGCCTA | TTGGGCGCTT | CCAGAACCGC | GTACACTTGA | TGGGGGACAA | 420 |
| CTTATGCAAT | GATGGCTCTC | TCCTGCTCCA | AGATGTGCAA | GATGTCGAG | | 469 |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGAGGGGACT | CGCCGCCATC | TCAGGTCTCT | TGGCTTTGCC | 60 |
| AGGGCCACCC | GGAGAAAAC | TGACACCCGT | TTCTGTAATC | CTTATGGGAG | ACCAACCTTG | 120 |
| TGCTCCGGG | AGATCCACTC | TCCACCTGG | AAACGCACGG | GAAGCCAAGC | CTCCAAAAAA | 180 |
| GCGCTGCCTC | CTCGCTCCGC | GTTGGGATTA | TCCGGAAGGA | ACTCCCAACG | GAGGTAGTAC | 240 |
| CACTCTACCC | TCCGCACCTC | CTCCTGCATC | AGCCGGCCTG | AAGTCGCACC | CTCCTCCTCC | 300 |
| GGAGAAGTAG | AGAAATAAAT | TTCTCCAC | CTAAACCACT | CTTTGAGTGA | TTGCAGTATG | 360 |
| ACTCCATTTT | CCTGGTGAT | TCATATAATA | GTTACCTGG | TGAAAAAAT | GAAGATTATT | 420 |
| TACAATGCTA | CCCCG | | | | | 435 |

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
GAATTCGGCC AAAGAGGCCT AACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT    60
GCCATGCTGT TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT    120
CTTCTGCAGG AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA G            171
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
GAATTCGGCC AAAGAGGCCT AGTCATGACT CCCCTGATTT GGCTCCTAAT GTCACCTATT    60
CCCTGCCCAG AACCAAAAGT GGTAAGGCC CAGAAAGAGC CTCTAGCAAG ACTTCTCCAC    120
ATTGGAAGGA GTCAGGAGCC TCCCATTTGT CATTCCCAAA GAACAGCAAA TATGAGTATG    180
ACCTTGACAT CTCTCCTCCA CGAAAAAGC AAGCAAAATC CCATTTTGA GACAAGAAGC    240
AGCTTGATTC CAAAGGTGAC TGCCAGAAAG CAACTGATTC AGACCTTTCT TCTCCACGGC    300
ATAAACAAAG TCCAGGGCAC CAGGATTCTG ATTCAGATCT GTCACCTCCA CGGAATAGAC    360
CTAGACACCG GG                                                    372
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTCGGCC NAAGAGGCCT AGGGTGGGAC AAGAGAGTGA GACTAGAATA TAAATATCCG    60
TAAACAGCAT CTGAGCATTG GTCTTTAACA GGGAGGAGGA ACCACTGGTG TATATTAATT    120
TAGGACACAG GATCATTATA GGGGTNGGGC CAGCTGGTGT TAATGGCATG CAGGCATATG    180
TGATGCCAAC CATGAGGGCT GGAAGAACCA GAAGCCAAAG AAGAATATGA CCGCATCTAT    240
TCTAAAGCTA CTGTGGTGGT TTCTCATGCT TCAGAGTCTC GTAAGTCTCC TGGTTCCTGG    300
TGCTCAGGCC CGTGTAACA CCATCTGATT TCTCATAGCT GGTATAGCT GCCTTTCGCA    360
CTTGGATCTT CAGTCGAG                                                    378
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGGTGCCGCG GTCCTGTCTT GCTGTGCCTG CGGCAGGGGC | 60 |
| TCGGAACCAA TTCATTCTTG CACGGCCTGG GGCAGGAGCC CTTCGAGGGA GCTCGGTCAC | 120 |
| TGTGTTGCAG GTCCTCGCCT AGAGACCTGC GAGATGGAGA AAGAGAGCAC GAGGCGGCAC | 180 |
| AAAGGAAAGC CCCAGGAGCA GAGTCTTGCC CATCTCTCCC TCTGAGCATC TCGGACATTG | 240 |
| GGA CTGGATG TCTTTCGTCA CTGGAAAACC TCAGACTGCC GACGCTGCCG GAAGAGTCAT | 300 |
| CCCCTCGAGA GCTCGAGGAC TCGAGCGGAG ACCAGGGCCG GTGCGGTCCC ACACACCAGG | 360 |
| GATCCGAGGA TCCTTCGATG CTCTCGCAGG CCCAGTCCGC TACCGAGGGT CGAG | 414 |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | |
|--|-----|
| AAGCGTGCTC GTGCCCGTAT TNCCNAGGGG NTCAGTCTGT NNCGCCCCANA GNCCAAGNCC | 60 |
| AAGCCCAAGN CCNAGNCCAA GGATCCANNC CAAGGCCAG GCTGCAGCCC CAGCTTCAGT | 120 |
| TCCAGCTCAG GTCCCACAC GTACCCAGGC CCCCACAAAG GCTTCAGAGN AGATATCTCT | 180 |
| CCCAACATGA GGACAGAAGG ACTGGTGCGA CCCCCACCC CCGCCCCTGG GCTACCATCT | 240 |
| GCATGGGGCT GGGTCCTCCT GTGCTATTTG TACAAATAAA CCTGAGGCAG TCGAG | 295 |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

| | |
|---|-----|
| ATGGACTTCC TCTTTTCTGC CANCCACAC CCATACATCG GGAGCCTATA ATACCCTTCG | 60 |
| TTGNTCTCCC TAACATGTAG GTGGCGGAGG GGAGATATAC AATAGAACAG ATACCAGACA | 120 |
| AGACATAATG GGCNNAACAA GACNACACCA ATTACNTNC CTCATTGATG GTGGNACATA | 180 |
| ACGAGCTAAT ACTGTANCCC TAGACNTGAT AGCCATCATC ATATCGAAGT TTCACTACCC | 240 |
| TTTTTCCATT TGCCATCTAT TGAAGTAATA ATAGGCGCAT GCAACTTCTT TTCTTTTTTT | 300 |
| TTCTTTTCTC TCTCCCCGN TGTGTCTCA CCATATCCGC AATGACGTCG AG | 352 |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACGTTATCCG CGATGCGTTT CCTGGCAGCT ACATTCCTGC | 60 |
| TCCTGGCGCT CAGCACCGCT GCCCAGGCCG AACCGGTGCA GTTCAAGGAC TGCGGTTCTG | 120 |
| TGGATGGAGT TATAAAGGAA GTGAATGTGA GCCCATGCCC CACCCAACCC TGCCAGCTGA | 180 |
| GCAAAGGACA GTCTTACAGC GTCAATGTCA CCTTCACCAG CAATATTCAG TCTAAAAGCA | 240 |
| GCAAGGCCGT GGTGCATGGC ATCCTGATGG GCGTCCCAGT TCCCTTTCCC ATTCCTGAGC | 300 |
| CTGATGGTTG TAAGAGTGGA ATTAAGTGCC CTATCCAAAA AGACGTCGAG | 350 |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCGT CGACCTCCCCT TCCAGCCCCC | 60 |
| AGAAAGCTCG GTCACCTGAG TGTTCCTAG AATCCTGGGG TGCTCCCGGG CCGCTCTCAG | 120 |
| AGAAGTGGCA GGTTCACGT TCAGCCGTGT GCGGATCGT GTGGCTTCCA AAGCCTTTTA | 180 |
| CAGCCCCCGC CCCCATCCC GTGGTCTGTC TGCAGGAACT CTCCGCTCTG TGAGAAGCCT | 240 |
| CTTCCGAGT CGAG | 254 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTAGAGGGG TCAGTGGCCC CGCACGGTGG GGTGGCCGCT | 60 |
| CAGGGCCTAG GGAGCAGGTG GGAGGGGCTT GGAGGGCAGA ACAGAGGGCC TGGGGGCTGC | 120 |
| TCTGCTGGCC ACCACTGCTT TCTGGTTGAA CCAGATAAGT AGCTGGTGGT GACGGCTGTG | 180 |
| GGCCCTGAGT CGGGGGAGAA GAGGCAGAGG GAGCAGTGGG CTGGGCTAGT GGGGACATGA | 240 |
| GTGGGTGGTG ATCATGCCTG TGTCGGGGGA GCTGAGGCAG AGAGTGGGGC AGCGAGCATC | 300 |
| CCCTGAGGGC AGGAGGAGAG GGGTGGGGAC AGGGAAGGGT CGGGGGTGGT CCCAGCCCTG | 360 |
| AAGACAGGAG TGGCGAGGGC AGGTGTGCTC TAGGTGCTTG TCGAGGTGGA CAACATGGGT | 420 |
| CGAG | 424 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

GAATTCGGCC AAAGAGGCCT AATGGCGTCC AGGTCTAAGC GCGGTGCCGT GGAAAGTGGG      60
GTTCCGCAGC CGCCGGATCC CCCAGTCCAG CGCGACGAGG AAGAGGAAAA AGAAGTCGAA      120
AATGAGGATG AAGACGATGA TGACAGTGAC AAGGAAAAGG ATGAAGAGGA CGAGGTCATT      180
GACGAGGAAG TGAATATTGA ATTTGAAGCT TATTCCTAT CAGATAATGA TTATGACGGA      240
ATTAAGAAAT TACTGCAGCA GCTTTTTCTA AAGGCTCCTG TGAACACTGC AGAACTAACA      300
GATCTCTTAA TTCAACAGAA CCATATTGGG AGTGTGATTA AGCAAACGGA TGTTCAGAA      360
GACAGCAATG ATGATATGGA TGAAGATGAG GTTTTGGTT TCATAAGCCT TTAAATTTA      420
ACTGAAAGAA AGGGTACCCA GTGTGTTGAA CAAATTCAAG AGTTGGTTCT ACGCTTCTGT      480
GAGAAGAACT GTGAAAAGAG CATGGTTGAA CAGCTGGACA AGTTTTTAA TGACACCACC      540
AAGCCTGTGG GCCTTCTCCT AAGTGAAAGA TTCATTAATG TCCCTCCACA GATCGCTCTG      600
CCCATGTACC AGCAGCTTCA GAAAGAACTG TCGGGGGCAC ACAGAACCAA TAAGCCATGT      660
GGGAAGTGCT ACTTTTACCT TCTGATTAGT AAGACATTG TCGAG                          705

```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

GAATTCGGCC AAAGAGGCCT ACCCAGCTCA GAATCTTGCT GCTCGGCCCC CAGGAGAGCA      60
ACAACACAAC GGGAACGATG TGAAGGTGT CAGCTCTGCT CTTCTTTTG GGAAGCGCGT      120
CGCTCTGGGT CCTGCCAGAA GGAGCCAGCA CAGGCCAGCC AGAAGATGAC ACTGAGACTA      180
CAGGTTTGA AGGCGGCGTT GCCATGCCAG GTGCCGAAGA TGATGTGGTG ACTCCAGGAA      240
CCAGCGAAGA CCGCTATAAG TCTGGCTTGA CAACTCTGGT GGCAACAAGT GTCAACAGTG      300
TAACAGGCAT TCGCATCGAG GATCTGCCAA CTTCAGAAAAG CCGATCGAG                      350

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

GAATTCGGCC AAAGAGGCCT AGTGGACAGG AAGTAGAATT TATTGGTGAG TATTAAGAGG      60
GGGGCAGCAC ATTGAAGCC CTCATGAGTG CAGGGCCCGT CACTTGTTCA GAGGGCCACG      120
ACTGGGGATG TACTTGACCC CACAGCCATC TGGGATGAGC CGCTTTTCAG CCACCATGTC      180
TTCAAATTCA TCAGCATTGA ACTTGGTGAA GCCCACTTC TTTGAGATGT GGATCTTCTG      240
GCGGCCAGGA AACTTGAAGT TGGCCCTGCG CAGGCCTCA ATCAGATGCT CCTTGTCTG      300
CAGCTTGGTG CGGATGGACA TGATAACTTG GCCAATGTGA ACCCTGGCCA CAGTGCCCTG      360
GGGCTTTCCA AAGGCACCTC GCATGCCTGT TTGGAGCCTG TCAGCCCCAG CACAGGACAA      420
CATCTTGTTG ATGCGGATGA CGTGGTCGAG                      450

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC | 60 |
| TTTGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTC ACTTCTTTGG CTTAATTCTC | 120 |
| TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT | 180 |
| TCTCTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT | 240 |
| TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAACCT TTTCTTAGG CATTTTGAAG | 300 |
| AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTTACTTC | 360 |
| AACTTTTTTA AAACTTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG | 420 |
| GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTTGAAAAAG | 480 |
| CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAATCATC | 540 |
| CAAGTGNITGG CTGAACTGTC GCCAGCAGCT AAAACAGGGG TCGAG | 585 |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTGGAGTTT GAGTATAGTA AATTATGATC CTTAAATATT | 60 |
| TGAGAGTCAG GATGAAGCAG ATCTGCTGTA GACTTTTCAG ATGAAATTGT TCATTCTCGT | 120 |
| AACCTCCATA TTTTCAGGAT TTTTGAAGCT GTTGACCTTT TCATGTTGAT TATTTTAAAT | 180 |
| TGTGTGAAAT AGTATAAAAA TCATTGGTGT TCATTATTTG CTITGCCTGA GCTCAGATCA | 240 |
| AAATGTTTGA AGAAAGGAAC TTTATTTTGT CAAGTTACGT ACAGTTTTTA TGCTTGAGAT | 300 |
| ATTTCACAT GTTATGTATA TTGGAACCTC TACAGCTTGA TGCCTCCTGC TTTTATAGCA | 360 |
| GTTTATGGGG AGTCACTTGA AAGAGCGTGT GTACATGTAT TTTTTTCTN GGCAAACATT | 420 |
| GAATGCAAAC GTGTATTTT TTAATATAAA TATATACTT CCGCGTCGA G | 471 |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATGTTTGGCA ACTGGGGTGA AGGGATTGCC CTCCCCCTGC | 60 |
| TGGGATCCC2 CCAGCCCCTC CGGTCTGGCA GGAAGGGGGC AGCCTGCAAC CCCCAAGGGC | 120 |
| AGGTGTGGGG CTGCCAGATG CTCCAGGCAG GGGGCCAGAA GGGGCTCACA AAGGCTTGCC | 180 |
| CTCCAGGGAG ATGACGGCAC TGCCCCCAG CTCTCTGCC AGGGTGCAGC GGTCTTGAC | 240 |
| CTCCTCGTAG CAGTTTGCTT GCAATTCATG CTTGATCCCT GTCAGCTTCT TCTTGATGGC | 300 |
| GTCCTTGGAG CTGGCATAAA TCATTTTGCT CTTAAGGGGS GCAGACTCGG GGGCCCAGAA | 360 |
| GATAAACACC AGATCCTCCT TCTTGCTCTC CYTGGTCTCA TAGGTTGCAT CATAGAGGGC | 420 |

ATAGCGGCAG TCCTTATCTG GCAGCATCTT GACAAAGGTG GCGTAGGGAT CGTCGAG

477

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|---|-----|
| GAATTCGGCC CAAAGAGGCC YMAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC | 60 |
| TTTGGACTTG ATCAGCTTGA TACAAGAACT ACTGATTTC ACTTCTTGG CTTAATTCTC | 120 |
| TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTGGGT | 180 |
| TCTCTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT | 240 |
| TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAAGTC TTTTCTTAGG CATTTTGAAG | 300 |
| AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTC | 360 |
| AAACTTTTAA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTCGA G | 411 |

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | |
|---|-----|
| GAATCGGCCC AAAGAGGCCT ACTGAAGATC AGCTATTAGA AGAGAAAGAT CAGTTAAGTC | 60 |
| CTTTGGACCT GATCAGCTTG ATACAAGAAC TACTGATTC AACTTCTTTG GCTTAATTCT | 120 |
| CTCGGAAACG ATGAAATATA CAAGTTATAT CTGGCTTTT CAGCTCTGCA TCGTTTGGG | 180 |
| TTCTCTTGGC TGTTACTGCC AGGACCCATA TGTAAGAGAA GCAGAAAACC TTAAGAAATA | 240 |
| TTTAATGCA GGTCAATCAG ATGTAGCGGA TAATGGAAGT CTTTCTTAG GCATTTTGAA | 300 |
| GAATTGGAAA GAGGAGAGTG ACAGAAAAAT AATGCAGAGC CAAATTGTCT CTTTACTT | 360 |
| CAAACCTTTT AAAAATTTA AAGATGACCA GAGCATCCAA AAGAGTGTGG AGACCATCAA | 420 |
| GGTCGAG | 427 |

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGAGAAGATA AACTGGACA CTGGGGAGAC ACAACTTCAT | 60 |
| GCTGCGTGGG ATCTCCAGC TACCTGCAGT GGCCACCAGT TCTTGGGTCC TGCTGCCTGT | 120 |
| ACTTTGGCTC ATTGTTCAA CTCAAGCAAT AGCCATAAAG CAAACACCTG AATTAACGCT | 180 |
| CCATGAAATA GTTGTCTTA AAAAATTTCA CATTTTACAC AAAAGAGAGA TCAAGAACAA | 240 |

| | |
|---|-----|
| CCAGACAGAA AAGCATGGCA AAGAGGAAAG GTATGAACCT GAAGTTCAAT ATCAGATGAT | 300 |
| CTTAAATGGA GAAGAAATCA TTCTCTCCCT ACAAAAAACC AAGCACCTCC TGGGGCCAGA | 360 |
| CTACACTGAA ACATTGTACT CACCCAGAGG AGAGGAAATT ACCACGAAAC CTGAGAACAT | 420 |
| GGAACACTGT TACTATAAAG GAAACATCCT AAATGAAAAG AATTCTGTTG CCAGCATCAG | 480 |
| TACTTGTGNC GGGTTGAGAG GATACTTCAC ACATCATCAC CAAAGATACC AGATAAAACC | 540 |
| TCTGAAAAGC ACAGACGAGA AAGAACATGC CGTCTTTACA TCTAACCAGG AGGTCCAG | 598 |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS: --

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT | 60 |
| TGGTGTGGGG TCCAAAGCAC TCTTATTTAA CATAGATTCC AAACCTTTTA CACCCATGGG | 120 |
| GTCAATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC | 180 |
| CCCCGTGTCC AAAGGAATCG CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAG | 238 |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT | 60 |
| TGGTGTGGGG TCCAAAGCAC TCTTATTTAA CATAGATTCC AAACCTTTTA CACCCATGGG | 120 |
| GTCAATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC | 180 |
| CCCCGTGTCC AAAGGATTCT CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAGGT | 240 |
| TCTCCCTATA GTGAGTCGTA TTAATTTTCT AGGAGTATTT AGAAGAGAAG CTGAAGCTGT | 300 |
| CGAG | 304 |

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACGACAGTTG GTGTAAAGGA AAACCTTCTGA GCTCCGTCAG | 60 |
| TTCACCTGGT ACATTGGAAT TAAAGTGCTT GGATGTTTTT CCCCCACTTT AAAAAAACTT | 120 |
| TTGAGGTTTT TTTTTTTTTT TGTCTTTTAA AAACATCGTA ACATTAACAC ATGGCCGTTT | 180 |
| ACCGTCCCCC AGCGATGGGA GCTGGCCTGG GGCCCAAGGT CCTCCAGGAT CTTCACTCAT | 240 |

TCACAGTAAC GGTTCGACC AGTCCTCCAG GTCGCACGTG GATGCGACAG GGGTGGGGAG 300
 GGAGGAGGAA GTGACTGTCC CACCTCTGCA GGACCATGGG AGTGGGCAAG GTGTTCTCCG 360
 GGGCGCACCC CTGAACCCAG GGGTGCTGCA GGACNTG 397

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC AAAGAGGCCT ATAAGAATTT AAGATGCATT TTTGCATTGG CTATATTTCT 60
 TTAAATTCTA GATAGTTATT TTCAAGTGTT GGTAACATA AATCTTAGGC TTAGGAACCA 120
 TTGGATTAGT AACAGCATTG TGCTAATCAA AACTTTAAAA AAATGAGTTC AAAATTGTTA 180
 TAATGTAATT TTATAGATTT TCTTTTATCC TCAACCTGCA GAAGCCGGAA AGTGAGGCAC 240
 ATAGCCCCAC ATAGGCAGAA ATTAAGCCT AGGCAATAAC TTAGTGAAAA TGGAAATTTT 300
 AGAACATTCC ACTTCTTGTT TAGTACAATT TTATGGCCAT GGTGCTAGCT AATGGAAATG 360
 GCTAGTATAC TATTTATAGG CCAGCAATAT TTTGGTGAAT TTAAGCGAAA CTATGCTCAG 420
 TATCATTGAA ATGGGGGTGG GGTGGGCTTG AGACATGAAA TCAATCATAC AAAGTCAAAA 480
 ACTATTTTAA CCCAGGAATA AGTTAAATTC CTGTCACCCA GTCCAGGTTT TCCCTATAGT 540
 GAGTCGTATT AATTCAGAG GAGTATTTAG AAGAGAAGCT GAAGCTGTCG AG 592

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC AAAGAGGCCT AGATGATGAT ATGTTTAACC ACCAAGTTCC TTATTTGTGG 60
 CTGATTTACT GCCTTTGTCA TCCTCTTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT 120
 GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT 180
 CTTGTCTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT 240
 TTTACTGATT TAGTGAATAG ATGTTTGGTT ACAGNCCCTG CCCGATACCC CATTCCTTTT 300
 AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTCATAATA GGGTCGAG 348

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC AAAGAGGCCT ACAGAATTGA GAGTTTGTTC TTACACACAA GTTTAATGCC 60

```

ACCTTCCTCT GTCTGCCATG GACCAACAAG CAATATATGC TGAGTTAAAC TTACCCACAG      120
ACTCAGGCCC AGAAAGTTCT TCACCTTCAT CTCTTCCTCG GGATGTCTGT CAGGGTTCAC      180
CTTGGCATCA ATTTGCCCTG AAACCTTAGCT GTGCTGGGAT TATTCTCCTT GTCTTGTTG      240
TTACTGGGTT GAGTGTITCA GTGACATCCT TAATACAGAA ATCATCAATA GAAAAATGCA      300
GTGTGGACAT TCAACAGAGC AGGAATAAAA CAACAGAGAG ACCGGGTCTC TTAAACTGCC      360
CAATATATTG GCAGCAACTC CGAGTCGAGG TTCTCCCTAT AGTGAGTCGT ATTAATTTC      420
GAGGAGTATT TAGAAGAGAA GCTGAAGCTG TCGAG                                455

```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

GAATTCGGCC AAAGAGGCCT AAAATCTCT TATTAAAGGT AGAACCTCTG CTAGCCAGAC      60
AACTATATTA TTTTGCTCAA CAAACAGTG GACATTTCTT GAGGGGCTAC GATTTACCAG      120
AACACATCAG CAATCCAGAA GATTACCACA GATCTATCCG CCATTCTCTT ATTCAAGAAT      180
GAAAAATGTC AAGATGAGTG GTTTTCTTTT TCCTTTTTTT TTTTTTTTTT TTTTGATACG      240
GGGATACGGG GTCTTGCTCT GTCTCCAGG CTGGAGTGCA GTGACACAAT CTCAGCTCAC      300
TGTGACCTCC GCCTCTGGG TTCAAGAGAC TCTCTGCCT CAGTCGAG                        348

```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

GAATTCGGCC AAAGAGGCCT ACCTTAAAGC CGTATACTTA TGAATTTAAA GTGGAAAATT      60
TTTTTGGTGG CCCTGGCCCC CTTGCCAGAT TCCAGCTGGC CGTCAGTGCT CCGTGTCTC      120
TCTGAAGAGG CTCTGCGGTT CTGGTCCCTG TGCTGAGCT CCAGGTGCCG CCAGACATTA      180
TACAACGTGA AGGCTGAGAT CTTTCCCCCT TCGGGAATGG AGTATTGCAG AACAGGCTCC      240
CTCTGCTCCC TGGAGGTTT GATCAGGAG CTCTCAGACC TCTTGAGGT GGATAAAGAT      300
GAAGCACTGA CTGAATCTGA TGAGCATTTT TCGACAAAGC TTATGTATGA AGTTGTCGAG      360

```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

GAATTCGGCC AAAGAGGCCT ACTCATCTTG GGTCCCAGCC AGGCCCCCCC AAAACCAAAG      60

```

| | |
|--|-----|
| CCCCTTCAAG TCCTGGGGTC CCAGCCTGTG CCCCCAGCTT CCTGCCACC CAGCCCCGAG | 120 |
| CATTCTCACA CAGAGAAAGA ACAAGCAAGG GCTCCAGGGG GACAGGATGG GGCAGGGCAT | 180 |
| ACAGTGGGGG GTGGGGGGGC AGCTGGGAGG AGGGAGGGAC AAAACAAAAC ATTTTCTTTT | 240 |
| GGGTTTTTTT TTTCTTTCTT TTTTCTCCCC TTTACTCTTT GGGTGGTGTT GCTTTTCCTT | 300 |
| TCCTTTTCCC TTTGAGATTT TTTTGTGTGTT GTTTCCTTTT TGTATTTTAC TGATATCACC | 360 |
| AGGATAGTTT ACTCTCCTTC TAGCTTTCTG CTTACCGCAC ACTGGATAAC ACACACATAC | 420 |
| ACACCCACAA AAATGCTCAT GAACCCAATC CGGAGAAGGT TCCAGCAGGT CCCCCACCCT | 480 |
| CCCCTCTCC TCCTACTTCT CCTCTTGACA GCGAGGACAG GAGGGGGACA AGGGGACACC | 540 |
| TGGGCAGACC CGCCGGCTCT CCCCCACCC CACCCCGTCG AG | 582 |

(2) INFORMATION FOR SEQ ID NO:155: --

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAAATAAAA CATTCTACAC CGTCTCCTAC CAAATATTCA | 60 |
| CTATCACCAA GTAAAAGTTA CAAGGTAAAC AGGAAAGAAT GGAATCATTT CATTGTGAAA | 120 |
| TTGTTTCTGT TCTAAGTGTT TTAAATGCTG TTTTGTATT TTTATTTTTT TTTTCAGTAT | 180 |
| TCTCCCGAAA CACCACCTCG ATGGACAGAA GATCGGAATT CTTTACTGAA TATGATTTGC | 240 |
| CAACAAGTAG AGGCCATGTC GAG | 263 |

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATTCTCAG CTCCAAGCAT TAGGTAAACC CACCAAGCAA | 60 |
| TCCTAGCCTG TGATGGCGTT TGACGTCAGC TGCTTCTTTT GGGTGGTGCT GTTTTCTGCC | 120 |
| GGCTGTAAAG TCATCACCTC CTGGGATCAG ATGTGCATTG AGAAAGAAGC CAACAAAACA | 180 |
| TATAACTGTG AAAATTTAGG TCTCAGTGAA ATCCCTGACA CTCTACCAA CACAACAGAA | 240 |
| TTTTTGGAAT TCAGCTTTAA TTTTTCCTT ACAATTCACA ATAGAACCTT CAGCAGACTC | 300 |
| ATGAATCTTA CCTTTTGGGA TTAACTAGG TGCCAGATTA ACTGGATACA TGAAGACACT | 360 |
| TTTCAAAGCC ATCATCAATT AAGCACACTT GTGTTANCTG GAAATCCCCT GATATTCATG | 420 |
| GCAGAAACAT CGCTTAATGG GCCCAAGTCA CTGAAGCATC TTTTCTTAAT CCANNCGGGA | 480 |
| ATATCCAATC TCGAGTTTAT TCCAGTGCAC AATCTGGAAG ACTTGGAAAG CTGTATCTT | 540 |
| GGAAGCAACG TCGAG | 555 |

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

| | |
|--|-----|
| GAATTCGCCC AAAGAGGCCT AGATGATGAT ATGTTTAAACC ACCAAGTTCC TTATTTGTGG | 60 |
| CTGATTACT GCCTTTGTCA TCCTCTTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT | 120 |
| GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT | 180 |
| CTTGCTCTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT | 240 |
| TTTACTGATT TAGTGAATAG ATGTTTGGTT ACAGNCCCTG CCCGATACCC CATTCCCTTT | 300 |
| AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTTATAATA GGGTCGAGGT TCTCCCTATA | 360 |
| GTGAGTCGTA TTAATTTCAG AGGAGTATTT AGAAGAGAAG CTGAAGCTGT CGAG | 414 |

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

| | |
|---|-----|
| GAATTCGGCC NAAGAGGCCT AAGCAGATGC TGATCTCATT ATGCTTGGCC TTGCCACACA | 60 |
| TGAACCGAAC TTTACCATT TTAGAGAAGA ATTCAAACCA AACAAGCCCA AACCATGTGG | 120 |
| TCTTTGTAAT CAGTTTGGAC ATGAGGTCAA AGATTGTGAA GGTTTGCCAA GAGAAAAGAA | 180 |
| GGGAAAGCAT GATGAACTTG CCGATAGTCT TCCTTGTGCA GAAGGAGAGT TTATCTTCCT | 240 |
| TCGGCTTAAT GTTCTTCGTG AGTATTTGGA AAGAGAACTC ACAATGGCCA GCCTACCATT | 300 |
| CACATTTGAT GTTGAGAGGA GCATTGATGA CTGGGTTTTT ATGTGCTTCT TTGTGGGAAA | 360 |
| TGACTTCCTC CCTCATTGTC CATCGTTAGA GATTAGGGAA AATGCAATTG ACCGTTTGGT | 420 |
| TAACATATAC AAAAATGTGG TACACAAAAC TGGGGGTTAC CTTACAGAAA GTGGTTATGT | 480 |
| CAATCTGCAA AGAGTACAGA TGATCATGTT AGCAGTTGGT GAAGTTGAGG ATAGCATTTT | 540 |
| TAAAAAGAGA AAGGATGATG AGGACAGTTT TAGAAGACGA CAGGGTCGAG | 590 |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGACGGGCCT CGGTCAGCAG CACGGGGTGC TCCTCGGGAG | 60 |
| CCACACGCAG CTCATTGTAG AAGGTGTGGT GCCAGATTTT CTCCATGTCC TCCAGTTGG | 120 |
| TGACGATGCC GTGCTCGATG GGGTACTTCA GGGTGAGGAT GCCTCTCTTG CTCTGGGCCT | 180 |
| CGTCGCCAC ATAGGAATCC TTCTGACCCA TGCCACCAT CACGCCCTGG TGCCTGGGGC | 240 |
| GCCCCAGAT GGAGGGGAAG ACGGCCCGGG GGGCATCGTC CCCCSCGAAG CCGGCCTTGC | 300 |
| ACATGCCGGA GCCGTTGTCTG AG | 322 |

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|--|-----|
| GGGTTGACAA ATATGGACTT CCTCTTTTCT GCCNNCCCAA ACCCATACAT CGGGATTTCCT | 60 |
| ATAATACCTT CGTTGGTCTC CCTAACATGT AGGTGGCGGA GGGGAGATAT ACAATAGANC | 120 |
| AAGATACCAG ACAAGACATA ATGGGCTAAA CAAGACTACA CCAATTACAC TGCCTCATTG | 180 |
| ATGGTGGTAC ATAACGAACT AATACTGTAG CCCTAGACTT GATAGCCATC ATCATATCGA | 240 |
| AGTTTCACTA CCCTTTTTC ATTTGCCATC TATTGAAGTA ATAATAGGCG CATGCAACTT | 300 |
| CTTTTCTTTT TTTTCTTTT CTCTCTCCCC CGTTGTTGTC TCACCATAG | 349 |

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTATAAGAG AGATCCAGCT TGCCTCCTCT TGAGCAGTCA | 60 |
| GCAACAGGGT CCCGTCCTTG ACACCTCAGC CTCTACAGGA CTGAGAAGAA GTAAAACCGT | 120 |
| TTGCTGGGGC TGGCCTGACT CACCAGCTGC CATGCAGCAG CCCTTCAATT ACCCATATCC | 180 |
| CCAGATCTAC TGGGTGGACA GCAGTGCCAG CTCTCCCTGG GCCCCTCCAG GCACAGTTCT | 240 |
| TCCCTGTCCA ACCTCTGTGC CCAGAAGGCC TGGTCAAAGG AGGCCACCAC CACCACCGCC | 300 |
| ACCGCCACCA CTACCACCTC CGCCGCCGCC GCCACCACTG CCTCCACTAC CGCTGCCACC | 360 |
| CCTGAAGAAG AGAGGAACC ACAGCACAGG CCTGTGTCTC CTTGTGATGT TTTTCATGGT | 420 |
| TCTGGTTGCC TTGGTAGGAT TGGCCTGGG GATGTTTCAG CTCTTCCACC TACAGAAGGA | 480 |
| GCTGGCAGAA CTCGAGAGT CTACCAGCCA GATGCACACA GCATCATCTT TGGAGAAGCA | 540 |
| AATAGGCCAC CCCAGTCCAC CCCCTGAAAA AAAGGAGCTG AGGAAAGTGG CCCATTTAAC | 600 |
| AGGCAAGTCC AACGTCGAGG TTCTCCCTAT AGTGAGTCGT ATTAATTCA GAGGAGTATT | 660 |
| TAGAAGAGAA GCTGAAGCTG TCGAGACA | 688 |

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATGATTTTG ATAGGAAGAA TGTCAGCCCA GGTTCCTATG | 60 |
| AACATGACCA TCACAGGTTG TATGATGACG TTTTACAGGA CTACGCCGGC TGTGCTGTTT | 120 |
| TGGCAGTGGA TTAACCACTC CTTCAATGCC GTCGTCAATT ACACCAACAA AAGTGTCCAG | 180 |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGNC | AAAGAGGCCT | ACCACCTTCT | CTGCCAGAAG | ATACCATTTC | AACTTTAACA | 60 |
| CAGCATGATC | GAAACATACA | ACCAAACCTC | TCCCCGATCT | GCGGCCACTG | GACTGCCCAT | 120 |
| CAGCATGAAA | ATTTTATGT | ATTACTTAC | TGTTTTTCTT | ATCACCCAGA | TGATTGGGTC | 180 |
| AGCACTTTT | GGTGTGTATC | TTCATAGAAG | GTTGGNCAAG | ATAGAAGATG | AAAGGRAWYY | 240 |
| TYMATKRARR | WTTTCKKWTY | MWKRAAACSR | WVMCARRRRW | KSMAMMMMRG | RRRRRRRWCC | 300 |
| YYWWCYTWC | YTKRWSYTKK | KRRGRRRW | AAARCCMRKT | TKGWRGGSYT | TKKKRWRGRW | 360 |
| TTWTWWKKTW | AAMMAMRRRG | RRRMSRCGRR | RARRAAAMMR | CYTTTGNAAT | NCNCCNAGGT | 420 |
| GATCAGAATC | CTCACATTGC | GGGACATGTC | ATAAGTGAGG | CCANCAGTAA | AACAACATCT | 480 |
| GTGTTACAGT | GGGCTGANAA | AGGATACTAC | ACCATGAGCA | ACAACTTGGT | AACCCTGGAA | 540 |
| AATGGGAAAC | AGCTGNCCGT | TAAAAGACAA | GGACTCTATT | ATATCTATGC | CCAAGTCGAG | 600 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| NCCTGTTTCA | TTAATTAAAT | TTCCCGAAAG | AACCTGAGTC | ATTTTCCNAC | ATGAGAATAC | 60 |
| TAGAAGAATG | ACCAAGACTT | GCGAGACGCG | ATTNCCGGG | TGGTGCGAAC | AATAGANCGA | 120 |
| CCATGACCTT | GAAGGTGAGA | CGCGCATAAC | CGCTAGAGTA | CTTTGAAGAG | GAAACANCAA | 180 |
| TAGGTTGCTA | CCAGTATAAA | TAGACAGGTA | CATACAACAC | TGGAAATGGT | TGTCTGTTTG | 240 |
| AGTACGCTTT | CAATTCATTT | GGGTGTGCAC | TTTATTATGT | TACAATATGG | AAGGGAACCT | 300 |
| TACACTTCTC | CTATGCACAT | ATATTAATTA | AAGTCCAATG | CTAGTAGAGA | AG | 352 |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AAAGAAGACA | AAGATGATAG | GCGGCACAGA | GATGACAAAA | 60 |
| GAGATTCCAA | GAAAGAGAAA | AAACACAGTA | GAAGCAGAAG | CAGAGAAAGG | AAACACAGAA | 120 |
| GTAGGAGTCG | AAGTAGAAAT | GCAGGGAAAC | GAAGTAGAAG | TAGAAGCAAA | GAGAAATCAA | 180 |
| GTAAACATAA | AAATGAAAGT | AAAGAAAAAT | CAAATAAACG | AAGTCGAAGT | GGCAGTCAAG | 240 |
| GAAGAAGCTG | CAGTGTTGAA | AAATCAAAAA | AACGGGAACA | TAGTCCCAGC | AAAGAAAAAT | 300 |
| CTAGAAAGCG | TAGTAGAAGC | AAAGAACGTT | CCCACAAACG | AGATCACAGT | GATAGTAAGG | 360 |
| ACCAATCAGA | CAAACATGAC | CGTCGAG | | | | 387 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGGAAGTTG GATGTTTTGA TTTTACTGTT TATAGATGTT | 60 |
| AGATTGTACA GATTGTCTG TATTTCTCAC CATATCTAAT GATACTTTTT TCATTAGATT | 120 |
| GGTCTTCAAG AACAGTATTA GTTATAATTA TTTTGGTTAT TCAGTATATA GTTAGCTCTT | 180 |
| ACAGTTTAGC TTTATTCACC ATATTTATAC TGTGGATTCA CAGCGAGAGG TAGAGGTTAT | 240 |
| TCCAGGAGAG TTGATGACCT TCATTTAAAG TCCAATAAAA ATCAGTAGTA GAAACATAAG | 300 |
| AAAACATCTT TGCAATATTT ACTTTTGTTC CTGTTTGCCG TAAATAGTAA CATTGTTTTT | 360 |
| TTTTATTTTG TGTGTGTTAT AAAACAGTTG CATTACAAT ATTATTGGCC TGAGATATTG | 420 |
| ATGATATTGT GATGGTATGA AAATGTGTAC ATTCCCTGTG CAACATCAGA TTTGCAGGAA | 480 |
| AAATGAAGCA CTTACTGAAA TCGCTGGTAC TCGTCGAG | 518 |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTTTTTCT | 60 |
| TTCTTTTTTC TCCCCTTTAC TCTTTGGGTG GTGTGCTTT TCCTTTCCTT TTCCCTTTGA | 120 |
| GATTTTTTTG TTGTTGTTTC CTTTTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT | 180 |
| CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATAACACACC CACAAAAATG | 240 |
| CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCCT CCTCCTCCTA | 300 |
| CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG | 360 |
| GCTCTCCCCC CACCCACCC CGGCACCCTC GAG | 393 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACGAAGTTAC AGAACTGAGA TTCTCGGGTC CCAGACACGC | 60 |
| ACCTATGTAC CTCCCCTGG TGTCCCTGCA AAGCCTGGCG CTTTGTACAT CAATAATAAA | 120 |
| AGTGGCAGGG CTGAGCAACA CCTCAGGAGT TACTCTGGAA GGATGGAGGA GTTATGTAAC | 180 |
| ACACGAGAGT CAGGAGCCCT GTGGAAGTGC TTTTATTAGC AGTAAGGCTG ATCGTACAAA | 240 |
| AAATTCTCAG AGCTTCATAG GACAAGGTAG TACAAGTATG GATGATACAG GACTGAGGAA | 300 |
| CGGGGGACGG CTCAAAAGAA ATCAACATCG TCTGGGGCAT CCAGGTCCCG ATATTCCACA | 360 |
| ATGGCCCTTG GGTCTCCAG AACCATCCTG TGAGGTGAGA GGTACAGGAT CAGACCTCGA | 420 |
| G | 421 |

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

TAGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA GAGTGCCCAT GGAAGACGGG      60
GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG TGCTCCTGAT CATCGTGATT      120
CTGGGGGTGC CCTTGATTAT CTTACCATC AAGGCCAACA GCGAGGCCTG CCGGGACGGC      180
CTTCGGGGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC TGCAACAAGA GCTGACCGAG      240
GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA CCTGCAACCA CACTGTGATG      300
GCCCTAATGG CTTCCCCTGG ATGCAGAGAA GGCCCAAGGA CAAAAGAAAG TGAAGNATC      360
TCGAG                                     365

```

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA      60
CATTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTT AAGGACAGAA      120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA      180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAAGTGCT ATTGCTCAGG      240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT      300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG      360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCCAGCTA CGCCGGACAA TAGAATGTTG      420
TCGGACCAAT TTATGTAACC AGTATTTGCA ACCCAGCTC GAG                                     463

```

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

GAATTCGGCC AAAGAGGCCT ACTTAGCTTC AAATCCCTAC TCCTTCACTT ACTAATTTTG      60
TGATTTGGAA ATATCCGCGC AAGATGTTGA CGTTGCAGAC TTGGCTAGTG CAAGCCTTGT      120
TTATTTTCTT CACCACTGAA TCTACAGGTG AACTTCTAGA TCCATGTGGT TATATCAGTC      180
CTGAATCTCC AGTTGTACAA CTTCACTTCTA ATTTCACTGC AGTTTGTGTG CTAAAGGAAA      240
AATGTATGGA TTATTTTCAT GTAAATGCTA ATTACATTGT CTGGAACACA AACCATTTTA      300
CTATTCCTAA GGAGCAATAT ACTATCATAA ACAGAACAGC ATCCACGCTC GAG                                     353

```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

GAATTCGGCC AAAGAGGCCT ACACTCGTCT CTTTTTTTCC CCATCTCATT GCTCCAAGAA      60
TTTTTTTCTT CTTACTCGCC AAAGTCAGGG TTCCCTCTGC CCGTCCCGTA TTAATATTTT      120
CACTTTTGGG ACTACTGGCC TTTTCTTTT AAAGGAATTC AAGCAGGATA CGTTTTTCTG      180
TTGGGCATTG ACTAGATTGT TTGCAAAAGT TTCGCATCAA AAACAACAAC AACAAAAAAC      240
CAAACAAC TCCTTGATCT ATACTTTGAG AATTGTTGAT TTCTTTTTT TATTCTGACT      300
TTTAAAAACA ACTTTTTTTT CCACTTTTTT AAAAAATGCA CTAAGTGTGT CTGAGCGCTT      360
TTCTGATCCT GCATCTGGTC ACGGTCGCGC TCAGCCTGTC TACCTGCAAC ACACTCGAG      419

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GAATTCGGCC AAAGAGGCCT ACCCAGAAAC ATCCAATTCT CAAACTGAAG CTCGCACTCT      60
CGCCTCCAGC ATGAAAGTCT CTGCCGCCCT TCTGTGCCTG CTGCTCATAG CAGCCACCTT      120
CATTCCCAA GGGCTCGCTC AGCCAGATGC AATCAATGCC CCAGTCACCT GCTGCTATAA      180
CTTCACCAAT AGGAAGATCT CAGTGCAGAG GCTCGCGAGC TATAGAAGAA TCACCAGCAG      240
CAAGTGTCCT AAAGAAGCTG TGATCTTCAA GACCATTGTG GCCAAGGAGA TCTGTGCTGA      300
CCCCAAGCAG AAGTGGGTTT AGGATTCCAT GGACCACCTG GACAAGCAAC CCAAATCCGA      360
G

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

TAGGACAAAA CAAAACATTT TCCCTTGGGG TTTTTTTTTT CTTTCTTTTT TCTCCCTTT      60
ACTCTTTGGG TGGTGTGCT TTTCTTTCC TTTCCCTTT GAGATTTTTT TGTTGTGTGTT      120
TCCTTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT      180
ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCCAATCCGG      240
AGAAGGTTCC AGCAGGTCCC CCACCCTCCC CTCCTCCTCC TACTTCTCCT CTTGACAGCG      300
AGGACAGGAG GGGGACAAGG GGACACCTGG GCAGACCCGC CGGCTCTCCC CCCACCCAC      360
CCCGGCAC

```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GAATTCGGCC AAAGAGGCCT AGACTAACCC AGAAACATCC AATTCTCAAA CTGAAGCTCG      60
CACTCTCGCC TCCAGCATGA AAGTCTCTGC CGCCCTTCTG TGCCTGCTGC TCATAGCAGC      120
CACCTTCATT CCCCAAGGGC TCGCTCAGCC AGATGCAATC AATGCCCCAG TCACCTGCTG      180
CTATAACTTC ACCAATAGGA AGATCTCAGT GCAGAGGCTC GCGAGCTATA GAAGAATCAC      240
CAGCAGCAAG TGTCCCAAAG AAGCTGTGAT CTTCAAGACC ATTGTGGCCA AGGAGATCTG      300
TGCTGACCCC AAGCAGAAGT GGGTTCAGGA TTCCATGGAC CACCTGGACA AGCAAACCCA      360
AACTCCGAAG ACTTCAACCG AG

```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

GAATTCGGCC AAAGAGGCCT AGTATAATAC TAAGTTGAGA TGATATCATT TACGGGGGAA      60
GGCGCTTTGT GAAGTAGGCC TTATTTCTCT TGTCCTTTCG TACAGGGAGG AATTTGAAGT      120
AGATAGAAAC CGACCTGGAT TACTCCGGTC TGAAGTCAGA TCACGTAGGA CTTTAATCGT      180
TGAACAAACG AACCTTTAAT AGCGGCTGCA CCATCGGGAT GTCCTGATCC AACATCGAGG      240
TCGTAAACCC TATTGTTGAT ATGGACTCTA GAATAGGATT GCGCTGTTAT CCCTAGGGTA      300
ACTTGTTCCG TTGGTCAAGT TATTGGATCA ATTGAGTATA GTAGTTCGCT TTGACTGGTG      360
AAGTCTTAGC ATGTACTGCT CGGAGGTTGG GTTCTGCTCC GAGGTCGCCC CAACCGAAAT      420
TTTTAATGCA GGTTTGGTAG TTTAGGACCT GTGGGTTTGT TAGGTACTGT TTGCATTAAT      480
AAATTAAAGC CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

TTNGGCCAAA GGGGCTTAGG ACAAACAAA ACATTTTCCT TTGGGTTTNA NTTTCTNTCT      60
TTNTTCTCCC ATTTANTMNT GGGGTGGTGT TGCTTTTCCT TTCCTTTTCC CTTGGAGATT      120
TTNINGTTGT NGTTTCCTTT TTGTATTNTA NTGATATCAC CAGGATAGTT TACTCTCNTT      180
NTAGCTNTGT GCTTACCGCA CANTGGATAA CACACACATA CACACCCACA AAAATGNTCA      240
TGAACCCAAT CCGGAGAAGG TTCCAGCAGG TCCCCACCCC TCCCCTCCTC CTCNTACTTC      300
TCCTCTNGAC AGCGAGGACA GGAGGGGGAC AAGGGGACAC CTGGGCAGAC CCGCCGGGCTN      360
TTCCCCCCCAC CCCACCCCGG CACCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | | | | | | |
|------------|------------|------------|---------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGCAAT | TCTCAAAC | TG AAGCTCGCAC | TCTCGCCTCC | AGCATGAAAG | 60 |
| TCTCTGCCGC | CCTTCTGTGC | CTGTGCTCA | TAGCAGCCAC | CTTCATTCCC | CAAGGGCTCG | 120 |
| CTCAGCCAGA | TGCAATCAAT | GCCCCAGTCA | CCTGCTGCTA | TAACTTCACC | AATAGGAAGA | 180 |
| TCTCAGTGCA | GAGGCTCGCG | AGCTATAGAA | GAATCACCAG | CAGCAAGTGT | CCCAAAGAAG | 240 |
| CTGTGATCTT | CAAGACCATT | GTGGCCAAGG | AGATCTGTGC | TGACCCCAAG | CAGAAGTGGG | 300 |
| TTCAGGATTC | CATGGACCAC | CTGGACAAGC | AAACCCAAAC | TCCGAAGACT | CTCGAG | 356 |

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACCGAGACTG | ACACACTGAA | CTCCACTTCC | TCCTCTTAAA | 60 |
| TTTATTTCTA | CTTAATAGCC | ACTCGTCTCT | TTTTTTCCCC | ATCTCATTGC | TCCAAGAATT | 120 |
| TTTTTCTTCT | TACTCGCCAA | AGTCAGGGTT | CCCTCTGCCC | GTCCCGTATT | AATATTTCCA | 180 |
| CTTTTGGAAC | TACTGGCCTT | TTCTTTTTAA | AGGAATTCAA | GCAGGATACG | TTTTTCTGTT | 240 |
| GGGCATTGAC | TAGATTGTTT | GCAAAAGTTT | CGCATCAAAA | ACAACAACAA | CAAAAAACCA | 300 |
| AACAACCTCT | CTTGATCTAT | ACTTTGAGAA | TTGTTGATTT | CTTTTTTTTA | TTCTGACTTT | 360 |
| TAAAAACAAC | TTTTTTTTCC | ACTTTTTTAA | AAAATGCACT | ACTGTGTGCT | GAGCGCTTTT | 420 |
| CTGATCCTGC | ATCTGGTCAC | GGTCGCGCTC | AGCCTGTCTA | CCTGCAGCAC | CACTCTCGAG | 480 |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGCCTA | ACACAGGAAA | CATTACAATT | GAACAATGCC | TCAGCTATAC | 60 |
| ATTTACATCA | GATTATTGGG | AGCCTATTTG | TTCATCATTT | CTCGTGTTC | AGGACAGAAT | 120 |
| CTGGATAGTA | TGCTTCATGG | CACTGGGATG | AAATCAGACT | CCGACCAGAA | AAAGTCAGAA | 180 |
| AATGGAGTAA | CCTTAGCACC | AGAGGATACC | TTGCCTTTT | TAAAGTGCTA | TTGCTCAGGG | 240 |
| CACTGTCCAG | ATGATGCTAT | TAATAACACA | TGCATAACTA | ATGGACATTG | CTTTGCCATC | 300 |
| ATAGAAGAAG | ATGACCAGGG | AGAAACCACA | TTAGCTTCAG | GGTGTATGAA | ATATGAAGGA | 360 |
| TCTGATTTTC | AGTGCAAAGA | TTCTCCAAAA | GCCAGCTAC | GCCGGACAAT | AGAATGTTGT | 420 |

CGGACCAATT TATGTAACCA GTATTTGCAA CCCACGCTCG AG

462

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AACACAGGAA | ACATTACAAT | TGAACAATGC | CTCAGCTATA | 60 |
| CATTTACATC | AGATTATTGG | GAGCCTATTT | GTTCATCATT | TCTCGTGTTT | AAGGACAGAA | 120 |
| TCTGGATAGT | ATGCTTCATG | GCACTGGGAT | GAAATCAGAC | TCCGACCAGA | AAAAGTCAGA | 180 |
| AAATGGAGTA | ACCTTAGCAC | CAGAGGATAC | CTTGCCTTTT | TTAAAGTGCT | ATTGCTCAGG | 240 |
| GCACTGTCCA | GATGATGCTA | TTAATAACAC | ATGCATAACT | AATGGACATT | GCTTTGCCAT | 300 |
| CATAGAAGAA | GATGACCAGG | GAGAAACCAC | ATTAGCTTCA | GGGTGTATGA | AATATGAAGG | 360 |
| ATCTGATTTT | CAGTGCAAAG | ATTCTCCAAA | AGCCCAGCTA | CGCCGGACAA | TAGAATGTTG | 420 |
| TCGGACCAAT | TTATGTAACC | AGTATTTGCA | ACCCACGCTC | GAG | | 463 |

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TACGAGAAGT | CCTGTAAGAC | GTAAATATTT | TTAAAATTCA | CTGAATTTT | GTCTTTCTCG | 60 |
| GTACCATAGA | ACACCACAGC | CAAGAGATCT | CGATCACTGC | TTATGATCTT | ACTGATGTAC | 120 |
| ACACTTTGGA | TACACTGGAT | GCTCATGTCA | AAAGGTGTCA | ACTCATCTTC | ATCTCCATCC | 180 |
| TCTTCCTCAC | CATCACCTTC | TTCTTCTCCT | TCCTCTTCTC | CCCCACCTTC | TTCTCTTCT | 240 |
| TCGTCTACCT | CATTGTCAGC | CTCCTGCTCC | CCATTTTCTC | CATTAGCATT | CCCGTTAGCA | 300 |
| GGGGCGTCTC | TTCCATTTTC | TGCCTCTTCC | ACAACTTCTC | TCTTCTCCTT | TAAGTCCTTG | 360 |
| GTGGTGAGT | | | | | | 369 |

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | NAAGANGCCT | ATGATCNTCT | TCTTTGAAGA | AACATGAAGT | TACACTATGT | 60 |
| TGCTGTGCTT | ACTCTANCCA | TCCTGATGTT | CCTGACATGG | CTTCACAAT | CACTGAGCTG | 120 |
| TNACAAAGCA | CTCTGTGCTA | NTGATGTGAG | CAAATGCCTC | ATTCAGGAGC | TCTGCCNGTG | 180 |
| CCGGCCGGGA | GAAGCAATTG | CTCCTGCTGT | NAGGAGTGCA | TGCTGTGTCT | TGGGGCCCTT | 240 |

TGGGACGANT GCTGTGACTG TGTTGGTATG TGTAATCCTC GAAATTATAG TGACACACCC 300
CACCTCNAG 309

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AATTCTGGTT TAAGATTCTA TCCATTTCTC ACTCTCAGAT 60
 CTGTTTGTTT CACCCTCTCC CCCTAAATAT TTGGATTTTA TATAGACCAG TAGGCTAAGG 120
 TAGGGAAGAC CACTGACAAG TATAAATTTA AGAGTTTACA AAACCAAGGA GGCCATCCAG 180
 CCCCTAGTTC TAAGCCATGT TCAGCACAGT GCCAACTTTG CCTTCCCTGG CTGTCCTTGC 240
 TTGCTTTCTG GTTGCTGTAA TTCTGAGGGG CAACCAGGCT TGCTGTAGAG AGGAGAGCCA 300
 GATGATGTGG AAGCCTAAGG CCACACCCCT CGAG 334

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 522 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TAACCGCCT TGAAAAGCCC TTCCTCTGGC TTGCTAGGAA GCTCATTGGA GACCCTAACT 60
 TGGAATTTGT TGCCATGCCT GCTCTCGCCC CACCAGAAGT TGTCATGGAC CCAGCTTTGG 120
 CAGCACAGTA TGAGCACGAC TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG 180
 ATGACCTGTG AGAATGAAGC TGGAGCCCAG CGTCAGAAGT CTAGTTTTAT AGGCAGCTGT 240
 CCTGTGATGT CAGCGGTGCA GCGTGTGTGC CACCTCATT TATCTAGCT AAGCGGAACA 300
 TGTGCTTCAT CTGTGGGATG CTGAAGGAGA TGAGTGGGCT TCGGAGTGAA TGTGGCAGTT 360
 TAAAAAATAA CTTTATTGTT TGGACCTGCA TATTTAGCTG TTTTGGAAAC CAGTTGATTC 420
 CTTGAGTTTC ATATATAAGA CTGCTGCAGT CACATCACA TATTCAGTGG TGAATCTTGT 480
 TTGTTACTGT CATTCCCAT CTTTTCGTT TAGAATCAGA AT 522

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTTTTTCT 60
 TTCTTTTTTC TCCCCTTAC TCTTTGGGTG GTGTTGCTTT TCCTTTCCTT TTCCCTTTGA 120
 GATTTTTTTG TTGTTGTTTC CTTTTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT 180

CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATAACACACC CACAAAAATG 240
 CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCTT CCTCCTCCTA 300
 CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG 360
 GCTCTCCCCC CACCCACCC CGGCACCCTC GAG 393

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC AAAGAGGCCT ATTCTAGGAC AAGAGCCAGG AAGAAACCAC CGGAAGGAAC 60
 CATCTCACTG TGTGTAAACA TGAATCCAA GCTGGCCGTG GCTCTCTGG CAGCCTTCCT 120
 GATTCTGCA GCTCTGTGTG AAGGTGCAGT TTTGCCAAGG AGTGCTAAAG AACTTAGATG 180
 TCAGTGCAATA AAGACATACT CCAAACCTT CCACCCCAAA TTTATCAAAG AACTGAGAGT 240
 GATTGAGAGT GGACCACT GCGCCAACAC AGAAATTATT GTAAAGCTTT CTGATGGAAG 300
 AGAGCTCTGT CTGGACCCA AGGAAACTG GGTGCAGAGG GAGCTCGAG 349

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC AAAGAGGCCT ACAAGAAAGC AAGCTCATCA TACTGGCTAG TGGTGGACCC 60
 CAAGCTTTAG TAAATATAAT GAGGACCTAT ACTTACGAAA AACTACTGTG GACCACAAGC 120
 AGAGTGCTGA AGGTGCTATC TGTCTGCTCT AGTAATAAGC CGGCTATTGT AGAAGCTGGT 180
 GGAATGCAAG CTTTAGGACT TCACCTGACA GATCCAAGTC AACGTCTTGT TCAGAAGTGT 240
 CTTTGGACTC TCAGGAATCT TTCAGATGCT GCAACTAAAC AGGAAGGGAT GGAAGGTCTC 300
 CTTGGGACTC TTGTTAGCT TCTGGGTTCA GATGATATAA ATGTGGTCAC CTGTGCAGAT 360
 CTCGAG 366

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 421 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TACAGCCACA TCTGGATACA CACACACACT CTTACATTCA TACCCAGAGA CTGGTGCACA 60
 GACACACACA CATCCCCCGT CCTGCCAATC AGTCCCAGGA ACACACAGGT CTCTATCAAC 120
 ACCCAGAAAT TCTGACACCA, CAAGCACAGG CCAACCTACA GCTAGAGGAT TAATGTCCAG 180

| | |
|---|-----|
| ACCCACAGGC TGGTGTGCGC ATGTCCTTCC ACGTGAATGT CACATGGGAG GACAGACTGC | 240 |
| ATGGATTTTT TTAATGACAC TATTTTATTT ATTTTTTGAG ACAGAGTCTC ACTCTGTCCG | 300 |
| CCAGGATGGA GTGCAGTGGC GTGATCTCGG CTCCTACAA CCTCCGCCTC CTGGGTTCAA | 360 |
| GCGATTCTCG TGCCTCAGCA TCCCAAGTAC CTGGGATTAC AGGCGCATGC CACCACGTCC | 420 |
| A | 421 |

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA | 60 |
| GAGTGCCCAT GGAAGACGGG GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG | 120 |
| TGCTCCTGAT CATCGTGATT CTGGGGGTGC CCTTGATTAT CTTCAACATC AAGGCCAACA | 180 |
| GCGAGGCCTG CCGGGACGGC CTTCGGGCAG TGATGGAGTG TCGCAATGTC ACCCATCTCC | 240 |
| TGCAACAAGA GCTGACCGAG GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA | 300 |
| CCTGCAACCA CACTGTGATG GCCCTAATGG CTTCCTGGA TGCAGAGAAG GCCCAAGGAC | 360 |
| AAAAGAAAAA GGAGGAGCTC GAG | 383 |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA | 60 |
| ACCTGGCCAT CAGCATCGCT CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG | 120 |
| TGACCAGCCT AACGGCCTGC CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA | 180 |
| ATACCAGCAG TTCACCCATC CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCAGC | 240 |
| TGCTCTTTGG CACTGTGGGG GTGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA | 300 |
| GCAAATACAA CATGAAGGTC CTCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT | 360 |
| ACACGTGTGC ACTCCACCAC TCTGGCCATT CCCCACCCAT CTCCTCCCAG AACGTCACCA | 420 |
| GTCTCGAG | 428 |

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

GAATTCGGCC AAAGAGGCCT AAAGAGCTCT CACTTCAGTC TTAATTACCC CACTGCTATT      60
CCCTGTGGAG AAAGCCGGCT AATTGTTTTG ATAAGGCTAT CTGCCATTGT AGAATACCTT      120
TCTCTAGTAG CTGAATGACA ATCAACTATA CGTTCCATAC TAAACATGCC AGAGATAGGA      180
CTTTTAGGCC TTGCTTTACA AAAGTGGTTT TTAACAGCTG ACATGAATAT TTCCCGTTTC      240
TATTTTCTTT TTTTCTTTT TTTTCTTTT TGAGACGGAG TCTCGCTCTA TCCCCACGC      300
TCGAG                                     305

```

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS: --
- (A) LENGTH: 0 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

GAATTCGGCC AAAGAGGCCT AANAGAAGAT GCCCCTGCTG ATCACTCTAA CCTGCTCCTC      60
TTCTGGCTCT CAGGCTACTC CATTGCCACT CAAATCACCG GTCCAACAAC AGTGAATGGC      120
TTGGAGCGGG GCTCCTTGAC CGTGCACTGT GTTTACAGAT CAGGCTGGGA GACCTACTTG      180
AAGTGGTGGT GTCGAGGAGC TATTTGGCGT GACTGCAAGA TCCTTGTTAA AACCAGTGGG      240
TCAGAGCAGG AGGTGAAGAG GGACCGGGTG TCCATCAAGG ACAATCAGAA AAACCGCAGC      300
TTCCTGTGTA CCATGGAGGA TCTCATGAAA ACTGATGCTG ACACTTACTG GTGTGGAATT      360
GAGAAAACCTG GAAATGACCT TGGGGTCACA GTTCAAGTGA CCATTGACCC AGCACCAGTC      420
ACCCAAGAAG AAAGTAGCAG CTCCCCAACT CTGACCGGCC ACCACTTGGG CAACAGGCAC      480
AAGTCCTGA AGCTCAGTGT CCTCCACCC CTCGAG                                     516

```

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

GAATTCGGCC AAAGAGGCCT AGCGCCCTGA AGACAGAATG TTCCATATCA GAGCTGTGAT      60
CTTGAGAGCC CTCTCCTTGG CTTTCTGCTG GAGTCTCCGA GGAGCTGGGG CCATCAAGGC      120
GGACCATGTG TCAACTTATG CCGCGTTTGT ACAGACGCAT AGACCAACAG GGGAGTTTAT      180
GTTTGAATTT GATGAAGATG AGATGTTCTA TGTGGATCTG GACAAGAAGG AGACCGTCTG      240
GCATCTGGAG GAGTTTGGCC AAGCCTTTTC CTTTGAGGCT CAGGGCGGGC TGGCTAACAT      300

```


TGCTATATTG AACAACT TGAATACCTT GATCCAGCGT TCCAACCACA CTCAGGCCAC 360
 CAACGATCCC CCTGAGGTGA CCGTGTTC CAAGGAGCCT GTGGAGCTGG GCCAGCCCAA 420
 CACCTCATC TGCCACATTG ACAAGTTCTT CCTACCAGTG CTCGAG 466

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TAGGCAGAAT GGGACTCCAA GCCTGCCTCC TAGGGCTCTT TGCCCTCATC CTCTCTGGCA 60
 AATGCAGTTA CAGCCCGGAG CCCGACCAGC GGAGGACGCT GCGCCAGGC TGGGTGTCCC 120
 TGGGCCGTGC GGACCCTGAG GAAGAGCTGA GTCTCACCTT TGCCCTGAGA CAGCAGAATG 180
 TGGATCGACG T 191

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 614 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT 60
 TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG 120
 GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT 180
 CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCGCCAGGG AAGGGGCTGG 240
 AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC 300
 GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA 360
 CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA 420
 CGTCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCAA 480
 CCTTTTCCC CCTCGTCTCN TGTGAGAATT CCGGTCGGA TACGAGCAGC GTGGCCGTTG 540
 GCTGCCTCGC ACAGGACTTC CTTCCCGACT CCATCACTTT CTCCTGGAAA TACAAGAACA 600
 ACTCTGAAC TCGAG 614

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 0 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

GAATTCGGCC AAAGAGGCCT ANACTGCAGC TCTTTTCATT TTGCCATCCT TTTCCAGCTC      60
CATGATGGTT CTGCAGGTTT CTGCGGCCCC CCGGACAGTG GCTCTGACGG CGTTACTGAT      120
GGTGCTGCTC ACATCTGTGG TCCAGGCGAG GGCCACTCCA GAGAATTACC TTTTCCAGGG      180
ACGGCAGGAA TGCTACGCGT TTAATGGGAC ACAGCGCTTC CTGGAGAGAT ACATCTACAA      240
CCGGGAGGAG TTCGCGCGCT TCGACAGCGA CGTGGGGGAG TTCCGGGCGG TGACGGAGCT      300
GGGGCGGCCT GCTGCGGAGT ACTGGAACAG CCAGAAGGAC ATCCTGGAGG AGAAGCGGGC      360
AGTGCCGGAC AGGATGCGCA GACACAATA CGAGCTGGGC GGGCCCATGA CCCTCACAGA      420
ACTCGAG                                         427
  
```

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

TAGGGATGTC AACATGATCT TTTCATATAT GCTGGCTATA GAAATTGGTC TCGGTGAAGT      60
AATGGTCTGT CTGTCAAGCA TGACATCCTT GCTGTGTGTA AGTTTTGTG GCTCTTCTGG      120
GATGTTGATC GTGACGTCTT GTCCGGGATT GAGAAGCTTC TGTGCTCTT CTGGGATGTC      180
ATTCATGATC TCTTCATATA TGCTGGCTAT AGAAATTGGG CTCTGTGAAG AAATAGTGTG      240
TCCCCAACCT TGGTACAGNC CCCCTGGGGA GGTACCTTT GAAGAACCAG AAGTTAGANC      300
TTGTGAAGAA GAAGAAAGTA GG                                         322
  
```

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

GAATTCGGCC AAAGAGGCCT ATGGAGTGTG AGAACAGCAA AAAATAATAA TTCAACCAGT      60
TGGTTATTAT GAACATCATT TTCATATTTT TAAAAATATG CTATATCATG GAATTC AATG      120
TAAAACCTCA AGAGATGCCA TCCTTGAGAG GGGCTGCACC AGCCTGTGCC CCAAGTTACC      180
CAGGATCACC CCCTACTTCT CCTGACGGCC CCCCGAGAAA GGCCTGCATT CTGGGCGACG      240
TGGCCTTCAG GGGCTCAACC CTTGGCCTCG AG                                         272
  
```

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

GAATTCGGCC AAAGAGGCCT AGCCAATTTG GTTTTCTAAG TATTTTCACG CCTTCTCCTC      60
GTGTCCGCGT CACTGCTCTG ATTCAGGCCC TTGTCAATTC TCATCTTTGC CATTTTAGTA      120
GTTTTTGGAT TGGGCTCCCG GCTGCTAATT TTGTCCCCTT TTCCACTATC TTCCACATG      180
TCACCGCAGT CATGTTTCTA AGGCAGAATC TCACTGTGCC CCACATCGTG TTGCTGGGCC      240
CTTGTCATGCC GTACCCTGGC CTTTGTGAAA TGCCCTTCAT CTGTGCTCTT CCCTCCACCT      300
GGAAATGTCCG TCTCTCTTTT TCTGCCAACC CACNCGACCC CTCCCTCCTN CAAGCCCGTG      360
AGTGTCCCN CCCTCCATGT CCTGTGGTGA CAGAGCTCGA G                                401

```

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

GAATTCGGCC AAAGAGGCCT ACGATATTTG CTGCGACCCG CAGGCGCTAT CCGCTGCCGG      60
GTTCTGGCGC GCCCTTTCAG TTCTGCTTGC TGTCGACACC GNTGCGTTAC CCGGAACCGC      120
CGGGCCGAAC AGCATGACGT CCGCTTTGGA GAACTACATC AACCAGACTG TTGCCGTTAT      180
TACATCAGAT GGGAGAATGA TTGTGGGAAC ACTGAAAGGT TTTGACCAGA CCATTAATT      240
GATTTTGGAT GAAAGCCATG AACGAGTATT CAGCTCTTCA CAGGGGGTAG AACAAAGTGGT      300
ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA      360
AACAGATTCT GCGCTTGATT AGGGGAACAC TCGAG                                395

```

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

GAATTCGGCC ANAGAGGCCT AAGAGCCAGT AAAAAAATTG TTAGAAAGCA GATACCATCA      60
AATTGGTTCT GGAAGTGTG AAATCAAAGT TGCACAACCC AAAGAGGTAT ATAGGCAGCA      120
ACAGCAACAA CAAAAAGGTG GAAGAGGTGC TGCAGCTGGT GGACGAGGTG GTACGAGGGG      180
TCGTGGCCGA GGTCAGGCC AAAACTGGAA CCAAGGATTT AATAACTATT ATGATCAAGG      240
ATATGGAAAT TACAATACTG CCTATGGTGG TGATCAAAAC TATAGTGGCT ATGGCGGATA      300
TGATTATACT GGGTATAACT ATGGGAAC TAAGATATGGA CAGGGATATG CAGACTACAG      360
TGGCCAACAG AGCACTTATG GCAAGGCATC TCGAG                                395

```

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTTTGGTCG TTCGTTGGGC GGTGCTGGTT TTTCGCTCGT | 60 |
| CGACTGCGGC TCTTCCTCGG GCAGCGGAAG CGGCGCGGCG GTCGAGAAG TGGCCTAAAA | 120 |
| CTTCGGCGTT GGGTGAAAGA AAATGGCCCG AACCAAGCAG ACTGCTCGTA AGTCCACCGG | 180 |
| TGGGAAAGCC CCCCGCCAAA CAGTTGNCCA CGGAAANCCG CCAGGAAAAG CGCTCCNTCT | 240 |
| ACCGGCGGGG TGAAGAAGCC TCATCGCTAC AGGCCCGGGA CCGTGGCGCT TCGAGAGATT | 300 |
| CGTCGTTATC AGAAGTCGAC CGAGCTGCTC ATCCGGAAGC TGCCCTTCCA GAGGTTGGTG | 360 |
| AGGGAGATCG CGCAGGATT CAAAACCGAC CTGAGGTTTC AGAGCGCAGC CATCGGTGCG | 420 |
| CTGCAGGAGG CTAGCGAAGC GTACCTGGTG GGTCTGTTG AAGATACCAA CCTGTGTGCC | 480 |
| ATCCACGCTA AGAGAGTCAC CATCATGCC AAAGACATCC AGTTGGCTCG CCGGATACGG | 540 |
| GGAGAGAGAG CTTTCTCGAG | 560 |

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTAGTTTAC TTTATCCCAT CCATTTATAT ATACATATAT | 60 |
| ATACACATAT ATGTGTGTTG TTTTGTGTTT GTTTTGTGTT GTTTTTTGA GATGGAGTCT | 120 |
| CGCTCTGTCG CCCAGGCTGG AGTGCACTGG TGTGATCTTG GCTCACTGCA ACCTCTGCCT | 180 |
| CCTGGGTTCA AGCAATTCTC CTGCCTCAGC TTCCCCGAGT AGCTGGGACT ACAGGTGTGC | 240 |
| GCCACCACGC CCGGCAAATT TTTTTTTTTT TTTTTTTTTT TTGATATTTT TAGCAGAGAT | 300 |
| GAGGTTTCCC CACGTTGGCC AGGCTGGTCT CGAACTCTTG ACCTCAGGTT ATCTGCCTGC | 360 |
| CTTGGCCTCC CAAAGTGTTG GGATTACAGG CGTGAGCCAC CGAACCTCGA G | 411 |

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 0 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACGTGGTGCG CGAGAGCGTA TCCCCAACTG GGACTTCCGA | 60 |
| GGCAACTTGA ACTCAGAACA CTACAGCGGA GACGCCACCC GGTGCTTGAG GCGGGACCGA | 120 |
| GGCGCACAGA GACCGAGGCG CATAGAGACC GAGGCACAGC CCAGCTGGGG CTAGGCCCGG | 180 |
| TGGGAAAGGA GAGCGTCGTT AATTTATTTC TTATTGCTCC TAATTAATAT TTATATGTAT | 240 |
| TTATGTACGT CCTCCTAGGT GATGGAGATG TGTACGTAAT ATTTATTTTA ACTTATGCAA | 300 |
| GGGTGTGAGA TGTCCCNCCT GCTGTAAATG CAGGTCTCTT GGTATTATT GAGCTTTGTG | 360 |
| GGACTGGTGG AAGCAGGACA CCTGGAAGTG CGCCAAAGTA GGCGACTCGA G | 411 |

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

| | |
|---|-----|
| GAATGCTGAT TGACCAGCTA AAAATCAAAT TACAAGATAG CAAAATAAC TTACAGATTA | 60 |
| ATGTATCTGA ACTTCAGACA TTGCAGTCTG AACATGNTAC ACTGCTAGAA AGGCACAACA | 120 |
| AGATGCTGCA GGAAACTGTG TCTCAGCTCG AG | 152 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACACNTCTGC ACCTCAACCA CAGACTACAC TTGCTGAACT | 60 |
| GGCTCCTGGG GCCATGAGGC TGCTACTGCC ACTGCTGCTG CTGCTGCTGG GAGCCTGGGC | 120 |
| CATCCCAGGG GGCCTCGGG ACAGGGCGCC ACTCACAGCC ACAGCCCCAC AACTGGATGA | 180 |
| TGAGGAGATG TACTCAGCCC ACATGCCCGC TCACCTGCGC TGTGATGCCT GCAGAGCTGT | 240 |
| GGCTTACCAG GTGAGTCCTT CACCACTGTC ACCCTGCCCT GCTCACACCC CTTCTCAAGC | 300 |
| CAGACCCCTC CACCCACCTC ACATTCCACC ACCGGCCTTT GATCCCCGCC TCGAG | 355 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AATTATAAGC ACTCAATAAT ACATTATCAA CTATTATTAC | 60 |
| TCAATTAAAA CTGGTAACT TTAATTGAAT TTGAACTGCC ACCTAGAATA GACAAGAAAA | 120 |
| TGAAACACAA TTCTGTATGG ATGTCAGAAA CATGAAATAT AAAATGTAAT AAATAAAAAAT | 180 |
| ATTAAAAACC CCTTAGCAAA TGTTAAGGAG CGTGTCAAAT GATTCCTGTG TTGAACCTTA | 240 |
| AGCATTTAGG TGGCTGGAGC CTTGAAAGTT ACCATCCCCC AATTTTCTGC TGTGTCATA | 300 |
| GGTTTTTTTC TATTGAGCAA TTCTTTCAGG TCGCTCCAC TCTGCTCTGC CTAAGGACA | 360 |
| ACTTCATATA GTGCATTCTG GTCTTAGACT CCACGATCTC GAG | 403 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGCGCTAAG CCTGGAGTGT GGGCACTGCA GTTTCAGAGG | 60 |
| CACCGATTAT GAGAATGTGC AGCTCCACAT GGGCTCCATT CATCTGAGT TCTGTGATGA | 120 |
| TATGGATGCC GGGGGCCTGG GCAAGCTCAT CTTTTACCAG AAGAGTGCAA AGCTCTTCCA | 180 |
| TTGCCATAAG TGCTTCTTCA CCAGCAAGCT GTACGCCAAT GTGTACTATC ACATCACGGC | 240 |
| CAGACACGCA GCCTCGGACA AGTGGAGTGA GCAGCCGAAA GAGCAGCCGA GCAAAGACAC | 300 |
| CCGTCGAG | 308 |

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACTGTGGTAA TTCTAGAGCT AATACATGCC GACGGGCGCT | 60 |
| GACCCCTTC GCGGGGGGGA TGCGTGCATT TATCAGATCA AAACCAACCC GGTCAGCCCC | 120 |
| TCTCCGCCCC CGGCCGGGGG GCGGGCGCCG GCGGCTTTGG TGA CTCTAGA TAACCTCGGG | 180 |
| CCGATCGCAC GCGGGGCGTG GCGGGCGACG CCCATTGCAA CGTCTGCCCT ATCAACTTTC | 240 |
| GATGGTAGTC GCCGTGCCTA CCATGGTGAC CACGGGTGAC GGGGAATCAG GGTTCGATTC | 300 |
| CGGAGAGGGA GCCTGAGAAA CGGTTACCAC ATCCAAGGAA GGCAGCAGGC GCGCACCTCG | 360 |
| AG | 362 |

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTCTTTTTT AACTAATCA CCATATTGTA AATTCAGGG | 60 |
| TTTTTTTTT GGTTAAGCT GACTCTTNGC TCTAATTTTG GAAAAAAGA AATGTGAAGG | 120 |
| GTCAACTCCA ACGTATGTGG TTATCTGTGA AAGTTGCACA GCGTGGCTTT TCCTAAACTG | 180 |
| GTGTTTTTCC CCCGCATTTG GTGGATTTTT TATTATTATT CAAAAACATA ACTGAGTTTT | 240 |
| TTAAAAGAGG AGAAAATTTA TATCTGGGTT AAGTGTATAT CATATATATG GGTACTTTGT | 300 |
| AATATCTAAA AACTTAGAAA CGGAAATGGA ATCCTGCTCA CAAAATCACT TTAAGATCTT | 360 |
| TTCAAGCTG TTAATTTTTC CTAGTGTGTG GGACACTGCA GACTTGTTCA GTGCTCCAC | 420 |
| GGCCTGTACG GACACGACTC TCGAG | 445 |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTTCACTCT CTCATTCTTA GCTTGAATTT GGAAATGACT | 60 |
| TTTGATGACC TAAAGATCCA GACTGTGAAG GACCAGCCTG ATGAGAAGTC AAATGGAAAA | 120 |
| AAAGCTAAAG GTCTTCAGTT TCTTTACTCT CCATGGTGGT GCCTGGCTGC TCGACTCTA | 180 |
| GGGGTCCTTT GCCTGGGATT AGTAGTGACC ATTATGGTGC TGGGCATGCA ATTATCCAG | 240 |
| GTGTCTGACC TCCTAACACA AGAGCAAGCA AACCTAACTC ACCAGAAAAA GAAACTGGAG | 300 |
| GGACAGATCT CAGCCCGGCA ACAAGCAGNA GAAGCTGTTT TCGAG | 345 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTGGGGAGT CTGCTATATT GTTGTTAAGG TCTCTTTGTT | 60 |
| AGTGGTGGTA GAAATTGGAG TATTCCTCT CATTGTGGT TGGTGGCTGG ATATCTGTTC | 120 |
| CTTGGAATG TTTGATGCTA CTCTGAAAGA TCGAGAACTG AGCTTTCAGT CGGCTCCAGG | 180 |
| TACTACCATG TTTCTGCATT GGCTAGTGGG AATGGTATAT GTCTTCTACT TTGCCTCCTT | 240 |
| CATTCTATTA CTGAGAGAGG TACTTCGACC TGGTGTCTG TGGTTTCTAA GGAATTTGAA | 300 |
| TGATCCAGAT TTCAATCCAG TACAGGAAAT GATCCATTG CCAATATATA GGCATCTCCG | 360 |
| AAGATTATT TTGTCAGTGA TTGTCTTGG CTCCATTGTC CTCCTGATGC TTTGGCTTCC | 420 |
| TATACGTATA ATTAAGAGTG TGCTGCCTAA TTTTCTTCCA TACAATGTCA TGCTCTACAG | 480 |
| TGATGCTCCA GTGAGTGAAC TGTCCTCGA G | 511 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```
GAATTCGGCC AAAGAGGCCT AGTTTATACC CACAGAATTT TTTCAATAAA TTAACCAAAC    60
CCTTTTCACT TTGCTTAAGA CTTTCAGTTT GTCCCATAC TCTTTAAGGT TAAGACCATC    120
TATAAAATCC TCTGAAGTGG ACAAATAC ATTCTCTTTA NCAAAATCCA TATTCCTATG    180
CCTTCTTATA ATCTTTTACC AAAACACCT TCCCTATACA CCTTGTACGT AAAACTGTTT    240
CTCCAGTGGT CTCAACTACA TATTATACTG TTAACCTTA CTCCTTTAG CATAGCTAGT    300
AGGCATGGCT CTCCATATGT TCCAGGCAT CTCGAG    336
```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```
GAATTCGGCC AAAGAGGCCT AGTGGGTAGA TACAGACCCT AACTTTGAGC TCTAAGATGA    60
AATTTGTTTA TAAATCCCTA GTTTCATTC AGTTTTTCA ATATTATCA AACACCTACT    120
GTGCCAGGCA TTGTTTAGGC ACAGGGGATA CAGCAGAAA ACTCGAG    167
```

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```
GAATTCGGCC AAAGAGGCCT ACACAGCCT TTGGCACAAT GAAGTGGGTA ACCTTTATTT    60
CCCTTCTTTT TCTCTTAGC TCGGCTTATT CCAGGGGTGT GTTCGTCGA GATGCACACA    120
AGAGTGAGGT TGCTCATCGG TTTAAAGATT TGGGAGAAGA AAATTTCAA GCCTTGGTGT    180
TGATTGCCTT TGCTCAGTAT CTTCAGCAGT GTCCATTGTA AGATCATGTA AAATTAGTGA    240
ATGAAGTAAC TGAATTGCA AAAACATGTG TTGCTGATGA GTCAGCTGAA AATTGTGACA    300
AATCACTTCA TACCCTTTT GGAGACAAAT TATGCACAGT TGCAACTCTT CGTGAAACCT    360
ATGGTGAAAC CCTCGAG    377
```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:


```

CTTGGGGGTG GGTTCNNMNT ANNAAAAATT ANAGNCGTTG GGGTTGGGG GGCNGAGAAG      60
GAANANAGAA CCCNCGNAA AATTTGAAAA CNGGGTNATT TATCCNGTNT TTTNAANGAG      120
AATCCCANNC CCGGAAAAAA AAAAAAANG AGGAANANAN AGATTGTAAG TTAAACAAA      180
AATCTATCTG TATAAGTCTT TACTTGTAAG AGTCTGTACA AGTCAGTNAG GTTTGGTCTC      240
TGCAGAGCCA GAACTTCAGA GAAGGTGATT TAATTGTAGG CNTCTTTGGT AGGCCTCTTT      300
GGCCGAATTC                                     310

```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

GAATTCGCCC AAGAGGCCTA AAGAGGCCTA GAAGCCAAAA AACTTTTCCC GAAAGGAGTC      60
TTCACCAAAG AGCTCCCATC TGGCAAGAAA TACCTCCGCT ACACACCCCA GCCTTAAGTC      120
TCTTGAGAA GCTGGTGCTG TGAGCCAGAG GATGTCAGCT GCCAATTGTG TTTTCCTGCA      180
GCAATTCCAT AAACACATCC TGGTGTATC ACAGCCAAGG TTTTAGGTT GCTATACCAA      240
TGGCTTATTA AATGAAAATG GCACTAAAAG TTTCTTGAGA TTCTTTATAC TCTCTGCCTT      300
CAGCAATCTC GAG                                     313

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

GAATTCGGCC AAAGAGGCCT AGGAACCACT GGCTTGGTGG ATTTTGCTAG ATTTTCTGA      60
TTTTTAACT CCTGAAAAAT ATCCCAGATA ACTGTATGG AGCTGGTAAC TATCTTCCTG      120
CTGGTGACCA TCAGCCTTTG TAGTTACTCT GCTACTGCCT TCCTCATCA CAAAGTGCCC      180
CTTCTGTTG ACAAGTTGGC ACCTTTACCT CTGGACAACA TTCTTCCCTT TATGGATCCA      240
TTAAAGCTTC TTCTGAAAAC TCTGGGCATT TNTGTTGGGC ACCTTGTTGA GGGGCTAAGG      300
AAGTGTGTAA ATGAGCTGGG ACCAGAGGCT TCTGAAGCTG TGGAGCAACC GCTCGAG      357

```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

GAATTCGGCC AAAGAGGCCT ATTAATGTG TCATTGGAAG CCATCCCTTT TTTTACATT      60
CATACAACAG AAACCAGAAA AGCAATACTG TTTCCATTTT AAGGATATGA TTAATATTAT      120

```

TAATATAATA ATGATGATGA TGATGATGAA AACTAAGGAT TTTTCAAGAG ATCTTTCTTT 180
 CCAAAACATT TCTGGACAGT ACCTCGAG 208

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNAAACCAAT AGTTTTTTAA AAGACAAGCT TGGGTGGGTG CANGNTGGGG ACAGTGCTGG 60
 TCTTTCACNG CAGCCCAGGC ACCCNTTGAG AGTCCCAGNG NGNGTNATGC CCCGAGCCAG 120
 TNAAGATGAA GGGAGAGCGG GTGCGGGGGC CATCNTCGGN GTCCAGCCC GGCCCATGGG 180
 ANTGAGTNGC GGCCTCTGCT TGTCGACNTG GGNGCTGGCT GTCCNATTTT ACTACTATTG 240
 ACCCTGAAGG CCATCGAGGA GGGCACGATG GAGGAGATCG AAGAGGAGGT CCGGCAGAAG 300
 AAATCATCAC GGAAGCGCAA GCGAGACTAG GCNTCTNTGG CCGAATTC 348

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCGGCC AAAGAGGCCT ACTTTCTCTG CAGATCATGG GGCCCTTGAT TGTGCTTGTG 60
 GGATTGTGTT TCTTCGTGGT TGCCCATGTT AAGAAGAGAA ACACGCTGAA TGCTGGCCAG 120
 GATGCCTCTG AGAGAGAAGA GGGACAGATC CAGATTATGG AGCCTGTCCA GGTCAGTGTA 180
 GGTGACTCGG TAATAATATT TCCACCCCTT CCACCACCTT ACTTTCCTGA ATCTTCAGCT 240
 TCTGCGGTCTG CTGAGAGTCC TGGAACTAAC AGTCTGCTTC CGAATGAAAA CCCCCCTTCA 300
 TATTACAGTA TTTTCACTA TGGCAGGACC CCAACTTCAG AGGGTGCAGC CTCTGAAAGA 360
 GATTGTGAAT CTATATATAC CATTCTGGG ACGAATTCAT CTTCTGAGGC CTCACACACT 420
 CCACATCTC CATCTGAATT GCCTCCTAGA TATGAAGAAA AAGAAAATGC TGCAGCACTC 480
 GAG 483

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC AAAGAGGCCT ACGATTACAA TCATGATTTC CAGAATGGAG AAGATGACGA 60
 TGATGATGAA GATATTGATT ATGTTTGCTC TTGGAATGAA CTACTGGTCT TGCTCAGGTT 120
 TCCCAGTGTA CGACTACGAT CCATCCTCCT TAAGGGATGC CCTCAGTGCC TCTGTGGTAA 180

| | |
|--|-----|
| AAGTGAATTC CCAGTCACTG AGTCCGTATC TGTTCGGGC ATTCAGAAGC TCATTAAAAA | 240 |
| GAGTTGAGGT CCTAGATGAG AACAACTGG TCATGAATTT AGAGTTCAGC ATCCGGGAGA | 300 |
| CAACATGCAG GAAGGATTCT GGAGAAGATC CCGTACATG TGCCTTCCAG AGGGACTACT | 360 |
| ATGTGTCCAC AGCTGTTTGC AGAAGCACCG TGAAGGTATC TGCCAGCAG GTGCAGGGCG | 420 |
| TGCATGCTCG CTGCAGCTGG TCCTCCTCCA CGTCTGAGT TTACAGCAGC GAAGAGATGA | 480 |
| TTTTTGGGGA CACTCTCGAG | 500 |

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGAGAAAGA AGATATTGAC ACCATCTACG GGCACCATGG | 60 |
| AACTGCTTCA AGTGACCATT CTTTTCTTC TGCCAGTAT TTGCAGCATT AACAGCACAG | 120 |
| GTGTTT TAGA GGCAGCTAAT AATTCATTG TTGTTACTAC AACAAAACCA TCTATAACAA | 180 |
| CACCAAACAC AGAATCATTA CAGAAAAATG TTGTCACACC AACAACTGGA ACAACTCCTA | 240 |
| AAGGAACAAT CACCAATGAA TTACTTAAAA TGTCTCTGAT GTCAACAGCT ACTTTTTTAA | 300 |
| CAAGTAAAGA TGAAGGATTG AAAGCCACAA CCACTGATGT CAGGAAGAAT GACTCCATCA | 360 |
| TTTCAAACGT AACAGTAACA AGTGTTACAC TTCCAAATGC TGTTCACAAC TTACAAAGTT | 420 |
| CCAAACCCAA GACTGAAACT CAGAGTTCAA TTAACAACAG AGAAATACCA GGTAGTGTTC | 480 |
| TACAACCAGA NCTCGAG | 497 |

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTTTTTTAA TATAAATTTT GTTGATATGG AATTAGGTAA | 60 |
| GTTTAAGTGT CTATGTGCAT ATGTTTTTAA TATAAGTTTT TTCTATTCAG TTTCACNGAT | 120 |
| CCAACTGGCA GTGGGTAAAT ATGGCGAGCT CGAG | 154 |

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGGAATGGTT TTNATTGGT CCTTATTTTT AACCTGCCCC | 60 |
| TGAGACTTAT ATGCTTGTTT ATACCATGTA CGTAGTGTGT GATTGTATGT GTTTGTATT | 120 |

| | |
|---|-----|
| GTCCACATGT CCCAAAACAT GGGCTGTTAC TCCCTTTTCT ATCTTGTTTT CCTTATTCCC | 180 |
| ACCCTTCTCT TTCCACCCAG GTATCTGGAC AGGAAGACTT CTACCATCAG CTTTACCAGA | 240 |
| GGAAGCTGCA GGCCCCACTG TGGCCCACT CCCTGGGCAT CACTGATTGC TATCAGTATG | 300 |
| TCACCTCCTG TCACCCCAAG AGATCAGAGA GACGCAAGTA TGGCCGAGAC TTCCTGCTAC | 360 |
| GTTCCCGCTT CTGCAGCATC GCTCGAG | 387 |

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs..
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACCTTCATTT GTTAGATTAT ATCAGTACCC CAACTTTGCT | 60 |
| GGACCTCATG CAGCTTTAGC TAATAAAAGT TTCTTTAAGG CAGATAAAGT TACAATGCTG | 120 |
| TGGAATAAAA AAGGTATGTT AAGTATATTT TATCCCTCCC TTTGTTTATC AGTTGTTAAT | 180 |
| TTAGGCTATA TTCCTATGTG TATAACAGAA GAATCAATGC CCATTTGTGT TTAAATCTA | 240 |
| ATTAAAGTTT TTAAGTTTAT AGCTACTGCT GTGTTGGTAA TAGCTAGCAC AGATGTTGAC | 300 |
| AAGACAGGAG CTTCTACTA TGGAGAACGA CTCGAG | 336 |

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGGACATTG GTTGAATTGG CATGACTAGA ATAGTTGGGA | 60 |
| ATGTTTGGGA ATGGGGAGAG ATTGCTAATG GGATGTCTGC CAGGGGCAAT ACTGAAATCT | 120 |
| GCTGGTTGGT AAAGGTAGTG CCTGAGCCCA GTGCTAACCA TAGTAGTTGG AAAATTGTGT | 180 |
| ACGTTGGCTG TGAATCCTT ATGCGAATAT TTGTCCAATC CATCTAAATT TCTCTCTGCA | 240 |
| GCATTTTAA AAAGACATAT AGCTGAAATT TTGTCAGTCC TAAAAATATT TTGTATTTCT | 300 |
| CTGCCCAGAT TTGCATTTGG GTAGATCGTG CTGTAGAAGA TATATCTTGC TTAAAGATAG | 360 |
| CTGCCACTGA TTAGTTTATT TTAGTCTATT TTAATCAACT TATTGCCTTG TAATCTTTCC | 420 |
| TTTTTCATTC TCTAAATTC TGAAATTCTA TCTTTCATGT TCCCCAGGAA AACTCTGAG | 479 |

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

| | |
|---|----|
| GAATTCGGCC TTCATGGCCT ACATGATGTC AACAACCGTG GCTCACAAGA TGAAAGAGCA | 60 |
|---|----|

| | |
|---|-----|
| CATTCCTTTT TTTGAAGATA TGTGTAAAGG CATTAAAGCT GGTGACACCT GTGAGAAGCT | 120 |
| GGTGGGATAT TCTNCCGTGT ATAGAGTCTG TTTTGGGAATG GCTTGTCTTCT TCTTTATCTT | 190 |
| CTGTCTACTG ACCTTGAAAA TCAACAACAG CAAAAGTTGT AGAGCTCATA TTCACAATGG | 240 |
| CTTTTGGTTT CTTTAACTT CTGCTGTTGG GGGCCATGTG CTCAGGAGCT TTCTTCATTG | 300 |
| CAGATCAGGA CACCTTTCTG AACGCCGGGC AGCTCGAG | 338 |

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

| | |
|---|-----|
| GAATTCGGCT TCATGGCCTA CCCCGAACCA CTCAGGGTCC TGTGGACAGC TCACCTAGTG | 60 |
| GCAATGGCTC CAGGCTCCCG GACGTCCCTG CTCCTGGCTT TTGCCCTGCT CTGCCTGCCC | 120 |
| TGGCTTCAAG AGGCTGGTGC CGTCCAAACC GTTCCGTTAT CCAGGCTTTT TGACCACGCT | 180 |
| ATGCTCCAAG CCCATCGCGC GCACCAGCTG GCCATTGACA CCTACCAGGA GTTTGAAGAA | 240 |
| ACCTATATCC CAAAGGACCA GAAGTATTCA TTCCTGCATG ACTCCCAGAC CTCCTTCTGC | 300 |
| TTCTCAGACT CTATTCCGAC ACCCTCCAAC ATGGAGGAAA CGCAACAGAA ATCCAATCTC | 360 |
| GAG | 363 |

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

| | |
|---|-----|
| GAATTCGACC TTCATGACCT AGCGTAAGAG GAGAGAGACA CATTGAGCAG CCAAAGGACT | 60 |
| CGGTGGAAAG AGCAGAACAC CATAGACAAT ATGTCGCTCT TGGGACCCAA GGTGCTGCTG | 120 |
| TTTCTTGCTG AATTCATCAT CACCTCTGAC TGGATACCCC TGGGGGTCAA TAGTCAATCG | 180 |
| AGGAGACGAT GTGACTCAAG CGACTCCAGA AACATTGACA GAAGATCCTA ATCTGGTGAA | 240 |
| TGATCCCGCT ACAGATGAAA CAGTTTGGC TGTTTGGCT GATATTGCAC CTCCACAGA | 300 |
| TGACTTGAG TGCTGGGATG AGAAATTAC CTGCAGCAAG GCTCTACTCT GTGCATCGGC | 360 |
| CGGTTAAACT CGAG | 374 |

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

| | |
|---|----|
| GAATTCGGCC TTCTGGCCTA GGGTGGGATA AGTGATTNGT ATTTGTTTNG GTTTAAAAAC | 60 |
|---|----|

| | |
|---|-----|
| ATACTTTGAT AGAAATTAGT CCCTTCTCTT TCCTTCTCTT CTACAATGTC AATTGCCCAT | 120 |
| TTCATTGTG TGTTCCTAAC ATTTCTTTT GTTAAGAAAT GTTGGGGCTA TAATTTT | 180 |
| GAAATCACTG AAGGAGGGG AAAAATAATT TTAACAACCT GTGTTGAAAC CTTCCATAGC | 240 |
| TTAATTGACT GGAATAATCC TGCCATCATT AATAAGATGT ACAAGGTGTA CTTGGAGAT | 300 |
| ATACCACTGA AGACANAGA GGAGCTCGAG | 330 |

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

| | |
|--|-----|
| TTACACCCTG GAAACCAAGC ATAAGCACAC TTTAGCAGA TGACTTAGAA ATTAAGTTGT | 60 |
| TTGAATCNAG TGAACACACT GAAGACTCCA ACAACCCACA ACTCGAG | 107 |

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCCGTCGTT AGTGAAGGGG AAATGGGTTG TATCCTAAGG | 60 |
| GATTGGGAAA TGGGAAGTGA ATTCAGGAG ATTGTGGAGT ACAAGGTATG TGTTCACGTT | 120 |
| AGGTGATGAG CAGTGTGAGG ATAGTGAAGT GTGGACAGTG TCAAATGCTT TTCTGTAGGG | 180 |
| AAGATGAAGT TAGCATCATC TTATCACTTT TGACATGCTT TTGTGGTTTA TTTTGTGTTG | 240 |
| TATTTCTGTT TTAGTAGAAA TGAAAGGCTT TGCCAAAGCC TCTGTACTAT GCTTCAGAGT | 300 |
| AGGACACACA ATTCTGAGAT TGCTGTAGAG GGCTCGAG | 338 |

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTCAGAGCC AAAGGAAAGC TGAAAAATG AAGACATTAG | 60 |
| CAGGACTTGT TCTGGGACTT GTCATCTTTG ATGCTGCTGT GACTNCCCCA ACTCTAGAGT | 120 |
| CCATCAACTA TGAATCAGAA ACCTATGATG CCACCTTAGA AGACCTGGAT AATTGTGACA | 180 |
| ACTATGAAAA CATACCTGTT GATAAAGTTG AGATTGAAAT AGCCACAGTG ATGCCTTCAG | 240 |
| GGAACAGAGA GCTCCTCACT CCACCCACAG AGCCTGAGAA GGCCAGGAA GAGGAAGAGG | 300 |
| AGGAGGAATC TACTCCAGG CTGATTGATG GCTCTTCTCC CCAGGAGCCT GAATTCACAG | 360 |
| GGGTTCTGGG GCCACACACA AATGAAGACT TTCCAACCTG TCTTTTGTGT ACTTGATAA | 420 |

GTACCACCGT GTACTGTGAT GCCCATGAAC TCGAG

455

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

GAATTCGGCC AAAGAGGCCT AGGGGGGTGA TGGTGTGTC TTTGGACTGT GTGCCTACAG      60
GGTTTTTTTG TTTTGTGTTG TTTTACTGTA ATGGAAATGG GTTTAGGATA AGCATACTCA      120
AAGCTCCACA GTGTATCCTT GAGCTTTCCA TGACTGCCAG TTACACACTG GAGAGGGTTA      180
AATGAATCTT AAAGTGTTCA TGATTACTAT TAAATATCAT TATAAAACAA ATTCTTTCGG      240
GGGGGCACAA ATGCTAATAT GTACAAGAAA ATCTTAGACT TGAAAATATC TTAAAAATGA      300
AAATAACTTT TTTTTCAGC TGACTGTATT CACAACCTTG ATGGATGTGA CCAAAGGTCA      360
ATTTGAAAGT CACCTTCGAG ATTGCCCAGA CCCTTGATA GGCTGGTGAG CACACGTTGG      420
CCAGCCTCGA G                                     431

```

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

GAATTCGGCC TTCATGGCCT ACTACAATCC GTGGCTGCTC NTTCTGCTT ACTTTACTCT      60
CCCCTGAAG CAGGTTANCG TTGAAGGTGG TATGGAAAAG CCTGCATGCC TGTTCAATTC      120
TTTTGTTTCT TCTCCTTCCC CCTCCCCCTA CCTCCTTCCC CTACCTCCTT CGCTCGAG      178

```

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

GAATTCGGCC TTCATGGCCT ACATCAACAG CATCAAGTCC AGACTAAGCA AAAGTGGGCA      60
CATACAAACT CTGCTTAGAG CATTTGAAGC TCGTGATCGA AACATACAAG AAAGCAACTT      120
TGATAGAGTC AATTTCTGGT CTATGGTTAA TTTAGTGGTC ATGGTGGTGG TGTCAGCCAT      180
TCAAGTTTAT ATGCTGAAGA GTCTGTTTGA AGATAAGAGG AAAAGTCTCG AG          232

```

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAAAAACCTA ACTT ¹ CGGCAG AAAACAAGAT GAGATTGGCA | 60 |
| TGGCTTTTATT TGTTTTTTTT GTTTTGT TTTT GGT TTTT TTTT TTTT TTTT TTTT TTTT | 120 |
| GATTTAAAAA CTGGAACGGT GAAGGTGACA GCAGTCGGTT GGAGCGAGCA TCCCCCAAAG | 180 |
| TTCCTGGGGC TCGAG | 195 |

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACATATCCTC AAATGGTAGT CATCTGGGGA CTAAGCAACA | 60 |
| GGTGTTCCTAA GGAACCTAAT CTCTGGGTTT GAAAAGTTCA CAGTCTGTGC AGTCTATTCTG | 120 |
| TCCTCCATAT AACCGAGCAG TGCTCTGGA TAGCCCTGTT TCTGTTGGCT CAAGTCTCTCC | 180 |
| AGTAAAAAAT ATCAGTGCTT TCCCCTGTT ACCAAAGCAA CCCATGTTGG GTGGGAATCC | 240 |
| AAGAATGATG GATAGTCAGG AAAATTATGG CTCAAGTATG GGAGACTGGG GCTTACCAAA | 300 |
| CTCAAAGGCC GGCAGCGGAC TCGAG | 325 |

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGAGGCTAT TTAGGATT CAATGAGAAG CAAAATCATA | 60 |
| TCCAAATCAA AGTAAAGGTC ATCGGTGGCC AATGAAGAGC GGAGAAAACG GAGGCGGGAG | 120 |
| AACAGACGCG ACCTCAAGAC AGAAGAATGG AAGACGCAAC TTTCAAGAAA AGAGGAACTG | 180 |
| AAACGAAAAG AGAGGCACAG TCCAAATGAG GAAGAGAACA AGGAGCCTTC AGTCTCCTGG | 240 |
| GGGCCAGGGA GCCTCGCCAC GCGGTACAG GTACACGGGG ACATTTAGAG GCCATCTCCT | 300 |
| TTAAAGCCAG ACATTCTTCT TACTGGAATC TAGGCCATGA AG | 342 |

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

GAATTCGGCC TTCATGGCCT AGGCGGGTGA CATTAGCCG GCGGTTCCGG GGGACGGANT      60
CTCCATTCCA GAACCATGGC CCAATTTGTC CGTAACCTTG TGGAGAAGAC CCCGGCGCTG      120
GTGAACGCTG CTGTGACTTA CTCGAAGCCT CGATTGGCCA CATTTTGGTA CTACGCCAAG      180
GTTGAGCTGG TTCCTCCCAC CCCTGCTGAG ATCCCTAGAG CTATTAGAG CCTGAAAAAA      240
ATAGTCAATA GTGCTCAGAC TGGTAGCTTC AAACAGCTCA CAGTTAAGGA AGCTGTGCTG      300
AATGGTTTGG TGGCCACTGA GGTGTTGATG TGGTTTTATG TCGGAGAGAT TATAGGCAGG      360
CGGGTCACTC GAG                                         373

```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

GAATTCGGCC TTCATGGCCT AAACAGGACC TGCTTCACAC CACCAAGCAT CAGGATGTGT      60
TGCTCAGTGA GCAGACCCGA CTCCAGAAGG ACATCAGTGA ATGGGCAAAT AGGTTTGAAG      120
ACTGTCAGAA AGNAGAGGAG ACAAACAAC AACCACTTCA AGTGCTTCAG AATGAGATTG      180
AAGAAAACAA GCTCAAACTA GTCCAACAAG GAAATGATGT TTCAGAGACT CCAGAAAGAG      240
AGAGAAAGTG AAGAAAGCAA ATTAGAAACC AGTAAAGTGA CACTGAAGGA GCAACAGCAC      300
CAGCTGGAAA AGGAATTAAC AGACCAAGAA AGCAAAGTGG ACCAAGTGCT CTNCAAAGGT      360
GCTGGCAGCT GAAGAGCGTG TTAGGACTCT GCAGGAAGAG GAGAGGTGGT GTGAGAGCCT      420
GGAGAAGACA CTCTCCCAA CTAACCGGCA GCTTTCAGAA AGGGAGCAGC AATTGGTGGA      480
GAAATCAGGT GAGCTGTTGG CCCTCACGCT CGAG                                         514

```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

GAATTCGGCC TTCTGGCCTA GGACTCTATA GAACCCACTG CCTCCTGATG AAGTCCCTAC      60
TGTTCAACCCT TGCAGTTTTT ATGCTCCTGG CCCAATTGGT CTCAGGTAAT TGGTATGTGA      120
AAAAGTGTCT AAACGACGTT GGAATTTGCA AGAAGAAGTG CAAACCTGAA GAGATGCATG      180
TAAAGAATGG TTGGGCAATG TCGGGCAAAC AAAGGGACTG CTGTGTTCCA GCTGACAGAC      240
GTGCTAATTA TCCTGTTTTC TGTGTCCAGA CAAAGACTAC AAGAATTTCA ACAGTAACAG      300
CAACAACAGC AACAACAAC TTAGATGATG CTACTGCTTC GATGTCTTCG ATGGCTCCTA      360
CCGTTTCTC CCACTGGTTG AACATTCCAG CCTCTGTCTC CTGCTCTAGG ATCCCCACGC      420
TCGAG                                         425

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```
GAATTCGGCC TTCATGGCCT ACAAAGGAA AGAAGAAAAA GGGCCAAAAG CCAAAATGAA    60
ACTGATGGTA CTGTTTTCA CCATTGGGCT AACTTTGCTG CTAGGAGTTC AAGCCATGCC    120
TGCAAATCGC CTCTCTTGCT ACAGAAAGAT ACTAAAAGAT CACAACTGTC ACAACCTTCC    180
GGAAGGAGTA GCTGACCTGA CACAGATTGA TGTCAATGTC CAGGATCATT TCTGGGATGG    240
GAAGGGATGT GAGATGATCT GTTACTGCAA CTTACGCGAA TTGCTCTGCT GCCCAAAGA    300
CGTTTTCTTT GGACCAAAGA TCTCTTCGT GATTCTTGC AACAATCTCG AG            352
```

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
GAATTCGGCC TTCATGGCCT ACACAATGGT GTTCGCATT TGAAGGTCT TTCTGATCCT    60
AAGTCGCCTT GCAGGTCAGG TTAGTGTGGT GCAAGTGACC ATCCCAGACG GTTTCGTGAA    120
CGTGACTGTT GGATCTAATG TCACTCTCAT CTGCATCTAC ACCACCACTG TGGCCTCCCG    180
AGAACAGCTT TCCATCCAGT GGTCTTTCTT CCATAAGAAG GAGATGGAGC CAATTTCTAT    240
TTACTTTTCT CAAGGTGGAC AAGCTGTAGC CATCGGGCAA TTAAAGATC GAATTACAGG    300
GTCCAACGAT CCAGGTAATG CATCTATCAC TATCTCGCAT ATGCAGCCAG CAGACAGTGG    360
AATTACATC TCGATGTTA ACAACCCCCC AAGACTCGAG                                400
```

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```
GAATTCGGCC AAAGAGGCCT AAGAGATTCA GGACCTGCAG AGTCGCCAGA AGCATGAAAT    60
TGAATCTTTG TATACTAAAC TGGGCAAGGT TCCCCCTGCT GTCAATTATC CCCCAGCTGC    120
TCCTCTGTCT GGGAGAAGAA GGAGACCCAC TAAAGCAAA GGCAGCAAGT CTAGTCGCAG    180
CAGCTCATTG GGCAATAAAA GCCCACAGCT TTCAGGCAAC CTGTCTGGTC AGAGTGGAAAC    240
TTCAGTCTTA CACCCCAAC AGACCCTCCA CAGTCGAG                                278
```

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTTTATATA CTTTCTCTGA AGGATCCTAA TGATAGTTAA | 60 |
| CCATTTCTCA TTTTATTTT GCTGGATTGT TTTCTGTTTT TTGCTTCAGC ATTCTTGCTT | 120 |
| TTGCTGTGCT TACTTTTGA GTTTTGATTC CCTGTGTCAC TGTTTTCTTT CGCATCCACC | 180 |
| ACTCGAG | 187 |

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTTCTCTGG AAAGGTCAC TATTGTTGT TTTTTCGAGA | 60 |
| CAGGGTCTCG CTCTTCACCC AGACTGCAAT GCAGTGGCAC AATCATAGCT TATTGCAACC | 120 |
| TCAAACCTCGT GGGCTCAAGC AATGCTCGCT CCTCCCAAGT AGCTAGGACC ACAGGCATGC | 180 |
| ACCACGATGC CCACCTAGTT TTTTGTATTT TCTATAGAGA NGGGGGTCTC ACTGTGTTTC | 240 |
| TCAAGCTGGT CACATACTCT TGGCCTCAGG CAGTTCTCCC ACATCAGANT CTCAAAGCAC | 300 |
| TGGGCTTACA GCTGNGAGCC NGNCCTTTT AAAAAAAAAA AAAAAATCAA AACAAAAACA | 360 |
| AACAAGATTA TGTCTTTCCC ACGCATCTCG AG | 392 |

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTTGGGAAT TAACATCTTC GATAAATCCC AGAAGTCTTT | 60 |
| AAGTGACAGT AGAGAGCCTA CAGAGAAGCC TGGGAAAGCA GAAAAATCTA AGAGCCCAGA | 120 |
| AAAAGTGTCA TCGTTCTCAA ACTCCTCCTC CAACAAGGAA TCAAAAGTAA ACAATGAGAA | 180 |
| GTTTCGTACT AAGAGCCCCA AGCCTGCCGA AAGCCCCCAG TCAGCCACTA AGCAGTTGGA | 240 |
| TCAGCCCCACT GCTGCTTATG AGTATTATGA TGCTGGCAAT CACTGGTGCA AAGACTGCAA | 300 |
| CACCATCTGT GGGACTCGAG | 320 |

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATCAGAAGC TTTTCAAAT TCCGTCTTCA AGAAGAAACA | 60 |
| CCCGTGGAGG AAGAAGACAT TATACAAAAC AAATTTAGAA ACTGGGATCA TGAGTGGAAG | 120 |
| AACAAAGGCA AGAAGGGCTG CCATGTTTTT TAGACGTTGC TCTGAAGACG CCAGCGGTAG | 180 |
| CGCCAGTGGC AATGCTTTGT TATCAGAGGA CGAAAATCCT GATGCGAATG GGGTAACTCG | 240 |
| ATCATGGAAG ATTATTCTAA GTACAATGCT TACACTGACT TTTCTTCTTG TAGGACTCCT | 300 |
| AAATCATCAG TGGCTTAAAG AAACAGATGT TCCTCAGAAA TCCAGACAAT TATATGCCAT | 360 |
| GCTCGAG | 367 |

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AAAGTAGTTC TGTTATAAAA AGCCAGGAAT CCTAAAACCA | 60 |
| AAATATTAGA ACGAAAACAG AAACATGGCT CACTATATTA CATTTCTCTG CATGGTTTTG | 120 |
| GTGCTGCTTC TTCAGAATTC TGTGTTAGCT GAAGATGGGG AAGTAAGATC AAGTTGTCGT | 180 |
| ACTGCTCCGA CAGATTTAGT TTTCATCTTA GATGGCTCTA ATTGTGTTGG CCCAGAAAAC | 240 |
| TTTGAAATAG TGA AAAAGTG GCTTGTCAT ATCACA AAAA ACTTTGACAT AGGGCCGAAG | 300 |
| TTTATTC AAG TTGGAGTGGT TCAATATAGT GACTACCTG TGCTGGAGAT TCCTCTCGGA | 360 |
| AGCTATGATT CAGGAGAACA TTTGACGGCA GCACTGGAAT CCATACTCTA CTTAGGAGGA | 420 |
| AACACAAAGA CAGGGAAGAA CCTCGAG | 447 |

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAATGAAGCA AAATTCCATA CATCATTTTG AAAATAGTGT | 60 |
| TTCTTTCCCT GATAGGCCTG TTCTGCATCA TTCTTTTAGC TTCCTTCTGC CCTGTTTATC | 120 |
| ACTTGGTCCC ACTTTTATAT TTTTCCTCTT CGGTCCAGAA TTTCTTATT AGTTTCTTGT | 180 |
| ATTTTGCTTA CTCCCTCCCT TCTCCATGAT TCAGCCTAGT CTTCCGTCC TCTGTGGAAT | 240 |
| TGGGTGTGCC TTCCTCTGGG CCACCTCGTC TTTTGCTGCT GTTAGCCCTC CCGCCTGCGC | 300 |
| ACCTGCCACT TCACCCTCGC CTGTGGTCCA CTTACGTTCC ACTCAGCCCG GTCAGTCTGT | 360 |
| CTTGTGTTCT CTCCACCGCC TAGGTCTCGA G | 391 |

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTTAAGT TCCAGTATGA GATCTTCAAA GCTGTCTTTT TTTTCTTC TTCCGTTCTC 60
AGATCCTGAG 70

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCGGCC AAAGAGGCCT AGTCAAATTC TTACCTCGCT CTTTCACTGC TAGTAAGATC 60
AGATTGCGTT TCTTTCAGTT ACTCTTCAAT CGCCAGTTTC TTGATCTGCT TCTAAAAGAA 120
GAAGTAGAGA AGATAAATCC TGTCTTCAAT ACCTGGAAGG AAAAACAAAA TAACCTCAAC 180
TCCGTTTTGA AAAAAACATT CCAAGAACTT TCATCAGAGA TTTACTTAG ATGATTTACA 240
CAATGAAGAA AGTACATGCA CTTGGGCTT CTGTATGCCT GCTGCTTAAT CTTGCCCTG 300
CCCTCTTAA TGCTGATTCT GAGGAAGATG AAGAACACAC AATTATCACA GATACACTCG 360
AG 362

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCTAGA CCTGCCTCGA GTGCGGATCC AGCCGGAGGC GAAGAGAAGC ACTTTGGGGG 60
CAAAAGAAGA GAAAAATGAA GACGGGACAT TTTGAAATAG TCACCATGCT GCTGGCAACC 120
ATGATTCTAG TGGACATTTT CCAGGTGAAG GCTGAAGTG TAGACATGGC AGATAATGCA 180
TTTGATGATG AATACCTGAA ATGTACGGAC AGGATGGAAA TTAAATACGT TCCCCAACTG 240
CTAAAGGAGG AAAAAAGCAAG CCACCAGCAA TTAGATACTG TGTGGGAAAA TGCAAAAGCC 300
AAATGGGCAG CCCGAAAGAC TCAAATCTTT CTCCCTATGA ATTTTAAGGA TAACCATGGA 360
ATAGCCCTGA TGGCATATAT TTCCGAAGCT CAAGAGCAAA CTCCCTTTTA CCATCTCTTC 420
AGTGAAGCTG TGAAGATGGC TGGCCAATC GAG 453

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

GAATTCGGCC TTATGGCCTA CTTTAAAAAA AAACCAATAC CAAAGAAGCC TACAATGTTG      60
GCCTTAGCCA AAATTCTGTT GATTTCACG TTGTTTTATT CACTTCTATC GGGGAGCCAT      120
GGAAAAGAAA ATCAAGACAT AAACACAACA CAGAACATNG CAGAAGTTTT TAAAAAATG      180
GAAAATAAAC CTATTTCTTT GGAAAGTGAA GCAAACCTAA ACTCAGATAA AGAAAAATATA      240
ACCACTCAA ATCTCAAGGC GAGTCATTCC CCTCCTTTGA ATCTACCCAA CAACAGCCAC      300
GGAATAACAG ATTTCTCCAG TAACTCATCA GCAGAGCATT CTTGGGGCAG TCTAAAACCC      360
ACATCTACCA TTTCCACAAG CCTCCCTTG ATCCATAGCT TTGTTTCTAA AGTGCCTTGG      420
AATGCACCTA TAGCAGATGA AGATCTTTTG CCCATCTCCC TCGAG                        465

```

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

GAATTCGGCC TTCATGGCCT AGCGGCGGGG CGAGCGCCTC CACGCAGCAA CTCCGGAGTC      60
CCCCGCTTGC CCGAGCGCAG TTTCTCCGCT GCTGTTTCCA CCGGCTTTGT AACACTGGGA      120
ATTTACATCC TCACCCGCAC CCCTCAGGCC CGAGGATTTT AAATCACCT TTAATCTCGA      180
ACTGAGAGTT GCGGTAGATG GGATTTTTC CTTTTCCCA GATGGTTGAA GGTTAAGATT      240
TTTGGAACCC CCCCCACCTC CTTATTTCTA TTATTATTC TGCNAGAAAA GTATAAAGAG      300
AGTTGTAGTG GAGGTGAGAT TTGTGATCGG GAAAGCCTTC GACTCCCTCC TTCTCCGTCT      360
TCCGCTTCTC TCTCTCTGAT TAGTTCCTAT CCAGCAGCAG ATTGAAGCAG GAGATGATTC      420
TTCTCAAGGT TTGTTTCAGCA GCTTCACTTC TAGGCGAAGG CTTCATGAAC CAAGTGACGA      480
ACAACCTCGA G                                     491

```

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```

GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC      60
AGTTGTATAT TTCCCCCTT TATACAGAAA TTTTACAATA ATTCAGATT TTTCTGAGTT      120
TTTTCAGATT TTTGATTCTA TAATATGAGA TTATCTTTC TTCCTCTTAT TTTTCTAGGT      180
TATTTATTTT TTCTTTTCTT TTTAATTGTC TCATACAGGT TTAATCTCGA G                231

```

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTAAATTT | AAAATACATA | CTAACATATA | ACCCAATTTT | 60 |
| AACATATTAA | GTGAATATGT | ATTCTTAAAA | GATCCACTAC | TTTACATTTA | GATGCGTTAG | 120 |
| GATGTATTAG | AAATAAAAAAC | AGAAGAAAAG | ATTTAGAATC | TAGTCTGTCT | TTGCCACTCA | 180 |
| AGCTAGTTAC | CCTCTCTGAG | TTTTATACCC | CCTTCATCTA | TTAAATGGG | GGGTAACGCC | 240 |
| AACCTGACTC | CTTTAAAATG | AGTTTGAGAG | TCAGGCAAAT | TAGAAAGATA | CATAGATGAA | 300 |
| AACCTTTTAA | AAAGTATATA | GTCTTTCATG | ATTTGTAGAA | CACTTTTATA | CTTTTCAGAG | 360 |
| TACTTTCACA | TTGATCATAT | TGTTTGTACT | TTATGAAAGT | CTTCTACAAA | TCAGAATTAT | 420 |
| GCTTATTATA | CAGATGTGGC | TCGAG | | | | 445 |

(2) INFORMATION FOR SEQ ID NO:264: --

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AATTACTTTA | TATTTTAAAA | GCTCTGTGAC | TTCAGTAGTG | 60 |
| CATTGAAATA | AAATTTTAT | TCATTATGAG | AGAGTCTGTG | AGGAACAGAA | TCATGGTTCC | 120 |
| TGTGTGTTG | AAGATATGGC | GTGGGGTGAT | AGTGCTGGCA | GCAGCTCTGT | TGCTCTTGTG | 180 |
| CCCATGGCAT | ACAGACTGGA | TCTGCTGGTC | CACGGCTCCT | GAGGTAAATG | TCCAAGCCCT | 240 |
| CTGCAATGCT | GACAGTCTTC | CTCATCCTCA | CACCTACCT | CTCAGTTTCT | ACCTGCCACC | 300 |
| TCCCAGTAA | TATTAGCCTC | TTGAGTCCCC | AACAACACTC | GAG | | 343 |

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ATTAAATTC | ATTTATCAGT | AGGATCATT | TGTTCTAGAC | 60 |
| AAGTTGGCTA | TATTATAAAA | CATTAAAGCA | GCAGGCACTA | AGTTAAATAT | TGTAGCAGTT | 120 |
| GAAATTTAAT | GCTAATCTTA | CAGTTTTACA | CAGTTAACAA | TCTAGGCCAA | ATCTATTGAT | 180 |
| ACCTTTGGAA | CTACCCTTTA | AATTCCATCC | TATGCTTGTG | AAAAGGTTGC | ATATAATTTT | 240 |
| TTTTCTTTT | TCTCTCTTCT | CTTCTCTTTC | TTTTTCTTTT | TTCTTTTCT | ATTTCCCTTT | 300 |
| TCTTCTTTT | TCTTTCACAG | AGTCTTGTA | TATCACCCAC | ACTCTCGAG | | 349 |

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGAATAAAAA | TGCTTGTC | AAAAATTCAA | ACATTTGTCT | 60 |
| CTTTCCTTTC | CATTCCAGTT | CTAGGTCTCG | TTCCAGATCA | TATTCTCCAG | CTCATAACAG | 120 |
| AGAAAGAAAC | CACCCAAGAG | TATATCAGAA | TCGGGATTTC | CGAGGTCACA | ACAGAGGCTA | 180 |
| TAGAAGGCCC | TATTATTTCC | GTGGGCGTAA | CAGAGGCTTT | TATCCATGGG | GCCAATATAA | 240 |
| CCGAGGAGGC | TATGGAACT | ACCGCTCAAA | TTGGCAGAAT | TACCGCAAG | CATACAGTCC | 300 |
| TCGTCGAGGC | CGTTCAAGAT | CCCGGCTCCC | TCGAG | | | 335 |

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGTGGAAATT | TGTGGCTAGT | GTGATTTTTG | TTTGTTTCCT | 60 |
| TTTAAGTACT | GTTGATCAGT | TGTGACACTT | ACTGGTTAAA | CTTACGTTGC | TAAAGATTTT | 120 |
| TCTATAATAA | GCCACACATT | ATATTTAGAC | TATATTAAGG | GACCTTGGTT | TTCTTCTAGA | 180 |
| TAGCAGCTGT | CCCAAAGAAA | ATATTTCTTC | TTTGCTCTGT | AAGATTTAGC | TATTATCTGC | 240 |
| CAGTTGTAA | GAGGTTTGG | TTCCAACTC | AACCAGCAAT | GTTGAGAGCT | GAACCTAAGA | 300 |
| TAGCTGTTGT | ACTTTTGTCT | TTCCATCTGT | TACTGTCCTT | CATTCTTGGC | TCCCTACTAT | 360 |
| CTATAAACAG | CAAGCTCGAG | | | | | 380 |

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ATCTAGACCT | GCCTCGAGTC | AGCAACAACA | ATTTTAAAA | 60 |
| TTTCTTCTG | GATTCTAGAG | TGAGTTTTTT | TCATAACACA | AGAGGATAAG | AGTGAGGACA | 120 |
| ACAGGAGGTA | TTGATGATCT | GCTGAGCACC | AGGCATTATG | CTAAGTGCAT | TCACACACAT | 180 |
| CTCAGTGCCT | ATTGCCTCGT | TGTGGACTTC | TCTATCCCAG | CTCGTCCCCC | TGGCAAATTC | 240 |
| TTTCTCATCC | TTCAACTCTC | AGACACCTCC | CCCGCGCCTC | GAG | | 283 |

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AACCAGGCAT | TTTTCAATTAG | GGTTCTAGGT | CCAGGTGAAT | 60 |
| TCTTGAGTTG | GTTCTGTGTG | TCATGTATTG | GCCTTTAATA | ATGCTCTTAT | TTTGGCCAC | 120 |

GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG

157

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTTCAGGT CCAGGTGAAT 60
 TCTTGAGTTG GTTCGTTGTG TCATGTATTG GCCTTTAATA ATGCTCTTAT TTTGGCCAC 120
 GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG 157

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GAATTCGGCC AAAGAGGCCT ACCCAAATAA AATCAGAGTC AGAAATGGAA ACAGACAGTG 60
 GAGTACCTCA AAACACTGGA ATGAAAAATG AAAAAACAGC CAACAGGGAA GAGTGTGCGA 120
 CCCAGGAGAA AGTTAATGCA ACAGGACCAC AGTTCGTGAG TGGAGTGATT GTGAAGATCA 180
 TTAGCACAGA GCCTCTACCT GGCAGGAAAC AAGTCCGGGA TACTTTGGCA GCAATCTCAG 240
 AAGTTCTTTA TGTGATTG CTAGAAGGGG ATACAGAATG CCATGCTAGA TTAAAACTC 300
 CTGAGGATGC TCAAGCAGTA ATAAATGCCT ATACAGAAAT TAACAAGAAA CACTGCTGGA 360
 AACTCGAG 368

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GAATTCGGCC AAAGAGGCCT ACAACGAACG GCTTGGNGC GGACTGGTAT CCGGGGACTG 60
 TGACTTGCAG GGTCCGCCAT GGAGCCAGAG CAGATGCTGG AGGGACAAAC GCAGGTTGCA 120
 GAAAATCCTC ACTCTGAGTA CGGTCTCACA GACAACGTTG AGAGAATAGT AGAAAATGAG 180
 AAGATTAATG CAGAAAAGTC ATCAAAGCAG ANG GTAGATC TCCAGTCTTT GCCAACTCGT 240
 GCCTACCTGG ATCAGACACT TGTGCCTATC TNATNACAGG GACTTGCTGT GCTTGCCAAG 300
 GANAGACCAC CACATCCCAT TGAATTTCTA GCATCTTATC TTTTAAAAA CAAGGCACAG 360
 ACTCGAG 367

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
GAATTGGGT CCTAGGATAT AAATATTTT CCCTTTATAA GATATTTATA GGATATTGCA      60
AACAAATTTCT GTTTTTTCAT ATCCTTGCCA GCAGTTAGGG TTATCAAATT CTTTGATTTC      120
TTACTGATTT GTAAGTTTTT TTGTTTGT TTAGGTATTT TCAGGATAGT TACAAATGTT      180
AGGAAAACCTT ATTTTATTTT GGCTTTTGAA GTTTCAGAT TTCTGAACA GTGACCAATA      240
TGGACTCGAG                                     250
```

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```
GAATTCGGCC AAAGAGGCCT ATCTTTTTTC CTCTTTTTTT GTTGCAGAAA TGATAACCTA      60
CTATTCAC TA TTCTGTGCCT TGCTTTGTTT GCATACTGAA AATTATCCAT GGAAGGATAC      120
AGCACCACTC GAG                                     133
```

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```
GAATTCGGCC AAAGAGGCCT AATGAAACAT TTCTGTAACC TGCTTTGTAT CTTGATGTTT      60
TGTAATCAGC AAAGTGTATG TGACCCGCCT TCACAAATA ATGCAGCAAA TATTTCCATG      120
GTTCAAGCTG CTTGAGCAGG ACCCCCATCT CTGAGAAAAG ATTCGACTCC AGTTATAGCC      180
AATGTAGTAT CATTGGCAAG TGCCCCTGCT GCTCAGCCTA CAGTGAATTC TAACAGTGTC      240
TTACAAGGTG CAGTTCCAAC AGTAACAGCG AAAATCATCG GTGATGCAAG TACTCAAACA      300
GATGCCCTGA AACTGCCACC TTCCCAACCT CCAAGGCTTT TGAAGAACAA AGCTTTATTA      360
TGCAAACCCA TCACACAGAC TAAAGCCACA CTCGAG                                     396
```

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACCCCTCCCC | ATTCTAGTT | TCATGAACTG | TGCACAGGGA | 60 |
| TATGGGGCTG | TTCGAGGTAC | TTTTGGGCTG | ACCAAGGCTC | AGAGGCTACT | GACAGCTTTG | 120 |
| CTGCAAGTAA | CTTCTAGGCC | TTGTGGGTCC | CAGTGCAGGG | AACCCATGTG | CGGTGACACT | 180 |
| GGAGAAGCCA | TCTGATCCAG | GTCTCTCACT | TGACAGATGG | GGAACTGAG | GTCCAAAGAG | 240 |
| GTACAGCAGC | TTGGTTTAAG | AGATAGAGAT | GGAAGTGGAA | CAAAAATAAT | AACCATTTGA | 300 |
| TAATATTTTA | ACATTTATTG | ATTTGTTTTT | ATATGCCAAG | ACCTTTTAAA | GCATTATCTC | 360 |
| CTTTAAACTC | TCATAACCAC | TCTTACTCGA | G | | | 391 |

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTGCTTCCT | GATCATTGT | CTTTTAAAT | AAAAATATGA | 60 |
| TATTTGAGAT | TCTTTTATTC | TCTTTAAATA | TTTGAATACA | GAGTCTATTT | GAAGGACCAG | 120 |
| TATATTGAAT | AGCAGTAATA | TTTGAAGGAC | TAGTCAGCTG | TAGAAGCCTT | GACTTCAGAT | 180 |
| CTTCACCCAA | GAAGTCTGT | GTATTTGCTT | TTCTGGGCC | ACTCAGATAG | ACAATTGTGT | 240 |
| TTTGATACA | GTAAGAGTTT | GCAGCTTAGC | TTAACTAGAA | ATAATCCGGA | TGCCTCGAG | 299 |

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTAGGATTT | GAGGAGGACG | CCTCTTTTGC | AGGAGGATGC | 60 |
| AGTGAACAGC | CAAAGTCATC | TGACATCCTT | TTCCATCTTT | TTCTTCTAG | TATCCCAGTT | 120 |
| TCAAGGCCCA | GGAAAGGCAG | GGACTAACAT | ATGGAGCAGT | TACCCAGAG | TTCAAAGGGT | 180 |
| TAATCTCTAA | GAATTCATTC | TCTGACACCA | GCCACAGCTC | TTGTCCCCAT | CTCTGGGACC | 240 |
| GTCCCCTCTG | AGCCCCAGGT | TGGCAGCTTC | CCTGAATTCC | TTCTATGATA | TAATTTGTAA | 300 |
| TTCGGCAGGG | CTCTGGGACC | CAGGCTCAGA | GACCCAGGCT | CTGCTCTCTC | CTCAGTTTCC | 360 |
| AGGAGTCAGG | GCTTGCTCTA | AGGGAGGAAG | TAAACAGGCC | TTTCCCTTGC | TCCCTCTCCT | 420 |
| TTTCTCGAG | | | | | | 430 |

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGGGAGTT AGATGTATTA TATAAAAATG TCCCCAGCAT | 60 |
| CAAAATGACT CAGAGTATGA CTGTATTTT AAATTAAATA TCAAGACCTA TCATCTGACA | 120 |
| AAACATATGA ATGACAATGA GATATAATAT TTGAAATTAG ATCCGTTCTG GGGAAATCAA | 180 |
| GATATTTTGT AACAGTATAC ACAGTAGGCA TTGGTAAGTA AATGAGAACT CTATGAGCTG | 240 |
| TTTTCTGGAA AAGTTTAAAA TGAAATTTGT CAAATATCAA ATGATTGTTA TAAGAAAATC | 300 |
| AGTGGAGGCA GTATCCTTGG AAAAATCCAG AAACAGTTTT GTNTGTTTGT TGTTTTTTAC | 360 |
| ATCAAGGCAG ATCAGCAGGT GAACAGCTCG AG | 392 |

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAAGAACT TTTTCTGGG AGCAAGGTAG TTATTTCAAA | 60 |
| GCACAGAAAA AGCGGCGGG GGGCACAGAG AAGCACAGAG AAGCGGGGGC AGTTGCTCAG | 120 |
| GTA AACATT CATCTTGGCT TTTCTTTTA AAAGATAAAC TTTGTCCAC GTAAAGAGGA | 180 |
| AACTGCATA GATATTCATT GAGATTATCT GATTGTGAC TGTGCCCCA GAAAAACAA | 240 |
| AGGTAAAATA CACGAGTTT TGCATTGAGA AGAAAGTATT TCAGGTAAAA ATTAATCTATT | 300 |
| AAGCACTTT TCTCAGCAGA AGAAATGCC AAATCTTAA GGACAGTACT CGAG | 354 |

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTTTGAGAT TTTTTTGTG TTGTTTCCTT TTTGTATTTT | 60 |
| ACTGATATCA CCAGGATAGT TACTCTCCT TCTAGCTTTC TGCTTACCGC AACTGGATG | 120 |
| ACACACACAT ACACACCCGC AAAAATGCTC ATGAACCCAA TCCGGAGAAG GTTCCAGCAG | 180 |
| GTCCCCCACC CTCCCCTCCT CGTCCTACTT CTCCTCTGA CAGCGAGGAC AGGAGGGGGA | 240 |
| CAAGGGGACA CCTGGGCAGA CCCGCCGGGT CTCCCCCAC CCCACCCGGC CCTCANATCA | 300 |
| TACTCGAG | 308 |

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGACCTGCCT TGTGTTTTCC ACCCTGAAAG AATGTTGTGG | 60 |
| CTGCTCTTTT TTCTGGTGAC TGCCATTCAT GCTGAACTCT GTCAACCAGG TGCAGAAAAT | 120 |
| GCTTTTAAAG TGAGACTTAG TATCAGAACA GCTCTGGGAG ATAAAGCATA TGCCTGGGAT | 180 |
| ACCAATGAAG AATACCTCTT CAAAGCGATG GTAGCTTTCT CCATGAGAAA AGTTCCCAAC | 240 |
| AGAGAAGCAA CAGAAATTC CCATGTCCTA CTTTGCAATG TAACCCAGAG GGTATCATTC | 300 |
| TGGTTTGTGG TTACAGACCC TTCANAAAAT CACACCCTTC CTGCTGTTGA GGTGCAATCA | 360 |
| GCCATAAGAA TGAACAAGAA CCGGATCAAC AATGCCTTCT TTGTAAANGA CCAAACCTG | 420 |
| GAATTTTAN AAATCCCTTC CACACTTGCA CCACATCTCG AG | 462 |

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGCAGATTCT TAATTTCCCT GTCCATATTT TCCCCTTTCC | 60 |
| TTTCTCCCTG CCGTTCCAT GGTCTTATCT GGCTGCTTTC TCAATTATT CTGTTGTTCT | 120 |
| TGTGGATTCC CTCTATTAA TCTTGAAGTC GTTACTGACA TGTTTGGCCC TATACCAGCT | 180 |
| AGACCATTGC CTGAAGACTT TTTGATGAAC AATCTGTGTA AAGAAAAAGG GAATCTCGAG | 240 |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCNT ACCAGGANTT TCTATTCAAT TGAGAAGAAC CCAGCAAAAT | 60 |
| GGGATCTCC ACAGTCATCC TTGAAATGTG TCTTTTATGG GGACAAGTTC TATCTACAGG | 120 |
| TGGGTGGATC CCAAGGACTA CAGACTACGC TTCACTGATT CCCTCGGAGG TGCCCTTGGA | 180 |
| TACAACTGTA GCAGAAGGTT CTCCATTTC CTGGAGTTG ACCCTGGAGT CAACTGTAGC | 240 |
| AGAAGGTTCT CCGATTTCT TGGAGTCAAC CCTGGAGTCA ACTGTAGCAG AAGGTTCTCT | 300 |
| GATTCCCTCA GAGTCAACCC TGGAGTCAAC TGTAGCAGAA GGACTCGAG | 349 |

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

GAATTCGGCC AAAGAGGCCT AAAAAAATAA GAAATAATCT ATTCCACATT TAATAATTTG      60
AATCTTCCTG CTATAGATAT TTGGTTATCT TGACTTTTAA ANATAACATA TTTCTACAGG      120
ATTTTGAGTC TGAGAAGAGA AAGGTAANAT GCAAGACACT TCGATTTGTT GCACATTATT      180
ATGGAGCATC ATTAATGGTT TGNACATTTT TTGTCCTTTG GGCTTGAATG GACAGTACCA      240
AATTTGGGGT AATCAGCAAC TTGATGCACA GCTACGAGGA ATAAATGCTT TTGCTAATGC      300
ACTCGAG                                         307

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

GAATTCGGCC AAAGAGGCCT AAAAGATTAA AAAAAAATTT GTGTGATTTG ACTATATATT      60
AAAATCTCTT TCATAATTAG TCAACAATTT AAGCAACAAT TAAATTATTA GTGCTGTGGA      120
AAATATAGAA GAAAGATAAT TTCTTATTCC CCTCCTGAGG AAAGCATTTG ATACACCTGG      180
AAAGGAGCTG CTATGAAGCC AATTTATCTG TTCTTTTAT CAATTCAGCA GCATTTAAGA      240
TCAGATTTTT TCTCTAGTGG TCCAGCAGAG GGAGCCCTAG CACATGAATT GTTTTCATTT      300
CGTGCTTGCA CCCAGGATCT CGAG                                         324

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

GAATTCGGCC AAAGAGGCCT AAGAGAGATC AGTAAAACCA CTGGNAAAGA AAAGATGGAG      60
AAAATGTTGG AAAACCAGAA CTGTNTGCTG TCAAGNTCAT GTGGAATGTT CAAGAAAGAA      120
TCTGACTCTA TTATCTAATA TCTTACATAC NTCCACCAGA CTGGACTTGC TATTTGAATT      180
TTAAGCAAGT TTCCTTTCCT TTTATACAAA TTGCAAATTT CATATTTTAA TAATCACATC      240
CTAGGAATAG CACAATAATT GGGAAATAGA ACCCTTATCA CTAGNAGAAC CATTTCCTG      300
CCACTCTCGA G                                         311

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

GAATTCGGCC AAAGAGGCCT ATGCCCCATA AAAGGGCTCC TGAAGCTCTT TGTGAAGGGG      60
TCTGAAAAGG GCAGATGAGG GTGTCTTTTG GGGCGGATGT GGGGTTTGGG ACAATTGCAT      120

```

GTGATTGTCA TTCTTTAGCT GTCTGCATCC CACAGAACT TTTTCTGAG TCTTCCAGCT 180
 GGCCCAAGTC CTGGGTCTCT TTTACTGTTT TTGTAGCTGA CTACAGTAGG CAGATGAGGA 240
 ACTCTTAGTC AATCTGGAAA AACTCGACTG ACTATAAACA ATCCTAAATT GAAAGAAAGG 300
 TCTCGAG 307

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GAATTCGGCC AAAGAGGCCT AGCCGGTGTG GGGAGGATTG GCTCAGCCAC CCGCTGGGAA 60
 TCGTGCAGGG ATTCTTCGCC CAAAATGGAG TTAATCCTGA CTGGGAGAAG AAAGTAATTG 120
 AGTATTTTAA GGAAAAGCTG AAGGAAAATA ATGCTCCTAA GTGGGTACCA TCACTGAACG 180
 AAGTTCCCTT TCATTATTTG AAACCTAATA GTTTGTGAA ATTCGTTGC ATGATTCCAGG 240
 ATATGTTTGA CCCTGAGTTT TACATGGGAG TTTATGAAAC GGTTAACCA AACACAAAAG 300
 CACATGTTCT TCATTTTGA AAATATAGAG ATGTAGCAGA GTGTGGGCCT CAACAAGAAC 360
 TTGATTTAAA CTCTCCACGA AATACCACTT TGGAAAGACA GACTTTCTAT TGTGTTCCGG 420
 TGCCTGGGGA ATCTACGTGG GTAAAAGAAG CCTATGTTAA TGCAAACCA GCTCGAG 477

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GAATTCGGCC AAAGAGGCCT AAAAAATCT TCTGGAAATA ATTCTTAGCT GTGTAAGAAA 60
 TTTGATACTT AAGGAGACAG CAGTGGAGTC ACTTAACATA TTTGTGTTGG TTTTGTACCT 120
 GCATAGTGAC TGCCATTAC TTTTATGTTT TGGTCAATTA GATACTAAGT AAAAAGATAG 180
 TTGGTATTTT GGCTTCAGAT CAGGTCTATT TCTCCTACTT CTATATATCC TTTCTGTGAT 240
 TAAACAAAT AAACAATCCT CAGTATCATC ATTTAACACC TCTAACTGAT AGAAAAAATG 300
 AGGTTGTGGG TCCTCGAG 318

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GAATTCGGCC AAAGAGGCCT AACCTTGGGA TTTTCTATAT ATATGATGGT CTCATTTGTG 60
 NATAAACACA ATTTTATTTT TTCCTTTCCA ATCTGGATGC TTTTTTTTTT TNCCTATTGC 120

ACTGCCTATT GCATTCCTAA AAAGTCCATT CCAATGTTCA ATAGAAATGG TGAAAGTGGG 180
CATTGGAATG GAGTTTTTAG GAATGCACTC GAG 213

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 544 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GAATTCGGCC AAAGAGGCCT AAAAAGAATT AACCAGCTCT TCAGTCAAGC AAATCCTCTA 60
CTCACCATGC TTCCTCCTGC CATTCAATTC TATCTCCTTC CCCTTGCATG CATCCTAATG 120
AAAAGCTGTT TGGCTTTTAA AAATGATGCC ACAGAAATCC TTTATTACACA TGTGGTTAAA 180
CCTGTTCCAG CACACCCAG CAGCAACAGN ACGTTGAATC AAGCCAGAAA TGGTTGCAGG 240
CATTTAGTA ACACTGGACT GGATCGGAAC ACTCGGGTTC AAGTGGGTTG CCGGGAANKG 300
CGNTCCACCC AAATACATCT CTGATGGCCA GTGCACCAGC ATCAGCCNTA NGAAGGAGNT 360
GGTGTGTGCT GGCGAGTGAC TTGCCCTGTC CAGTGCTCCN TAATTGGNTT GGAGGAGGCT 420
GTGGAACAAN GTANTGGAGC AGGAGGAGCT CCCAGGNGTG GCGGTGTGTC AATGACAAAA 480
CCNGTACCCA GAGAATCCAG NTGCAGTTCC AAGATGGCNG CACACGCACG TACAAAATCA 540
CAGTAGTCGG TGCCNGCAAG TGCAAGAGGT ACACCCGGCA GCACANNGAG TCCAGTCACG 600
ANTTTGAGAG CATNTCACGT GCCAAGCCAG TCCAGCAACT CGAG 644

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCGGCC AAAGAGGCCT ATTTNTGGAT GGTGCTAGCG AANTAGAGGC TAATCCCCAA 60
CATGAGGTTT TTCTAATTTT ANGGTTGTGA TTTTCCAGTG AAAGAAATNA ANAAGAATTT 120
GCAGATTCGT GGAGACTTGG GAAGGATATN AAGCTGTCTT ACAACCCAG ATTCAACCCAA 180
AATTCAGCAA ATCACTGAAT ATTCNNAATA AAAATTGAAG TATTTTCNAA CTTCAGTTTT 240
TATCTCCAGA GGTNACGTC CNATGTAATC CGAAATCCTC ACGANGACAT AACCTCGAG 299

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCGGCC AAAGAGGCCT ACAACAACAA CAAAAGAAGA ATACTAATTA GAATTTGAGT 60
TCTAGGGGTT TTTCTAGGT TTTTCATTCT AGACTTAGCT TTTATTCAA CCTGTTGATC 120

CTGCATAGGG GTAGTCTAGC TTTAAAAAAT AAAACAATAA ACATAAATGA GCCTATTGAG 180
 TTCAATCAGA GTAGGGAGCA GTTTTATTGA ACAGCACATT TTCAAATTCT TCAGTTGTGT 240
 TTTGTTTTTC AGCTACGTGT CTCTCTGTGA TAATGAAAAG ACAGGTTGCA AAGCCCGGGA 300
 TTCGCTCGAG 310

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATTCGGCC AAAGAGGCCT ACATCTATTG AGGAAAACCA CAAAAAATT CAAAACAGCT 60
 ACAACGGGAA AAAGAGAGTT TTGTCCACA GTCAGCAGGC CACTAGTTTA TTAAGTTCCA 120
 GTCACCTTGA TTTTGTCTAA AATGAAGACT CTGCAGTCTA CACTTCTCCT GTTACTGCTT 180
 GTGCCTCTGA TAAAGCCAGC ACCACCAACC CAGCAGGACT CACGCATTAT CTATGATTAT 240
 GGAACAGATA ATTTTGAAGA ATCCATATTT AGCCAAGATT ATGAGGATAA ATACCTGGAT 300
 GGAAAAATA TTAAGGAAAA AGAACTGTG ATAATACCCA ATGAGCTCGA G 351

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCGGCC AAAGAGGCCT AGAGTGAGAC CTTATCTTAA AAAAAAAAAA AAAAAAATTG 60
 TCTATGATTT TTTTAAAAGC TTTTATTTT GAAGTAATTT TAGACTTGCT TAAAGTTGCT 120
 AAAAATAAGA CACAAGTTTC ATATATCACT CAATCTGCTT CCTGTAATAT TAACAACATA 180
 AATAGCCACA GGGAAATCTT CAAGACCTGG AAATTAAGTG TAGGACAGCA CTATTACCTA 240
 AACCACAGCT CTAATTTGAA TTTTCATCAGT TTTTCTCCTA ATGCTGATTT TCTGTTCCAG 300
 GATCCTATCC AGGAGCCAC ATTGCTCGAG 330

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCGGCC AAAGAGGCCT AAAAAAATAT AAGTAACAGA GGNAGAAATA ACTGTTATTT 60
 GTCAAGTGAC AAGCTTTTAA TGTGAGAATG GCTCACCTAA AGCGACTAGT AAAANTACAC 120
 ATTAAAGAC ATTACCATAA AAAGTTCTGG NAGCTTGGTG CAGTAATTTT TTTCTTTATA 180
 ATAGTTTTGG TTTTAATGCA AAGAGAAGTA AGTGTTCAT ATTCCAAAGA GGAATCAAGG 240

| | |
|---|-----|
| ATGGAAGGG ACATGAAAA CCAAAACAAG ATGTTGGATT TAATGCTAGA AGCTGTAAAC | 300 |
| AATATTAAGG ATGCCATGCC AAAAATGCAA ATAGGAGNCA CCTGTCAGGC AAAACATTGA | 360 |
| TGCTGGTGAG AGACCTTGTT TGCAAGGATA TTATACAGCA GCAGAATTGA AGCCTGTCCT | 420 |
| TGACCGTCCA CGTCTCGAG | 439 |

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATTATTTCT TGTCTCTCCC CAAATGAAAT CTGGGACATT | 60 |
| ATGACAATTT ATTTTCTAA GGATGATCTT GGTTCGCTT ATTGAAATGT CCTCACTCAC | 120 |
| CTCCAAGAGG AAGGGGATG GCTTCAGAAA ATGTCCTTAA GTGTTTTTAT TTTTCACGAG | 180 |
| TTATTATTG CAACACTAGC TCTCCCTGC AGGAAGCTAT ATAATTGTGT GCTTAATTGG | 240 |
| TAACATAGAA GAATTCCTAG CTAATTCCTA GAGAATATAC TGTGAATTC CTTGTCACCT | 300 |
| AAGTATCTGT TAAAACTCA ACCGTGGGAA ACAATGTCTA TGGATGCCTT TGGGAAAATA | 360 |
| CACATTTTAC CTATTATTC ATCTTTTTTC TCACTTTGTC AAGTAGTAGG TACCCCACTG | 420 |
| TACTCGAG | 428 |

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AACATTATCG ATTCCATTTT TTTACTGTG TAATTCTGCT | 60 |
| TCTTATTGCC TGTGTAAATT TCTGCTCTAT ATTAGTTTCC TGATACCCTA TCATTAAATTC | 120 |
| AGTCTGCCCT TTTTCATAT CATTCTACTG TTTTGTCTCA TCTTCCTTAT ACTTTATTCA | 180 |
| GAGACTGTGT TTTTATGAAG TTTGTGAAAA ACATTTTAAA AATTGTTTAA AATGTACTCT | 240 |
| TTGTCTATTT CTTGCTATTT TTTCTTTTGG ATATTCTGGA ATATATCCAC AGCGCTCGAG | 300 |

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATAGATTGTT ACATTTGTTT TGTGCATTCC ATGAAGTTTC | 60 |
| TTACCCTTAG AGTTATTTCT GTCTTAGTAA CAGCAACAAG TGGGAATGGA GACTTTGGTG | 120 |
| ACTGGAGTGC CTTCAACCAA GCCCATCAG GCCCTGTTGC TTCCAGTGGC GAGTTCTTTG | 180 |

GCAGTGCCTC ACAGCCAGCG GTAGAACTTG TTAGTGGCTC ACAATCAGCT CTAGGCCAC 240
 CTCCTGCTGC CTCAAATTCT TCAGACCTGT TTGATCTTAT GGGCTCGTCC CAGGCAACCA 300
 TGACACTCGA G 311

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCGGCC AAAGAGGCCT AGCGCGGTGT GTCGTGGTGT GGCGCGGTGT GGCATGGCGT 60
 GGTGTCCAG CTTGCTACAC ATTTGTGTT TTTAAATGTT TGTGGATAC AGTAACACTT 120
 TGTTAATTTT AATTATATGC AAGATAACTT GATTGCCCTA AACAGCCAT TTGGGTCAAG 180
 ATAAAGCCAT CGCCCTCTGA AGGGGNTGA GCTGGGTGTC TCCTCCATCA GTCGNTGTGA 240
 TAACTCTATG CCAGTTTCGA TTTCCAAAGT CAGAAGTGCA AAGCAGGGCT GGTATTAAAT 300
 CNTGTCAAAT CGTCCAGGTC CTGTGTNGTC GNACTCCATT ANTTATNTAG GTCCATANGA 360
 TGTGTCTTAC NACGNAACAA ACCCTCTCG AG 392

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCGGCC TTCATGGCCT AATGGAATTT GAGTCCAAAG GTAAATATAT TAAACATATA 60
 GATAAGAAGA AAAGAAAAC GTTATTTAAG TATCTGATCA GCTCTGCACC CCAGGGACCT 120
 CCACTTTTGC CCAGGTTTGA GAATTTGATC TATAGAATTA CCTGCATTCT TTCCCGCTCA 180
 TCCATCCAAT CAGCCACCTT TCTCCCTTCA AAGAAGTGTC TTCATTTTTT TCCTTCTTTT 240
 GTTATTTTTA TTGACTGCCC ATCACTGTTA TTAAATCCTT CCCTCTTTT TTGAATGAAG 300
 CAGCAGAGCC TTTTATTTG TTTTCCTTGT TTTGTTTTT GTTTTTGTGT TTCAGAAATG 360
 ACAGGGCTGT ATCAGCAG TCTCGAG 387

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCGGCC TTCATGGCCT AAAAATTAAG CAAGCAATAC CTAGCCAATA GTTCTGCTTA 60
 ACTTTTNGGT TAAGTATTTT GTTGGGATTC CTATAAATAA TTTTTCACAC AAAGTTTTAA 120
 ATTTCTGGTG TACTTTGACT CTCAACTGAG AGTGGATAGA GTTTTCTTT TGAGGATTAC 180

ATCTTAAAT GTCCATCGCC TGGCTGGTTA TAAGCATTTG TCACCTTTG AAGGTAAAT 240
 ATACTCTGGC CCTTCTTGAC TCAGTTACAG GTCATTTTAG GTCCAGTAAT AAGAGTCAGG 300
 TGGTTGGTTA TTGCTTTCAG AGTCAGACAA ATCTCGAG 338

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC TTCATGGCCT ACGAAGAAAA AATATTTTNG AGAGAATTTT CCAGATTGAA 60
 AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC 120
 CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT 180
 GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC 240
 CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT 300
 GGAACGCTCC AAAAATAAAG AAGCCCAAGC ACGGGCGGAA GACATACTGC CCACNTACGA 360
 CCAAGAGGAC AGGGAGGATG AGGAAGAGAA GGCAGACTAT GTCACAGCTG CTGAAAAGAT 420
 TATCTATAAT CTTAGAAACA CCTTGAAGTA TGCCAAGAAA AACGTCCGTG CTCTCGAG 478

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTCATGGCCT AGACGAGCGG AGTAAATCT CCACAAGCTG GGAACAAACC 60
 TAGTCCCAAC TCCCACCCAC CGGCGTTTCT CCAGCTCGAT CTGGAGGCTG CTTCGCCAGT 120
 GTGGGACGCA GCTGACGCCC GCTTATTAGC TCTCGCTGCG TCGCCCCGGC TCAGAAGCTC 180
 CGTGGCGGCG GCGACCGTGA CGAGAAGCCC ACGGCCAGCT CAGTTCTCTT CTACTTTGGG 240
 AGAGAGAGAA AGTCAGATGC CCCTTTTAAA CTCCCTTTC AAAACTCATC TCCTGGGTGA 300
 CTGAGTTAAT AGAGTGGATA CAACCTTGCT GAAGNTGAAG AATATACAAT ATTGAGGNTA 360
 TTTTCTTCTT TTTTTTTTCA AGTCTTGATT TGTGGCTTAC CTCAAGTTAC CATTTTTCAG 420
 TCAAGTCTGT TTGTTTGCTT CTTCAAGAAAT GTTTTTTACA ATCTCAAGAA AAAATATNTC 480
 CCAGAAATTG AGTTTACTGT TGCTTGATT TGGACTCATT TGGGGATTGA TGTACTGCA 540
 CTATACTTTT CAACAACCAA GACTCGAG 568

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATCAAAAAT | ACCTTACCTT | GTTCTGCCCT | GTGAAAGTAG | 60 |
| CCTAAGGCCT | GTCAAAAACA | CAAAGAGCCC | AAACATAATA | AAAAAGATTA | AAGAAGACAA | 120 |
| TATTAAANAA | GCATTGTCTC | AAAGATCTAC | TGCTATATTA | TATTTAAGTC | AGGAAGTAAA | 180 |
| TCATCTTAAA | ATAATGGTCA | CTTCTTCAAC | AGTGAGAGTT | AACACCCAAA | GTGAACGTAA | 240 |
| CACTTCAATC | ATCAAGATTA | CAATATATGG | ACTACTTCTG | GTAATAACTT | GTTGCTGTT | 300 |
| TAGAACTTGT | ACCAAATAA | CATCATGTGC | AGAGAGGAAA | GAACTCGAG | | 349 |

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs--
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTGATGGGG | ATGTGATGTG | GGCATCTGCT | AATTCGTCTG | 60 |
| CAACTACATG | ACCTAAGATG | GCCTCATTA | TCTAAGGGGC | CTCAGCTGGA | ACACTTGCCT | 120 |
| CTGCTGGATA | ACCCAGGTCT | AGTGTATCC | TCCAGACTAG | ACCTGGCTTC | TTCTGTGGCA | 180 |
| GTCTCAGGCG | AGTGTTCCT | GACGGTGAGA | GCAGAAGCCT | AGGTTTGGCC | ACATATCCCT | 240 |
| AACTCATAGG | ATGGTGACAT | AAACTCTACC | TCTTATGGAG | AAATAGCAAG | TTACACTGCA | 300 |
| TACGGGACGA | CTCGAG | | | | | 316 |

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTGGCAACG | ACTTGGACAT | CTGAGCTGTC | ACTGCCGAAA | 60 |
| ACAGGCCGCA | AGAGAGATAA | TCAATATGCA | TTTCCAAGCC | TTTTGGCTAT | GTTTGGGTCT | 120 |
| TCTGTTTCATC | TCAATTAATG | CAGAATTTAT | GGATGATGAT | GTTGAGACGG | AAGACTTTGA | 180 |
| AGAAAATTCA | GAAGAAATTG | ATGTTAATGA | AAGTGAACCT | TCCTCAGAGA | TTAAATATAA | 240 |
| GACACCTCAA | CCTATAGGAG | AAGTATATTT | TGCAGAACT | TTTGATAGTG | GAAGGTTGGC | 300 |
| TGGATGGGTC | TTATCAAAAG | CAAAGAAAGA | TGACATGGAT | GAGGAAATTT | CAATATACGA | 360 |
| TGGAAGATGG | GAAATTGAAG | AGTTGAAAGA | AAACCAGGTA | CCTGGTGACA | GAGGACTGGT | 420 |
| ATTAAATCT | AGAACAAAAC | TCGAG | | | | 445 |

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGAAGTTCCT | TATGCTACTT | TCACTGAGCA | TCCTATGAAA | 60 |
| TACACCAGTG | AGAAATTCCT | TGAAATTGTC | AAGTTGTCTG | GGTTCATGTC | TAAGCTTGTT | 120 |
| CCAGCTATCC | AGAATGCCCA | CAAGAATTCA | ACTGGATCTG | GAAGAGGAAA | GAAACTGATG | 180 |
| GTGTTAACTG | AACCCATTTT | GATTGAGACC | TACACAGGGC | TGATGTCATT | CATTGGAAAC | 240 |
| CGCAACAAAC | TGGGCTATTC | CCTTGCCCGT | GGGAGTATTG | GTTTTTGAGA | GTCTTTTTTG | 300 |
| TACCATAAGC | ATATCATCCA | CAGATATGTC | ACTTTGAAAA | TTCCAGTTTG | ACCCACGCTA | 360 |
| TTTTTGGA | CTA | ATTATTTT | AATGACGCTT | TATGATTTAG | AAATTTAGTA | 420 |
| TTTCCGAAAA | TTTAAAGCT | TGATTGGACT | GATAGATACA | CACTTTAGAC | CTCATACAAG | 480 |
| AATAATCAAA | TTTTCTTAAA | ACTAGAAAAT | AAATGCTGCT | GATACCTCGA | G | 531 |

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACACTCATGC | TGCCAGTCCC | CAAAAGACTT | CATTCATTCA | 60 |
| ACATATATGT | GACCGCCTGC | TACGTGCCAG | GCGTGGGCCA | GGTCCTAGGG | ACAAAGGAGA | 120 |
| GGCCTCGCA | CCCCACCCCA | TGACCCATAC | CTCCTCTTCC | CCACCTCCCT | GGGCCAGCCT | 180 |
| GCCTTCCTTC | TCCTCCTCC | TCCTTCCTGG | GGGAAGGAAG | CCCCACCTTC | TGTGCGCAGT | 240 |
| CAGCTCCTAA | GCACGCTCCC | GCTTCCCCTG | GCCTCCCCAT | TTAAAAAGGG | AGGCAAAGGA | 300 |
| TGTCACCACT | GTCACACAC | TCATGGCTTT | GCTCTGGGAA | GTCTGCAAA | TAAAATGAAA | 360 |
| GTCTCCAAC | CGTACTCGA | G | | | | 381 |

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCT | TCATGGCCTA | CTTTGACGCA | CCAGGCACAA | CCCAGAAAGA | CGAGATTGTG | 60 |
| GAAATCCATG | AGGAGAATGA | GGTCGCATCT | GGTACCCAGT | CAGGGGGCAC | AGAAGCAGAC | 120 |
| GCAGTTCCTG | CACAGAAAGA | GAGGCCTCCA | GCACCTTCCA | GTTTTGTGTT | CCAGGAAGAA | 180 |
| ACTAAAGAAC | AATCAAAGAT | GGAAGACACT | CTAGAGCATA | CAGATTAAGA | GGTGTCAGTG | 240 |
| GAAACTGTAT | CCATTCTGTC | AAAGACTGAG | GGGACTCAAG | AGGCTGACCA | GTATGCTGAT | 300 |
| GAGAAAACCA | AAGACGTACC | ATTTTTTCGAG | GGGCTCGAG | | | 339 |

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCCTGCCTCG | AGTCTTGAT | ACATCACACT | TGAGTCAAAT | CCTGGATACT | GCCAAAGGAA | 60 |
| CCTGAAAATC | CAGGAGACAA | CGTAGCTAT | TCCTGTGAAC | CTCTAGAGGA | TTTGCGCCTG | 120 |
| CTCTTCAAAC | AACAACCAGG | AGGAAAGTAA | CTAAAATCAT | AAATCCCCAT | GGCCCTCCCT | 180 |
| TATCATATTT | TTCTCTTTAC | TGTTCTTTTA | CCCTCTTTCA | CTCTCACTGC | ACCCCTCCA | 240 |
| TGCCGCTGTA | TGACCAGTAG | CTCCCTTAC | CAAGAGTTTC | TATGGAGAAT | GCAGCGTCCC | 300 |
| GGAAATATTG | ATGCCCCATC | GTATAGGAGT | CTTCTAAGG | GAACCCCCAC | CTTCACTGCC | 360 |
| CACACCCATA | TGCCACACT | CGAG | | | | 384 |

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGGGGGGTGG | GCTGATGGAG | GGTAAGTAAA | ACCTCCTACT | 60 |
| GGAAGATGTT | CTCCTAAGAG | TTCCACTTCA | TTTTCTATCC | TTTGCAGAGG | CGATCGTGAT | 120 |
| TGCTGTGTTT | GGAAAGGGAC | AACTGGCCT | GGTGGTGGCA | AATGAGGAGG | ATGATGGGGA | 180 |
| GAAAGGTGAG | GAGGATGTAT | AAGAAATGGA | TCACTAGAAA | TAAGGGGTGG | GAATGCAGCA | 240 |
| TATGGTACTG | GTAAGTGCTG | AACTGAACAT | GCCTGAAGCA | TTGGAGGAGG | CACACTACAG | 300 |
| ACAGGGAGGT | GCTGTCCACT | GAAAACCACA | GAGCATCCTG | GGACCTGCTG | TGTACTACAA | 360 |
| GCAGGGATGT | GCTGGCCTGT | GCAGAGTGGA | ATCCCATGTG | GTGCCACTGT | TGTTACTGTG | 420 |
| TAAGAAACAG | GGACTGTTCC | TTGATGGAGC | TGATCATGTA | TGTCAACCAT | GACTGCATTG | 480 |
| TGCTGGGGTG | GATGAGCAGC | AGGATGTAGC | AGACGGGGAG | ATACATTCCG | AGGGTGAAG | 540 |
| GCTCCGAG | | | | | | 547 |

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATTTGTGGC | TTACCTCAAG | TTACCATTTT | TCAGTCAAGT | 60 |
| CTGTTTGTTT | GCTTCTTCAG | AAATGTTTTT | TACAATCTCA | AGAAAAAATA | TGTCCCAGAA | 120 |
| ATTGAGTTTA | CTGTTGCTTG | TATTTGGACT | CATTTGGGGA | TTGATGTTAC | TGCACTATAC | 180 |
| TTTTCAACAA | CCAAGACATC | AAAGCAGTGT | CAAGTTACGT | GTGCAAATAC | TAGACTTAAG | 240 |
| CAAAAGATAT | GTAAAGCTC | TAGCAGAGGA | AAATAAGAAC | ACAGTGGATG | TCGAGAACGG | 300 |
| TGCTTCTATG | GCAGGATATG | CGGATCTGAA | AAGAACAATT | GCTGTCCTTC | TGGATGACAT | 360 |
| TTTGCAACGA | TTGGTGAAGC | TGGAGAACAA | AGTTGACTAT | ATTGTTGTGA | ATGGCTCAGC | 420 |
| AGCCAACACC | ACCAATGGTA | CTAGTGGGAA | TTTGGTGCCA | GTAACCACAA | ATAAAAGAAC | 480 |
| CACACTCGAG | | | | | | 490 |

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGAAGTAAC AGTGTATCAT GTATGCCACT GATTCCAGGG | 60 |
| GACACTCCCC TGCTTTCCTC CAACCTCAGA ATGGAAATAG TCGTCACCCA TCTGGCTATG | 120 |
| TTCCAGGGAA GGTGTGCCA TTGCGTCCCC CTCCTCCTCC AAAGAGTCAA GCTTCAGCCA | 180 |
| AATTTACCTC CATCAGACGA GAAGACCGGG CAACCTTCGC ATTCTCACCT GAAGAACAGC | 240 |
| AAGCCCAGAG AGAAAGTCAA AAGCAAAAGA GACACAAAAA TACTTTCATT TGTTTTGCTA | 300 |
| TTACTAGTTT CTCATTTTTT ATAGCACTTG CAATCATTTT AGGAATATCC TCAAAATATG | 360 |
| CTCCACTCGA G | 371 |

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATTAAATG TGGACAGATT GGAGGGGAAA GGTTTGCAGC | 60 |
| AAAAATCATA AGTAGAAGGA AACAGAATGG TTAAGTACAC AGTGTAGTAG CCATTTAGGA | 120 |
| AAGTTATAAG CCATTTAAAT GCCATGTATA AAGTGTTTT GATAAGAAAA AATCAAAGTG | 180 |
| TAAAGGAGAA TACAAAATTA TATGTGTACT GCGGACACAT CTGTATTGTT CTGTGTATGG | 240 |
| AAAACAGACT GGGGAGAAAT AGCTTTAAGT CCTAATAGTA ATTTCTTTT TCTCTCTTCT | 300 |
| TTTTCTGCT TTCTCTTTT CCTGTCTCCC TCAATATTGC ATATCTTTCC CATTAAAAAG | 360 |
| TATTGTATTA TATATCTACC AACAAGACAT TTGTTTCAGA TTTTGGTT TTGTCTTCAA | 420 |
| GGAACATTCT TCTGCATACA AACTCGAG | 448 |

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAGATGGGG TTTTGCCACG TTGCCCAGGC TCATCTCCTC | 60 |
| GAATCTTGG ACTTAAATGA TCCTCCCGTC TTGGCCTCCG AAAGTGCTGG GATTACAGGC | 120 |
| ATGAGCCACA GTGCCCAGCC TCTACCCGCT TTCTGTGGTC AGAAATAGAC GCAGGACATT | 180 |
| CCATCCATAC CTTATTCTT TCCTGGCTCT TCTCCCATGT GTCCTCGTGG GTCCTGGTCA | 240 |
| CCCTCTTAGC TGCTGTGTAA TAACCCCTGT GCAGATGCAG CAGCCACGAT GTCATCAGTC | 300 |
| CCCCCCAGT GATGCATAGG GGGCTTCTTC CCCTCCCTGG GTACAGCACT ACCAATTCCT | 360 |
| GTGTATGGGC CGTGTACAGC AGGGGCCACG TCCTGGCCCC GCTTCAGTCC CGGCTCGGGC | 420 |
| TCCTCGCCGG GGTCTCCATG CCACTTCCCT CTCCCATCTC CACATCTCGA G | 471 |

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
GAATTCGCCT TCATGGCCTA CAGCATCGTC GGGAC2CAGAC TCCTCTCAGG CCAGTTGCAG      60
CCTTCTCAGC CAAACGCCGA CCAAGGAAAA CTCACTACCA TGAGAATTGC AGTGATTGTC      120
TTTTGCCTCC TAGGCATCAC CTGTGCCATA CCAGTTAAAC AGCTGATTCT GGAAGTTCTG      180
AGGAAAAGCA GCTTTACAAC AAATACCCAG ATGCTGTGGC CACATGGCTA AACCTGACC      240
CATCTCAGAA GCAGAATCTC CTAGCCCCNC AGAATGCTGT GTCCTCTGAA GAAACCAATG      300
ACTTTAAACA AGAGACCCTT CCAAGTAACT CCAACGAAAG CCATGACCAC ATGGATGATA      360
TGGATGATGA AGATGATGAC GACCATGTGG ACAGCCAGGA CTCCATTGAC TCGAACGACT      420
CTGATGATGT AGATGACACT GATGATTCTC ACCAGTCTGA AGAGTCTCAC CATTCTGATG      480
AATCTGATGA ACTGGTCTCG CTCGAG                                         506
```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
GAATTCGGCC TTCATAATTT TTCTTATCTT CATTCTTTTCG GGTGCCCAAA TAAGCTCATG      60
TTTTCCATGG TCGGTTTAGT TTTTACTAGT CGTTGGCTAG TTTCTAATT GCATGTGAGT      120
TAGCATGTGG TGATGGCGGA GTAATGTCAT GTCTTGGAGA GAACATTGCT TGAGTTCCAA      180
ACTTAGCTTT TCTACTTCTT GGTGAGACTT TGGACAAATT ATTTTGGAGC TTGTTTCCTC      240
ACTTAAAAAA ATGGGGTTTG TACCTTTAGT TGTTC2AACT GTTGTGAGGA CTTGAATAAT      300
AAAGTATATA GCTATAGATA AGAA2ACTTG GGGGACTCGA G                                         341
```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
GAATTCGGCC TTCATGGCCT AATTTT2TTTC AAAACCTTGA AATGACATGT TAAATGCTG      60
CTTTGA2CTG GTTTTCTTT AGCCTGTAGA AAAGAACTTT GAGTTACTGG TCAAGTAGTT      120
TTGACCATAC TGGCTTAGGA AAACAGCGCA TCAGCTGTCT GATTGCTATC ATGTAAAAAT      180
CTGTGAACGA CTTTGAGAAG TCATTGGTGG ATTATGTTGT TCAGGAATAG GAATGGAGCT      240
TTCTTCCTAT CACTTGTATT TTTT2TTTTT TTTGGAAGGG GGGAGGAGGA GGAATTATTT      300
CCNCCCTAAT AAANGNGGN NTTAATCCTG GGCC2CNNNA AGGCTGGNNN GGGTCCNGAT      360
KTGGGGGTNC NNTTTATTGG GAACTGACNG GGN2TTTAATT TTCCGGTTTT TTTT2TTTCT      420
TGAATGATCT TGTGTTGTAG AGTTGAATAC AGTTC2TAGGG AAGTATGATC ACAAATGAA      480
TGTTGCAGT TCCTCCTATG ATTAATATGT CAGACATGTC AAAATTCTCT CATCATGTGT      540
```

ATTTCGCGG TTTATTCACT CCAGGACTCG AG

572

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGATAACTTT GAACAGAATG GGAGGCAGGT TTACCCTAAG | 60 |
| CAGTTCCCCA CTTGAAGTTT TCCTTTAGTT TAGTGATTG AGGGGCCCAA AATACTTTCA | 120 |
| CATTTCCCCC CTTTCTTTT TAAAAATCTG TTGGAGAACG CATTTTAGAA GAAAATGAGT | 180 |
| CTCTGGCCTC AGGTTTCGTC TGATCTCTCA TGGCTAGGAT GGTTTATTCC TAGATAGATA | 240 |
| GGTCCTGAGT TATTAGGAAA GCTCCTTTT AGAAGGTTGT GAAGTCTCAT GTCCTGTGAA | 300 |
| GAGAAAATAG GGGGAGGACA ACAACAAACA AAAGAAGTCG AG | 342 |

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

| | |
|---|-----|
| GAATTCGGCC TTCATGCCTA CAATATTGTT TAATAATTAT TCAGAAATAT TCAAGTATAA | 60 |
| TACTTAATAA AAATTTCTGC TATGTGCAAG GCATGGTGCT AGGTACTGAG ACTATAAGGA | 120 |
| GGTAAAAGAT AGTTCCTGCC CTAAAGACT TCTATAATTT AATCAGAAAG GAGAGTATAT | 180 |
| GAAAATCATA CTGAATAAAA AGTGGCTCAT AATAAATGCC AAGGAATCAA CACAAAGTCC | 240 |
| TTTCCCTGGT AGGGAAAGTT TTTTGTAGGA AATGGGACAT GAATTTGGCT TTGAAGGATG | 300 |
| TGGAGGTTT AGATAAGAGG GAGAACTGT TGTGTTCTAG GTTAGAGGAA CAACATAAAC | 360 |
| TCAAAAGAGA CTAAGAAGA ACGGACTCGA G | 391 |

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCCTGAGCA GTGCCTGGCC CATACTGGAT ACACAGTGTG | 60 |
| CATTTTGTGG GGAAGCAAGG AAGGAAGGTA ATATTCCAGC TCAGGGTTCT CTCTGACCCT | 120 |
| GAATAGTGTT ATGGACTCTT TGGGAAGGAT AGAAGCTTTC TTAGTTTCT GACAGAGGCC | 180 |
| TGTAGGCTGC AAACGTTGTG TTTGTAGAAA GAGTTGTAAG GGTGTCATGA GCCTTTATTT | 240 |
| AAAAGTGTCT TTAATGTATC TTAGGCATCT TTTCTTTTC ATCTCACACT ATGGACAGTT | 300 |
| TTAAGTGCAA AAGGGGAAGT CGAG | 324 |

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

GAATTCGAGC TCGACTGGAT AGTTTTTCTT TTTAACTTA AAATGCTTT TAGTTGGCA      60
CTCCGTAGTA AAGGAGGTTT CAGAAGCCAG TAAGAGAACC TCTGCCAACT ATGAAAGAGA      120
AGATATTTCT ATCTACAAGT TATTTACGGA TCAATTATTC AATTAATATT TTATATAATA      180
GAAAGGTTTT ATTTGTTAGG ACTTTATCTT TAAGTTCCCC AAGAGTAAAA AGGTCTAGTC      240
ATTATTATAC TGTGGGAGAA TGATAGAAGA TTGATTACAT TGAAGTCCA GAACTTCTAT      300
TTATTTAAAA GATTTAAGAT TTGACACACT CTCGAG                                336

```

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

GAATTCGGCC GGCATGGCCT AANCTAAAAA TAAATNAAC CCAACGCATA NAANACGGGT      60
TTATCTCTCC TAAAAACANT TNAGTTTNGA CTTAAATGAA ACANATCATN NNACAACNTC      120
ATTTTNAAT GAAGATTTTA CCTGGACCCT AGGTGTGCTA TTCTTCTAC TAGTGGACAC      180
TGGACATTGC AGAGGTGGAC AATTCAAAAT GAAAAAATA AACCAGAGNA GATACCNCG      240
TGCCACAGAT GGTAAAGAGG AAGCAAAGAA ATGTGCATAC ACATTCTGG TACCTGAACA      300
AAGNATAACA GGGCCAATCT GTGTCAACAC CAAGGGGCTA GATGCAAGTA CCATTAAAGA      360
CATGATCACC AGGATGGACC TTGAAAACCN GNAGGAAGTG CATCTCGAG                                409

```

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

GAATTCGGCC TTCATGGCCT AGGCGGCGGC AGCCGAGGGC GTACTGGCGA CCCGGAGTGA      60
TGAGCCCGCC CGAGACGATG CCGCCGTGGA GACAGCTGAG GAAGCAAAGG AGCCTGCTGA      120
AGCTGACTTC ACTGAGCTCT GCCGGGACAT GTTCTCCAAA ATGGCCACTT ACCTGACTGG      180
GGAAGTGACG GCCACCACTG AAGACTATAA GCTCCTGGAA AATATGAATA AACTCACCAG      240
CTTGAAGTAT CTTGAAATGA AAGATATTGC TATAAACATT AGTAGGAAGT TAAAGGACTT      300
AAACCAGAAA TATGCTGGAC TGCAGCCTTA TTTGGATCAG ATCAATGTCA TTGAAGAGCA      360
GGTAGCAGTT TTTGAGCAGG CAGCTTACAA GTTGGATGCA TATTCAAAAA AACTGGAANC      420
CAAGTACAAG AAGCTGGAGA AGCGATGAGA AACTTATTTT TATGGGACAG AGTCTTTTTT      480

```

TTTTAATGTG GAAGGACTCG AG

502

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAATATTCC ATATCAGTAC ATATAGCACT GCCTCACTTT | 60 |
| TTAATGGCTA TATAAAATAG TACTATAATT TTTAACCAGT CACCTGATGG TGGGCTTAGT | 120 |
| AGTTATTCTG TGGCTGTAAC CAACATCACT GCCATGTGCA CTGGTACACA TACAGAAGTC | 180 |
| CACACAAGTA GGCCTGTATC TGTAAGGTAA ATACTGGTGG GATTACTGAG TGAAAGGAGA | 240 |
| CGTGAATTTT TAGATTTTCTA CTATGAAAGA CAACTGCTC TTTATGGGGA TTTTATTAAT | 300 |
| CTACAACCCC ATCAACAATG TATGAGAGCC CATTTTTCAC ACACTTGCCA ACTCAGTAGG | 360 |
| TTATTAAACC TTTTGGTCTC TGCCACTTGT ATATCCCAGA TCAACTTCTA ATTCTGCTTC | 420 |
| ATATTGTTTG CTATCCTTTA GAATATTTCT GTCCACCTT GTCTCGAG | 468 |

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGGAAAGGA AGTGACATAG TGGTATAAAA ATTTGAAATT | 60 |
| TGTGATGTGG CTTAGAAGCT TGATATATAC GGGTATGATT GCAGCTGCTA CATTTAGCCT | 120 |
| TTTTTTCTTT CTTTTTGGAG AATGAACCGC ATTAAGAAAT ACATTTTACA TCACAATTTA | 180 |
| GCAAGTATAT GTGCTAACAT ACTTCTGTTT CTACAAGGGA TGTATTGTGG TATTTTCTAT | 240 |
| TGCATTTTAC TCTAATTAG TTCATTTAAA AAAATGCTGA TTCTAACCCA TGAAGTCGAG | 300 |

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCACCACAC CCGGCTAATT TTTGTATTT TTAGTAGAGA | 60 |
| CGGGATTTCA CCATGTTAGC CAGGATGGTC TTGATCTCCT GACCTCGTGA TCCACCCGCC | 120 |
| TGGCCCCCCC AAAGTGCTGG GATTACAGGC ATGAGCCACC GTGCCTAGCC GACTCTTGAG | 180 |
| TTTTGACAAG AGGTGATATC TGGGAGATTA ATAAGTATTT AGTTTAAGAA AACATTTAGT | 240 |
| AAGCCTGTCC TGTGTTCCCA CACAAAGGGT ATAACAGCAA TATATTCCAT AAGAGTAAAG | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 523 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

GAATTCGGCC TTCATGGCCT ACATTACCAT CAGATTGACA TATTTAATTA TCAGATATCT      60
TTCTTTTGCC AAAAAGTTGT GGTGAGTTG GCCCTGGGAT TTATAAATAC ATGCACACAG      120
CACATTTCTG TCATTGTTCA CTGCAGTCTT TTAACACATC TTCTCAGCAA TATTCTTAAT      180
GTTTCCAGCG GGAAATTGT AAATTATTTA ACCACTGAAT TAGAGGTGTG TTGTTTTTTA      240
GCTAATCAAT AGCCATTGAA TGCTTAAATG GGCTTTAAAG TAGACAAAAG TAAAAGACAG      300
CAAAGAAAAT TAATCAGTAA GATTGCCCAT ACTCCATAGA CACTTGAGCA GCTACTTTAG      360
TCATTTTGAA ATACACGCTT TATGTTTTCC CTTGGACTGG CATATTCCTG TCATTTATAA      420
AAAGAATATA CATTTGTAAA TTTAAGGTGT GGACATTCAT TATTGAAGGT AGAAATAGTT      480
ATAATCATCA GTGTCTAGAT ATATCTGAAG AGAGGTACTC GAG                          523

```

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

GAATTCGGCC TTCATGGCCT AAAGTAGGCA AGGGATAATA ACCAAAGAAG NAAATTTTCAT      60
GAAGACTAGA CATCATAAAG CATAATTTTA ATAGTCACTC AACCAAGTAT TTTTATTTT      120
TTATGGATAC TCTGAATGGC AATTAAATGT GAAACCCAGT TTCTTGGGCA AGTCAAATTC      180
TGGAATCACA TCCACCTAAA TTAAATGAC TAGCTCGTAT TTTCCCCATC TTCAAGTTTC      240
ACATCCTGGT CATCAAAAGA CTCGACAGCA AGACTTAGAA TGAAAAAGGG TACTTGTTTA      300
TATTAATATT TTTTACTTGA ACACGTGTAG CTTGCAGCAG GTTCTTGATG AATGTGCTTT      360
GTGTCCAAAA TGCCTCCCA TTGTACACAG GTGTACACCA TGCATGCACC AACACCACTC      420
GAG                          423

```

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

GAATTCGGCC TTCATGGCCT ACAAGCCACA AACTGTGGT GAATGGAAAA GAATGTATAA      60
ACTTCGCTC ATTTAATTTT CTTGGATTGT TGGATAACCC TAGGGTTAAG GCAGCAGCTT      120
TAGCATCTCT AAAGAAGTAT GCGTGGGGA CTTGTGGACC CAGAGGATTT TATGGCACAT      180
TTGATGTTC TTTGGATTG GAAGACCGCC TGGCAAAATT TATGAAGACA GAAGAAGCCA      240

```

TTATATACTC ATATGGATTT GCCACCATAG CCAGTGCTAT TCCTGCTTAC TCTAAAAGAG 300
 GGGACATTGT TTTTGTAGAT AGAGCTGCCT GCTTTGCTAT TCAGAAAGGA TTACAGGCAT 360
 CCCGTAGTGA CATTAAAGTTA TTAAAGCATA ATGACATGGC TGACCTCGAG 410

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GAATTCGGCC TTCATGGNCT ACCTTAGCCT CAGCTCTTTC TTCTGGGTTG TTTGTATTTT 60
 CTTTCTGTG CCAAACAGTT TCCCCACAA AAAGAACTTT ATGTCTTTCT CTGTCTTCCC 120
 TCAGTCCTTC CAGTCAGCAG CCTGTGATTG GGCTTTTCCC CTCAGAAACG AACAAATCCAG 180
 AACCCTACTGT TAAAACAAC TGTATTTTGC CTTGGGAAGT CCCATTGCCT TCCCTGAAAA 240
 CATTAAACAT TCCTCCGATC CCCAGCCTGA GTCTCTCTGT CTCTGGGCCC CATCCTGCTC 300
 CACAGCAGG CTGGTGTGTC CAGCACAGAG TGACCCTCCG ATGCCCTTTC CCACCCGCCG 360
 CCNTGCCTCC CTCGAG 376

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GAATTCGGCC TTCATGGCCT ACGGGTTGTT ACATATTTAT TCTTTTTTGA AGCCCATCAC 60
 TACATCGCCA TTACGTTTTA CACTGTGTAT GTAACAAATG TTACCACTTT GTTCTTTATT 120
 CCTTTTGGGA TCATCTTCAG TGGGGGTAA ACAGTATCAA GCTCTAGAGC TCCCTCTGGT 180
 GGTTTTTGTG ACATATTTGA AGATGGCAGC TTGCTTTTGA AGAATTTCTG GCTCTGCTCT 240
 CCCTGTTTTT ATCTGTACTT TTTTCTCTCA TTGTGCCTCT TGCACACACA CACCCCCCCC 300
 ACTCGAG 307

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC TTCATGGCCT ACATTACTCA GCTTTCCTGA ACAACCAGGC ACGACCTCT 60
 GCCTGCAGGC CAGGCACGTG CTGCTGCCCC TGGAGGCGGG TGGGGGTGCC TCCGCGCTGG 120
 AGGACACGGG GTGCACTGAG GCTTCCCAT GGTGATGGGG GAATGTGGTG ATGAGGGGAT 180
 GCGGTGCCCC CGGACCGCAC ACATGCCATG TGTGGACACT CAACAGGAAG CTTGGGTCAG 240

CATTTTCAGCT GGAAATGCAG AGCCAGGGCC CTGGAAAGTC CCTCAGCAGC TGTGCACAGG 300
 CCTGCTCACC GTGCGTGTGC GGGCAGAGCC TCCCTGGGGA GGCAGAGGCC CCGCGTTCTG 360
 CACTCGAG 368

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TTCCTGCTCT TCTAGGTAGT 60
 CACACTTCAC TAAAGTGTCA TCCACCAGTG TGTTGAATCC GAAGAATGAC AATTTTCTAC 120
 CACTGGTGTA AAAAACAAC AATTGAAGAC CCTTGTGCAT TGTGTGTCAC AAAGCTAAAT 180
 ACATGGAAAT CGTTAATATC GCTGATATTA AGTAAATTCC CCACTCTGAG TGAATACTTT 240
 GATGATTGCC AACAGTGGCT AATAAAATGA CGGCTACCAC ACTCATGGGT CACTGGGGCT 300
 GCGCAGGGCT CTTTGAGGTG GGTGGCTTCT TTTGGAAAGT ACTATGAACG TCTCGAAGCA 360
 GTATTCTAGT GATAAGAATT CTTAACATAG CCAAGCGCCC CACGTTTGTG CCCCACGTTT 420
 GTTCCCCTTA TCTCGAG 437

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCGGCC TTCATGGCCT ACCAAACCCA ATTTATTTAA AAANATACTT CTATATCATT 60
 ATATGTATTA CCAATTGTTT TAGCCTTATA CAGGATGCGG TGTNCTGTGC TCCTTNGTGA 120
 ATGTCNGTTG CTGGTAGCTG GTTATGCTCA TGATGATGAC TGGGTTGACC CCACAGACAT 180
 GCTTAACATAT GATGCGGCTT CAGGAACAAT GAGAAAATCT CAGGCAAAAT ATGGTATTTT 240
 AGGGGAAAAG GATGTCAGTC CTGACTTGTC ATGTGCTGAT GAAATATCAG AATGTTATCA 300
 CAAACTTGAT TCTTTAACTT ATAAGATTGA TGAGTGTGAA AAGAAAAAGA GGAAGACTA 360
 TGAAAGTCAA AGCAATCCTG TTTTAGGAG ATACTTAAAT AAGATTTTAA TTGAAGCTGG 420
 AAAGCTCGAG 430

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GAATTCGGCC TTCATGGCCT AGAAATAGAT TTTTCTCAG ACTCTCATCT CACATTCCTT 60

| | |
|---|-----|
| TTTAAGATTT CCTNGTCCTA TCCCCACCCC AGACGTTTCC ATTTTGCTTT TATTTTCTAT | 120 |
| AATAATTCCT GGGGGCCTCT ATTAAAGGCC TTTTCTTTG ACTACTTACA TCCATTATAC | 180 |
| CAGTATCTTT GTCAGTAAAA TTTTATATAT CTTTATTCT GTCATCAGGT TAAGAAACAA | 240 |
| TAATTGTATT TTAAAGGAA AATATTTTAC GATGCTACTA AGCAGTTACT TTGTCCACTT | 300 |
| ATGCAGGATA CTCGAG | 316 |

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCTGGCTGG CACCTGGAGA ATCCCTGAGC TGGAAAAGCA | 60 |
| GCTTGGTCTG CAGAACTGAG TCACAAGACT GAGGCACTGG GGAGCCTCAG CCCCATCTGG | 120 |
| TTGTTGNTCC CTCTGTGACC TTGAGCTTGT CTTCCACTTG GTGCCGTAGG CCCTCATTTG | 180 |
| TCCATTGAAG TTAGCACCTG TCCCTCCCGT CCTCCAGAGA GGTCAGGAGG ATAAGCATT | 240 |
| GAAGACTCAC TGTGGTTTAT TGAGTGCTTA CTGTGCAGGT ACTGCTGTAG TTTTGTGCAA | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

| | |
|--|-----|
| CAAACCTTTTG AGTNNNACAG TTAAGATATT ATGTGAAGCT CAGAATCATG TTTCAGACCA | 60 |
| TTGAAATTAC TGGTTAAAAT ACAAATAGCT GAAGACATGA TGTAAGAT TAAGTACTTG | 120 |
| GTTTTGTAAC ATATTACCA ATTAAAGTCA CAAAATATTT CTCATTATTT ATTCATGCAG | 180 |
| GTAAGTGAAG AAAAGATAGT GCAGAAATCA ACTTTAAATA AAAAATTATT CCTCCCTTC | 240 |
| CTCCCACTCC CCTATACTCT ACAAATGTT TTCCCTGGGA CTAGGCCTTG AAAAGGCCAC | 300 |
| TACATATTAG TGTGACATGC ATTACTGTCT GCAATTAAAA AAGCTAACCT TGTGGTGATT | 360 |
| GTAATTACAT TATAAAAATG TCCACATGCA TAAATCTAAA AAAGGTTGAA AACCTACAGT | 420 |
| AAATCTACAA TATAGTGTAT ACATTTGACC ACTGGTTTGT GTTATGTAGA AGTCATAGAT | 480 |
| TTGGTAAAGC ATTGTAACAA TTTAGGAAGG CATCTAAATC TTTAAGTTCT GGACAAATTT | 540 |
| TATGTTTTAA TCTACAAAAT TGCATGAAGG CTAACCTCGAG | 580 |

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:


```

GAATTCAGAN TTNTGCTATG GTAGCACCAG ATGTCCAAAT TGAAGATGGG AAAGGAACCC      60
TCCTAATATC TTCCGAAGAG GGAGAGACGG AAGCTACTAA NTCACAAGAA GTTNTTCAGA      120
ATTTGGAATT AGAANTGGCA NCCGGCTTCA AGCAGATGAC TTCNTCCAGG ACTATACTTT      180
ATTGATCAAC ATCCTTCATA GTGAAGACCT AGGAAAGGAC GTTGAATTG AAGTTGTTGG      240
TGATGCCCCG GAAAAAGTGG GGCCCAAACA AGCTGAAGAT GCTGCCAAAA GCATAACCAA      300
TGGCAGTGAT GATGGAGCTC AGCCCTCCAC CTCCACAGCT CAAGAGCAAG ATGACGTTCT      360
CATAGTTGAT TCGGATGAAG AAGATTCTTC AAATAATGCC GACGTCAGTG AAGAAGAGGG      420
AAGCCAGCTC GAG                                                                433

```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```

GAATTCGGCC TTCATGGCCT AAAACTCTAA TAGTCTCTCT TCAGCGGAGC CACTGAAGGA      60
AGATAAGCCT GTCAGTGGTC CTAGGAACAA GACTGAAAAT GGACTGACTC CAAAGAAAAA      120
AATTCAGGTG AATTCAAAAC CTTCAATTCA GCCCAAGCCT TTATTGCTTC CAGCAGCACC      180
CAAGACTCAA ACAAACTCCA GTGTTCCAGC AAAAACCATC ATTATTCAGA CAGTACCAAC      240
GCTTATGCCA TTGGCAAAGC AGCAACCAAT TATCAGTTTA CAACCTGCAC CCAAACCTCGA      300
G                                                                301

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

GATTCAGATG GAGATGCCAA GCAGGCCCTT AGGTGAAGGA GTCTGGAGTC TGAAAGCATT      60
TGGGATGGGG ATATAGACTT GAGAGCCATC AGCTTATAAA TAGGACTTGG TCAAGAATGG      120
GTGGCCTCCA TCCTAGATGG ATATAAATAA GAAATAAATA TCAATTTTTC TTCTTATAAC      180
ATTCTAGGT TTTCAATTTT ATGACTTTAA GAAAAATATG AATGACAAAA ATAAACATA      240
AAATCAAATA TATCCGTATT GCCCTTTGGG GGACACCATC TCTTGCTCAC TTTACACAGT      300
AAGTGCCATT TCCTTCACCT CCATGGAAAA CATTTCTGTA ATTACTAAGT TGAATAACTT      360
AAAATATAGG ACGGGACATC TCGAG                                                                385

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

GCAGAAACCT TCAGGGAAC CCCATGCTAG CGGCAACTGC ACCACACTTT GAGGAGAGCT      60
GGGGGCAGAG ATGTCGTCGA CTCAGGAAAA ATACAGGGAA TCAAAAAGCT CTAGACAGTG      120
ATGCTGAGAG TTCCAAAAGT CAAGCAGAAG AAAAAATCCT AGGTCAGACT TATGCAGTTC      180
CCTATGAAGA CGATCATTAT GCAAAAGACC CAGACATTGA AGCACCCAGC AACCAGAAGT      240
CAAGTGAAC  GAATGAAAAG CCAACGACAG CTCTTGCCAA CACCTGTGGA GAGCTCGAG      299

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

GCATTGGTT CTTTTATAT CTTCTATTC TCTCACTATA TTCCTGTTT TCTTTTAATG      60
CTTGACATC ATTAACTCG CTGTTATCCT TGTCTGTGAG TCATCTGGTC ATTTCTGTGT      120
GTTTTATTA ACTGATTAT CTCCTGTCC TGGCCACATT TCTGTGCTTT TNGGCGTTTC      180
AGTAACTTCT GATTGGATGT TGGGTATTAT AAAGATTATA TTATTGAGTG TCTGGATTG      240
GGGTGGTAGT TACTTGTGGA TCAGTATGAT CCCTTTGAGG CCTATTTTGA AGCTTCAGCT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

GAATTCGGCC TTCATGGCCT AGATTACAAC ACGTGTGCCA CCACACCTGG CTAATTTTTC      60
TATTTTTAGT AGAGACGAGG TTTCACCATG TTGACCAGGT TGGTGGTCTT GAATTCCTGG      120
CCTCCAGCCT GGTGACAGAG CGAGACTCCA TTTCAAAAAA AAAAAACAAA CTTTCATGCTG      180
AGAAGTCTGA AGAAAAAAA GATTTTAAAG AGGAAATGT GTAAGAAAAA TACTTCAGCT      240
TCTGTTACAA AATCAAATA GAAAAAACA CAAAATTGGT GTTCCTCGA G                291

```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

GTAACCTTAG CTGTACCTTG CAAACCAGAA CATATGGTCA CCCTACCCTC CGGTCACTTT      60
TTCTTCTTTG TTTCATTCT TTTAATTTT TTCCCTTTTA AACACACAGC ATTATCTTTC      120
CCTGAGCACC ATTGTCTTTG CAAATGCTCT TGCAATCGGG ATATTTTGA CCTGGCAACA      180
TGCATATTCA GTCTGAACAG TCTCTCTGAA CCTACCCCAA AACCTGGTTT TAGCTTCCAG      240

```

GCAGAAGACT CTGTTCCCTG GCTTGCAACC CCCAAACTCG AG

282

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ATATCAATGC | AATTTTAAAT | TTTTGTTAAT | ATCAACAGCA | 60 |
| AAAGCCTAGT | GCATTGGGAG | ATGTGCAACC | TCCCTGAAAA | TCTTTTCTGT | TTCTGGAGTA | 120 |
| CTTCAGGGGT | GGCCTCTGGC | CCCAGAGCCT | TTGCCACAGT | GCTCCCACCA | GCCCCACCT | 180 |
| CATCCGCTCG | TTTGCAGAGC | CTCATCTACA | GGTCCCCACG | CTGCCTTCTT | TACTCACTCT | 240 |
| GCGCTTGGCC | GTTTTGTTAT | TTGGCTTAGT | CTACATTGGG | CGGAAGTCTG | TGTGCACAGA | 300 |
| TGTTGGTGTT | CTTCGAGCCC | CTTCCACTCA | GAGGGCCACA | CG | | 342 |

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TCATGGCCTA | CAAAGAGCTG | GGATTACTGG | TGTGAGCCAC | CGTGCCCGGC | 60 |
| CTGGACATCT | GGTTTTAACT | AGATGGAAGG | GAAGAACATT | ATGAATCTTT | AAAATACGGC | 120 |
| TGTTGCCATT | TTTCTCTCTT | CTTAACATGC | AGCATAGGTG | ACAAGCTTTT | CTGTCACTAT | 180 |
| CATGGAGCAT | TCTGAATCAT | GACATTTTTG | TTTGAGAGTT | CATTCTTGAA | TTTTCAGTTC | 240 |
| AAAATATTGT | TTGAACTATT | ATTCCACATT | CAAAGATTAT | ATAAGGTCCT | GTGCTTTTGA | 300 |
| ATCTTTTTC | AAAAATTAT | TTCTGCCTGC | TTAAAAAA | TACTTTTATT | TCCCCACAGA | 360 |
| GAGTTCAGGA | CTTCAGATTA | GTTTGTGTTT | AGCTCACTTA | ACTGGATAGA | CAATTTTGCG | 420 |
| TTTTGCAACA | CCATAGCTCG | AG | | | | 442 |

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AAAAAATGA | AATTCCTTAT | CTTCGCATTT | TTCCGGTGGTG | 60 |
| TTCACCTTTT | ATCCCTGTGC | TCTGGGAAAG | CTATATGCAA | GAATGGCATC | TCTAAGAGGA | 120 |
| CTTTTGAAGA | AATAAAAGAA | GAAATAGCCA | GCTGTGGAGA | TGTTGCTAAA | GCAATCATCA | 180 |
| ACCTAGCTGT | TTATGGTAAA | GCCCAGAACA | GATCCTATGA | GCGATTGGCA | CTTCTGGTTG | 240 |
| ATACTGTTGG | ACCCAGACTG | AGTGGCTCCA | AGAACCTAGA | AAAAGCCATC | CAAATTATGT | 300 |

ACCAAAACCT CGAG

314

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGCTACCAGA GTGTGAGAGA CCATTGTCTC GTTGGCTGGC | 60 |
| GCTCACGGAC ATGCAGTCAC GGTAGCGGGA GCAATCACAA AACTGTAATT TACTTACCAA | 120 |
| ATCTCTTCCT TTCCGTAGCC TCGCCTGCCT GACTTAGAGA AAGAAAAGCA ATAATTTTAC | 180 |
| AGGCAATTTG AGGTGTCTCT TTGGGTCTT TCTGTTTGA AGGATATTTG TCGAAAAAAA | 240 |
| GAGCAAAACC GTTTTAAATA AACTCCCCCT GGAAAAAAC CAAAACACT TGCATCTCGA | 300 |
| G | 301 |

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGCAAATACA CATTAAATAAG AATGCCTAGA AGAGGACTGA | 60 |
| TTCTTCACAC CCGGACCCAC TGGTTGCTGT TGGGCCCTGC TTTGCTCTGC AGTTTGGTAT | 120 |
| TATTATGTA CCTCCTGGAA TGTGCCCCC AGACTGATGG AAATGCATCT CTTCCTGGTG | 180 |
| TTGTTGGGGA AAATTATGGT AAAGAGTATT ATCAAGCCCT CCTACAGGAA CAAGAAGAAC | 240 |
| ATTATCAGAC CAGGGCAACC AGTCTGAAAC GCCAAATTGC CCAACTAAAA CAAGAATTAC | 300 |
| AAGAAATGAG TGAGAAGATG CGGTCACTGC AAGAAAGAAG GAATGTAGGG GCTAATGGCA | 360 |
| TAGGCTATCA GAGCAACAAA GAGCAAGCAC CTAGTGATCT TTAGAGTTT CTTTCATTCCC | 420 |
| AAATTGACAA AGCTGAGCTC GAG | 443 |

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATAGGCNTCT TTGGCCGGCC AAAGAGGCCT AAAAAAATCT | 60 |
| CAGCTATGGT TCATTATTAC TAGCTCAGCT TTAAATCTT TAAATTGGTT GAATTATTCT | 120 |
| CTATGTCAGT TATTTTATT GACCAGTTT GGAATATTT TGTTCAATTA TCAGGGAGTA | 180 |
| TGCGGTTAAT GAAGTTGTGG CAGGGATAAA AGAATACTTC AACGTAATGT TGGGTACCCA | 240 |
| GCTACTCTAT AAATTTGAGA GACCACAGTA TGCTGAAATT CTGTCAGATC ATCCCGATGC | 300 |

ACCCATGTCC CAGGTGTATG GAGCGCCAAC TCGAG

335

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACAGAGATTA TATTGGGGTT NCCATTTTGT GAAGCCANAG | 60 |
| ACATNTGGTC ATTGGGATGT GNGATTGCAG AATTATTTCT TGGANGCCCG NTNTACCCAG | 120 |
| GAGCCTNGGA GTATGCTCAG ATTCGANACA TTTCTCAGAN TCAAGNTTTN CCAGGAGNAC | 180 |
| AGTTGTTANA TNTGGGTACT AAATCCACAA GATTTTTTTG ACANAGAAAC AGATATGTCT | 240 |
| CNTTCTGGTT GGAGATTAAA GACACCGGAA GAGCATGNGG CAGAGACTGG AATGNAGTNT | 300 |
| TAAGAAGCCG GACTCGAG | 318 |

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGTGGGAATT TAAATACAA GATCCTGTTG AAAATATTGA | 60 |
| TATTCAAAGA AACAAACAGC TTTGGATCCA TAGCCACAAT TTAGGTTTTT CTAGATTAAA | 120 |
| ATCAGAAGTG ATTTTATTGT TGGGAAGATAC ATTAATTCTT TGAAGTCAGA ATAAGAGGCT | 180 |
| TGACAATTTA ATTTCTAATT AAGTGACTGA ATAGACAAAG GATCAAATAC AAACAGTAGT | 240 |
| GCAGGAAGAA AATAAATTGG AAGAAATAAT TGTTCAACCA GTAGTAATAA TTAAGACCAC | 300 |
| CATTTTAAAA TTTTCTATAC ACAAAGAATG AGAAAATATT GTTATTATTA TTATACTTCT | 360 |
| TTCTTCTTCA GTATTAGTGG ACCCACATTA TCTCCTGTCA ATTCATTGTG TTTATNATGT | 420 |
| GAACCATCTC TCGAG | 435 |

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACAGGCTCAC ATTGACTACA CACGTTTATA CCAGGCGCCA | 60 |
| TGTTCTTTGC CGAAACTCCC GCTCAGAGCC TGGATGATCT GCCCCTCACC TCTGCCCTCG | 120 |
| TTCCCATCCA CTCTCCCCTC CTTGCTCTGT TCCTCGAG | 158 |

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```
GAATTCGGCC TTCAAGGCCT ACTCTTCTTG GCATATTATT TTCCTGAATT GCTGCCTCTG      60
TTGTTCAAAC CATCCCGGAT TAATGACAAA AACTATCTT ATTCAAACCA AGAATTATCT      120
ACAACCCCTCC TTCTCAACTA GTTTNNGCAA GATCATTTCA GTTTTCTTT TTGTGCTACA      180
TCCTGGATTA ATTCTTCAGT TTNGTCTTCT CTGGAATCAC TACCTAAGGC TTATTCCATG      240
TTTCAAGTTT TTTGTTTTTT GTTTTTTTT ACTTTGATGA GTATGTTTAC CAACGCTCTC      300
GAG                                                                                   303
```

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
GAATTCGGCC TTCATGGCCT ACAAAGTGT GGAATTACAG GCGTGAAC TA CCGTGCCAG      60
CCTTTTTTTT CATAGCAGTT TTATTAAGTT GTATTGCCA TACCACCCAA TGTATCCATT      120
TAAGCACCTG ATTCAGTGGT TTTTCATGTA CTCATGGAGT TATGCAGCCA CAATCTTAGC      180
GCATTTTCAT TACCCAGAA AGAACTGTA CCCATTATGC ACCCCGTTCC CNTCNTCCGG      240
TCNTGGCAAC CACGAGTGTA CTGTCTGTCT TCATGGATTT GCTATTCTC GACGTTTCAT      300
TGGGATGAAA TCACACAGTG TATGGCTTCC ACACTTTACT GTGCTGTGT CAAGGTTTAT      360
CTATGTGTTG GGTGCAGCCA CCCCTTGGTA TCCACAGGGA TTGGACCCAG GAGCCTGCAC      420
CGATCCCTG CAGGGATGCC TGTGTCCAC AGTGCCCCCT GCAAACTCA CTGATATGAA      480
GAGTCGGCTC GAG                                                                                   493
```

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
GAATTCGGCC TTCATGGCCT AGTTAACATG ACACAAAATC TTTACCTGCA GTTCTAATAT      60
TTTGCAAGGC TGAAGTCCAT ATTTACAAC GTCTTAGATC ATCTCAATCT GATTATTTAA      120
CTATTCTCTC TAACTGCTAG TCCAGCCCCT AAAACTGCAT TTCTCTGCTC CTCCAAAGCT      180
TAGTGGCTTA TTGAAGTCCA TATTGCAATT GTGACAGAGC CAACTCCCAA GAATGGATTC      240
CCACTCAGTG TAATGCAATA GGAGCACTTT AATTTTATCT CCATTTTCTG GACCCAGTGC      300
ATCATCTAG CCCTTTTTTC TTGGAATGAA GTCTGGCTGA GAATGATGAT CCATTAGTAA      360
GAATTACTTA ATAAATCAAC TCTTGTTTAT GAGTGGCAGA AACTAAAGC CAGGCTCGAG      420
```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

GAATTCGGCC TTCATGGCCT AATGTCACCA CTGTGGAAAA CCATATAGGT CGAAGGCTGG      60
ACTTGCATAT CACCTGAGGT CAGAGCATGG GCCTATATCC TTCTTTCCAG AGTCAGGACA      120
GCCAGAGTGC TTAAAGGAGA TGAACCTAGA GTCAAAGAGT GGGGGCCGAG TTCAGAGACG      180
TTCTGCCAAG ATAGCTGTAT ACCACCTACA GGAGCTGGCC TCTGCTGAAC TGGCCAAGGA      240
ATGGCCCAAG AGGAAGGTGC TTCAGGACCT GGTACCTGAT GATCGAAAGT TAAATATAC      300
TCGTCCAGGG CTCCTACCT TCAGCCAGGA AGTACTACAT AAATGGAAGA CTCGAG      356

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

GAATTCGGCC TTCATGGCCT ACATGATGAA ATGTTGGCTA AAAGAGTCAC CCTAATATTA      60
ATAAAATGTT TTATTCTTCA TGTGACTAAA TCAGTGTGCA TCAAGAAAA AGAAAGAAAA      120
AATGCTTAGA TTCCTTTTTT AAATTATCTC CAGAATTTCT AATTTTATA AATTAAGGAC      180
CAACAAATCC CATTTTGTTT TCACGTTTGA CATTTGTTCC TTTGACTTAA ATAACCTCTC      240
CACTCTTTAT TTTCTATTT GTGGTGATTT GAATAATTTT TCAGAAAATA TGTACTTTCT      300
GATAAATTGT AGTGTGTCAG TAATGAAAAC TGCTCTATGG TGCTCCCTC GAG      353

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

GAATTCGGCC TTCATGGCCT ACGAACTACT CTAAGTAATG GGCCAAGTCA TGAGCTGCAC      60
AAAGGCCCCC AAGACCCAGA CCGGTTTAAT GTTAAGCAAA ATGCCGCCTG GTCTCAGGTA      120
GACACTCAGC CACCGCTAGC CCCAGTCAAC TGTCCCATGG GAAGGCAGAA GGCCCGGTGT      180
TGCCAGGTCT TAAGTTTTC AAGAGGAAATC CTTAAACGAT GGTGTTTCAC TATAATGGAT      240
TCATTTTAT GTTTTATAAA TCTCTATGTT CATGTACTGG TATTAGTACT TTTATGTGAT      300
AAAATCTTTT TTTTAAACAT TGGTAATTCA AAAACACAAC ACCCACATAC AGTGAGGACC      360
AAACAAAACC CGTCTGCAAG CAGGCTCTCT CCGAG      395

```

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```
GAATTCGGCC AAAGAGGCCT ACAAAGGACA GCCCTGTCTG CACACTGAGT TACTGTGGAT      60
TTTAAAGAAA CTTGCTATAA GAATTTAGGC ATTCTGATT CAGTTAAAGG ATTGCCAATT      120
CATCAGTCCC TGAAACTAGA GCAATCTCAA CAGGACAAGA AAAGAAAATG GGCTTTTAA      180
GTCCAATATA TGCCTTTTC TTCTGTTTG GAGTTAGAGT ATACTGCCAA TATGAAGCTT      240
ACCGATGGGA TGACGATTAT GACCAAGAGC AAAATGTCTG G          281
```

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```
GAATTCGGCC TTCATGGCCT AGTGCCACTG CACTCCAGCC TGGTGACAGA GTGAGNCTCC      60
GTCTCAAAAA AAAAAAAAAA AACTCAGCTT CTTGAGAGAG ATAAATTGG GGGAGGAGCC      120
CAGGGCCACA TACCAAGCTT TGGGACATGG TGCCTCATGC TCTCTGGGAT TGCAGACCAT      180
CCAGGTCTGT CTTGCCCCCT GTTAGTGCAC ATATATCCAC TCACATGTCT TCCCTCAGGC      240
TATCGGGCAG GGGGACTTCA CCAGGGGGTT TATGGATAGG CTCAAGAGG GTCTGTGAGC      300
CCCCAGAAAT TGTGTGTGAG ACTGAGTATG TGTCTTTTT TCCAGGAAAT TCTCGAG      357
```

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```
GAATTCGGCC TTCATGGCCT ATTACAATAT GCTTAAAGCT CAAAATGATC GAGAAACACA      60
AAGTTTGGAT GTCATATTTA CTGAAAGACA AGCGAAAGAA AAACAAATCA GAAGTGTCTGA      120
AGAAGAAATT GAACAGGAAA AACAGCAAC AGATGACATT ATCAAAAATA TGTCTTTTGA      180
AAACCAAGTC AAGTACCTAG AGATGAAAAC CACAAATGAG AAAGTGTAC AGGAATTAGA      240
TACACTTCAA CAACAATTGG ATTCACAGAA CATGAAAAAA GAGAGCCTGG AAGCAGAAAT      300
AGCTCACTCC CAGGTGAAAC TCGAG          325
```

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

GAATTCGGCC TTCATGGCCT AGTGAATTGA GTTTTGTAAA CTCCTTAGC ATATCACACA      60
ACACTAATTT TCCACTCTCA ATATGTGGCT GTAGAGTGTT TAATGTTTAC TTTCATATCG      120
CTTTTCCATA GTAGTGCAAG ACCTCAGTTT AGCTTGTTTA CATTATTTGC AGATTACTT      180
ACAGTGTACT ATTTATTTCT GTTTAAATA GTGTTTGCAA TAGGAGAAAA TCATATGATC      240
TTAAGCATAT ACACCAAAGG TAAGAAAGGA AGCCACTATT GTATCTTTT GATGAATTCC      300
AGATGAGCTG GGATCAAATT GAACTGCTTA GGCAGAAATT TAAGAGACAA GTAGAAGTGG      360
TGCAGAAAGA CATTGTGACT GCAATGCCTT ATTTACAGCT ACTGCCCAGA GGAGAACT      420
CCCAACATGA CAAAGAGTTC ATCAGCTTGA ATGTTAACTT TTGAAAACAA TTAATTGAGC      480
CACTGCACCC GGCCAATCTA GTGAATTGAG TTTTGTAAC CTCCTTAGCA TATCACACAA      540
CTACTCGAG                                     549

```

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

GAATTCGGCC TTCATGGCCT AGGAGGCGGA GGTGTCAGTG AGCCGAGATC ACGCCATTGC      60
ACTCCAGCCT GGGCGACAAC AGCAAGACTC CATCTCAAAA AAAAAAAGTG AGATCCTGCC      120
GATGGGCCCT TCCTGTCCAC CTGTCAGGAA AACCTGCAAA AGGTTCTTGT CGCACCATT      180
GAGCCAGTTT TTCCCAAATG ACACCCATAC CTGATTTTCC TTGTTCTTCT AAGACAGTTT      240
TAATTAGGAT AATCTCATAA GTGCTACATT TTCAGTGAAT TTTTCAATAT AGTGGCCCAT      300
GTTCTTTCTT TTTTTTTAAA GTCTTTTCC TCTGGTAGCA CATGTGATT AATGCTTGCT      360
TTCCTGAATT GTAGAAATAA AAGGAAATCA CAAGTATTTT CCAACAAAGT GGAAGTGGG      420
CCGAAGGGTG CAGAAAAAAA CTATAGAAAT TAGTTAAAAA TTAGGAAGGG GCACTCTCGA      480
G                                     481

```

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```

GAATTCGGCC TTCATGGCCT ACCAACTCAG AAGGGAATGG AATGTGGAAA AAAAGAAAGA      60
AAACCTGAGT AACTTTTCTT AAAAAAGTCT AGCTGTCTC AGTTTGTTGC ACCAAATGGG      120
GAGCAGGGAA TGTTCCAGTC GCAACTGACT AATTAGCCCA ACCCTNATT ATTGATAATA      180
ATAATGATAA ATAATAATGC TAGCTAACAC TTAGTGAGCA AATACTAGGT ATTATGTGAA      240
ATCATTTTCT TGTATTAAC CACTTAATCT ACACAGCAAC TCGAG                                     285

```

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

GAATTGGCCT TCATGGCCTA NGTGTGGATA GTGGAGGCAT TGGTAGCCAG AACATGTCAC      60
TTTATGACAG CATATGGACA GCAATATGGA AGCCCAGCAT GGTGGTAAA AAATGGGGCA      120
GCCTAAGGTC AATGACTTTT GGCTGAGTCT GTGAAGATCT CAAAGCTTGG TGGTTTTTAG      180
CATAGCCTTT ATACCATACT TAACTCCGGG TAAGGACCAG GACCACTGTA GCGACCAATT      240
GATTGACAGA GTAAAGTATG TGGGTTTTTT TTTTCCCCCA ACTGGGCTGA TTCTCTTAGA      300
ATAAAAATTG TATACCATTA TATTATGTTA ACTTGATCAC AAAGAACAAA ATGTTATTTA      360
TTAATAATAT AGCATTGTCA TCTGTTTGAT GAATTTTCTT GATTTAATGC TTGTTTAGAT      420
TCAGTAAGCC ATTTCAGGA ACTATAATAA ATGCTTCTTC CAACTTCTCG AG              472

```

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

GAATTCGGCC TTCATGGCCT ACGAGTGCTT GCTGGAATCG TTTACCCTNG TTAATTTTTA      60
TCATNTCCTC TTTATGAGCA TGATATGGCT TCAGCTGTTC CACTTTGATC CAGGCATGAT      120
CTTCTGTTCC AAAAAATTTC ACAAAGAAGC ATTCTTTTCC GCGAGGTTTC TTCAAGTCCT      180
TTGGTGGATT AACAATCTTT CCTGGCCAAG GAGGATATCG GCCGAGTTTC CCCCACACCA      240
AGTCGCCGAG CCGCAGACTC ACAGCCGCCA TCTTACCACC CAACCACCGC CGACGCACGG      300
GCCGCCG                                         307

```

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

GAATTCGGCC TTCATGGCCT ACAACGATCT TGTCTTCTTC TATCAGGTTT GCGAAGGTGT      60
TGCGAAGGCC AGCCATGCCT CCCACACAGC TGCCCAGGCT GGGCTTCCTG ACAAGCTTGT      120
GGCTCGTGGC AAGGAGGTCT CAGACTTGAT CCGCAGTGGG AAACCCATCA AGCCTGTCAA      180
GGATTTGCTA AAGAAGAACC AAATGGAAAA TTGCCAGACA TTAGTGGATA AGTTTATGAA      240
ACTGGATTTG GAAGATCCTA ACCTGGACTT GAACGTTTTT ATGAGCCAGG AAGTGCTGCC      300
TGCTGCCACC AGCATCCTCT GAGAGTCCTT CCAGTGTCTT CCCCAGCCTC CTGAGACTCC      360
GGTGGGCTGC CATGCCCTCT TTGTTTCCTT ATCTCCCTCA GACGCAAACT CGAG              414

```

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```
GAATTCGGCC AAAGAGGCCT ACTGGATGGC ATCTACTTCG TATGACTATT GCAGAGTGCC      60
CATGGAAGAC GGGGATAAGC GCTGTAAGCT TCTGCTGGGG ATAGGAATTC TGGTGCTCCT      120
GANCATCGTG ATTCTGGGGG TGCCCTTGAT TATTTTCACC ATCAAGGCCA ACANCGAGGC      180
CTGCCGGGAC GGCCTTCGGG CANTGATGGA GTGTCGCAAT GTCACCCATT TCCTGCAACA      240
AGAGCTGACC GAGGCCCAGA AGGGTTTTCA GGATGTGGAG GCCCAGGCCG CCACCTGCAA      300
CCACACTGTG ATGGCCCNAA TGGCTTCCCN GGATGCAGAG GAGGCCCAAG GACAAAAGNA      360
AGTGAGGNAG CTCGAG
```

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```
GAATTCGGCC AAAGAGGTCC TGTAAGTATG ACTATTTAAT TTATTTCTTT TCACAATATA      60
AAAAGCACAT GCGATATTTT GAAAGACTAT TAAAGGTGGG GACAAGAGGT TATTTAAATC      120
TATGTTTGGA TGCAACTTTT ATGGCTTAAA CTACAAAGAA TTATCCTTTT TATATATTAA      180
ATGATTGTAT AGTTCTTTTA ATACTGTTTT TTGATACAAG TGTGAAATNC TTAAGAAAAA      240
TGGCAAACAT CACTAACCAAC CATTACAATT CTAATAGCTA ACTTTTCTGA GCCATTACTT      300
GGAACCATGC ACTGTTTAAA ATGCCTCACT TGGCCAATGC TCGAG
```

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```
GAATTCGGCC AAAGAGGCCT AAAATGCGGA GTTATAATCC AGAAGGGGAG TCCTCAGGGA      60
GATACCGAGA AGTAAGGGAT GAAGATGACG ATTGGTCCTC TGATGAATTC TGAAGATAAT      120
CTCCTAAATC ACTGACGTTG AGATGTCATC ATCTTACATC AGACTTTCTA ACTAGTATCA      180
AGATCAGTGT CAGATATTGT TGAGGGAAGT AATTTTATAA AGTTACACAA AGGTAGTTAT      240
AAAAAAGGCC CAGTTGTCTT TTCAGAAGGT GACTTTCATG TGCTTGAAAA GTTTAATATT      300
TGAATATTGT GTTTAACCAC ATGGTATTAA AATTTTGCAA TATATTGTGT ATTGGTCTGA      360
TATTTTAGTA TATAGTAGAA CATACTTTT TTTTCTTTAA GCCAAATGAA AAGAGGTAAC      420
TTTGCTTTT TCCTTTTCT TACCTATCAA ATAGCATTTA TTACATGTCT TTCAGTGAAA      480
TACTTAGTTG TTCCAGGCAC GCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```

GGAACGAATA GAAGTGTGTTG TATCTGTGGG TTNGACACAC TACTGAATCA CAAAGTCTTT      60
GGAATAATTC TCAAAAGCCA TCACTTTTAG CCCACTTTCT CATTATTAA TGCTCTATTC      120
TTTTCTAGC ATGTCTAGCA GAATTCTCTT GAATTCTTGC AGTGAATTGG TGCTCCTTAA      180
ATACCTGCTA TTTTGAATA GTTTGACTT AAATACATTT TCCTTTTCTC CCAGTTGCAA      240
AATGTCAGGG CTGACAACTG AAAGGGCTTC TGAAGATTGT CAGTGTTCCTC ATATTCAGAT      300
AGGTAGCAAA GAATCTGACA CATTGGTAT AATAAACCCA CTGGAG                          346

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

GAATTCGGCC TTCATGGCCT AGGATGAATG ACCTTAAAGA TCGAATGA ATAAGAGACA      60
TCATTTACCC TCAAAGAAAC TAGAGTCTGA TTGGGCAGGG AGGAAAAGGT ATTAAAATTA      120
TGTCTTTCTG CATTGTGTGG ATTTGAAGTT TGTTTTTGT TGTTAAGAGT CTTATTATTA      180
GGATAATGAC ACTGTTTTTT CTTTATTAAG TTACTTGTGT GGCAGTTAAG ATGATTCTGG      240
TGGCTCTTAA CATTTTTTTT TTCTCCAGTC GGGAACATGC CCTGTGTGCC GCCGTCATTT      300
CCCACCTGCG GTTATTGAAG CATCTGCAGC TCCTTCCTCT GAGCCTGATC CTGATGCCCC      360
ACGGTCTCGA G                                     371

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

GAATTCGGCC AAAGAGGCCT AGGAACTGTT CTGTTGAAAA TACCCATCCA ACAGTTTCTT      60
ACTATGCTCA TCCCCAAGTG GCATCCTACA ATACCTACTA CCATAGCCCT CCTCACCTGC      120
CACCATATTC TGCTTATGAC TTTCAGCATT CCGGTGTCTT TCCATCCTCC CCTCCCTCTG      180
GACTTTCTGA TGAGCCCCAG TCTGCCTCTC CCTCACCCAG CTACATGTGG TCCTCAAGTG      240
CACCGCCCAA AACTCGAG                          258

```

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

GAATTCGGCC AAAGNGGCCT AATATAACTT AGCTGCTATT TACAACACTA GAAATTTAGT      60
ACTTTAAGTA ATTTACATC  TATGATAACA TTTGTTACTT TATTTTAAAT GATTTTTTTA      120
CAGTAGTTAT GACAGTAGGA TGGTTATGGA ATTGGAATTT AAACCTCCCA CTAATGAGCT      180
TAAGCTGCTT GGAATATTAA TTATGTAGTT TTTACATTCC ATTTTAAAC  AAAAACTTAG      240
NAAAGGTGCT GGCATTCTGA GGCCTGCAAT TAGGCCACAT AGCAGAAGCT TGCTCCTTCC      300
TTATCTGGGT GAAATATTTT ATTTTGCAC  TTTGAGTCAT ATTCCCACCC CTGTATAAGC      360
TACATAGGAG CCTGAATGAA TTGGGTAGGA AAGGAAATTA TGCAAACAAG TCTCAGCTAG      420
TGCTGAATGA CTCGAG                                     436
  
```

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

GAATTCGGCC AAAGNNGCCT AGCACATGCG TCCCCGCAGT TGTCTCTTTC TCCTTTCCAA      60
GTTTCGTGNC TAAAGGAGAT GGAAGTATTC TAAATTTTCC TACTTCTAAT TTTTACTATG      120
CAACCAGCAA AGGCGGGAAG GTTGCAAGGA AAATTGTCCG GTCTTTTACA ACTAAGNNGG      180
AAATTACTTC TCCTATGTTT TTATTCAAGA GTTGCTTTTA AAAGTGCCTG CCGGCTTTCC      240
CTTTTAACTT TTAGGATTAT AGTTAAGGTT ATGGAAAGTA GTCATTCATT AGTTCAGTAC      300
GTTTCATATA GTTCTCTAAC ATAGAAGAAA ACTCAGTCAC CAGACAGTGA AGTCATTTAG      360
CAGTGGTTAT TGGAAGATAA TCCACAGTGA TGGTAATGGA ATACTGGAAA CNCATCCTAA      420
ATAATCTGTA ATTATTATTA TTATTATTTT GGGACAGNGC GAGGCTCCGT CTCCAAAAAT      480
AAATAAATAA AATAAATAAA TAAATAAATA AATAAAGGAT GGTGCACGTC TCGAG          535
  
```

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

GAATTCTAGN CCTGCCTCGN GTCGCACCCA TGTTCAATCG TTCCTTCCTT CCTTCCTACA      60
TTCTTTTTTT TTNCCTTCTT CTCAGGGTTC TCACTCTGTC ACCCTGGGTC GAG          113
  
```

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

```

GAATTCGGCC AAAGAGGCCT ACACACATCG TTCATGTACA TGATCGCCCG ACTCTGCATG      60
CTGAAGCTCT ACCACAAGCG GCACCCGGAC ATCNACGCCA GCGCCTACAG TGCCTACGCC      120
TGCCTGGCCA TTGTCATCTT CTTCTCTGTG CTGGGCGTGG TCTTTGGCAA AGGGAACACG      180
GCGTTCTGGA TCGTCTTCTC CATCATTCAC ATCATCGCCA CCCTGCTCCT CAGCACGCAG      240
CTCTATTACA TGGGCCGGTG GAAACTGGAC TCGGGGATCT TCCGCCGCAT CCTCCACGTG      300
CTCTACACAG ACTGCATCCG GCAGTGCAGC GGGCCGCTCT ACGTGGGACC GATGGTGCTG      360
CTGGTCATGG GCAACGTCA+ CAACTGGTCG CTGGCTGCCT ATGGGCTTAT CATGCGCCCC      420
AATGATTTCG CTTCTACTT GTTGGCCATT GGCACTGCA ACCTGCTCCT TTACTTCGCC      480
TTCTACATCA TCATGAAGCT CCGGAGTGGG GAGAGGATCA AGCTCATCCC CCTGCTCTGC      540
ATCGTTTGCA CCTCCGTGGT CTGGGGCTTC GCGCTCTTCT TCTTCTTCCA GGGACTCAGC      600
ACCTGGCAGA AAACCCCTGC AGAGTCGAGG GAGCACAACC GGGACTGCAT ACCCTTCGAG      660

```

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

GAATTCGGCC AAAGAGGCCT AGTGTGTTGGA GCTGTGGGCT GTGCCCTTCC AGTCCCCCAC      60
AGCAGTGCTG TTGCCCAAGA ATCTCCTAGC GAGAGACCAG GGGCTACTGC CAGGTGACAG      120
AAAAGGGAAC ATCAGTTCCG CTATACCCAC AGCTCACCTG GCGGCCTGGG GCCTGCACAG      180
GGCCTGGTTG AGGCAGTGGA CCCCATTTT GGGCCGTCTG TGGAGTTGAT GTTCCTGCCA      240
GCTGTCCCT CTCTGTCTC CCTGGAACCT CACCTGCAGT TTGATGCCTG AGTTAAAATT      300
GTTCTTCTAA ATAATTCACT GTAGACTTTC TGTTTTTCAG TATGTGAAAA CTTCTGAGAA      360
ACTTGGAGAG TCTCGAG                                     377

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

GAATTCGGCC TTCATGGCCT ACTGGGCGGT CTTTGCAACA ATAACAATAT CTGCTCCATC      60
CTTTGCTGCT TTCAATGCAA TAGCTTTGCC AATGCCACGG CTTGCACCTG TGATAAAAAC      120
TGTACATCCT GCCAGCCTCC CGGTGTTGGG TAACATGACT TTCGTAGATC AGAGGAGGCG      180
GCGGGCGAAG CGCACGTCGA GCGGGGGAGC GCGCTGCCT GTGGAGATCC GCGGAGGCCG      240
ACAGGATTTC TTGGCTGCCG TCCCCGCTGC TGTGCATTGG GTTAAAAACG ACAACCAACT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

GAATTCGGCC AAAGAGGCCT ACTTATTTTA CACAGCTTGA TTAAGGTCTA TGTCGGTATA      60
ATTTTTTTTA TGAGTCTNAC ACGTGGGATT TGTTGAGCTT CTTGAATTTG TATGTTTATA      120
CAAATTTAGG AATTTTTTTC ATCCATTATT TATTTGAATA TATTCTCTGT CTTCACTGTC      180
CTTTGAGGAC TCCAATTACG CATATACCTA ATTGCCTGGA GTGTCCCAT AGCTTACTGA      240
TGCTTTGTTT ATTTTTTTCT TTCTTTTTTT CTCACCATGC TTTAGTTAGG ATAGTTTTTA      300
TTACTGTTTT TTAAAGTTTG CTAATCTTTT CTTNCAGCAT GCCAGCTCGA G      351

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

GAATTCGGCC AAAGAGGCCT AGCGTCTTGG ACATGCCAGG AATAAAAAGG ATACTCACTG      60
TTACCATTCT GGCTCTCTGT CTTCCAAGCC CTGGAATGC ACAGGCACAG TGCACGAATG      120
GCTTTGACCT GGATCGCCAG TCAGGACACT GTTTAGATAT TGATGAATGC CGAACCATCC      180
CCGAGGCCTG CCGAGGAGAC ATGATGTGTG TTAACCAAAA TGGCGGGTAT TTATGCATTC      240
CCCGGACAAA CCCTGTGTAT CGAGGGCCCT ACTCGAACCC CTACTCGACC CCCTACTCAG      300
GTCCGTACCC AGCAGCTGCC CCACCACTCT CAGCTCCAAA CTATCCACA TATCTCGAG      359

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

GAATTCGGCC AAAGAGGCCT ACTACATGTA AAACACTTTT ATTCATTAAA AAGAAAAGT      60
ACTGGCTTGG ACCTACAAAT TAGTTTCATT ATTTGTTAAT GTTTGAAAGC CATTAAAAGA      120
TGAATATTAA GGTTCCTTTA TACTCAATAC TTGTAGTTTT GTTTGGGGGA ATGAGAGGAT      180
GCCCTTGTA CCTTTGTGAG GCCTCTCCAC TGAGGGTCAA TCATGACTTC TGTTTAAAC      240
CAGCCCATCC CATCTTCTCC AGCTGCTCTC CTTATGTCTT GCTTCTCTCC CCTCCAACCT      300
TCTCAGCACC AGGACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

GAATTCGGCC TTCATGGCCT AGTGGGAGCT ATTTTCTTTT TTGTGCATAT AGATATTTCT    60
TAAATGAAGC TGCTTTCTTG TCTTTTATTT CTAAAAGCCC CCTTATACCC CACTTTGTGC    120
AGCAAAGATC CCCGTGCAGG TCACAGCCTG ATTTGTGGCC AGGCTGGACA AATTCCTGAG    180
GCACAACTTG GCTTCAGTTC AGATTTCAAG CTGTGTTGGT GTTGGGACCA GCAGAAGGCA    240
AACGTCCAGC CAACACACAG GACTGCAAGA GGTCTCGAG                                279
  
```

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```

GGTAGAAGCA GGAGGTTTTT AACCTAGTCA CAGAGCAGCA CCTACCCCCT CCTCCTTTCC    60
ACACCTGCAA ACTCTTTTAC TTGGGCTGAA TATTTAGTGT AATTACATCT CAGCTTTGAG    120
GGCTCCTGTG GCAAATTCCC GGATTAAAG GTTCCCTGGT TGTNAAAATA CATGAGATAA    180
ATCATGAAGG CCACTATCAT CCTCCTTCTG CTTCACAAAG TTTCTGGGC TGGACCGTTT    240
CAACAGAGGC TCGAG                                255
  
```

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

GAATTCGGCC TTCATGGCCT AGGCCACAT AGAAGAAATG AATGAAAAGA CTTTAGAAAA    60
GCTTGATGTG AAGCAAACAG AACTAGAATC ATTATCTTCT GAACTGTCAG AAGTATTAAA    120
AGCCCGTCAC AACTAGAAG AGGAACTTTC TGTTCTGAAA GATCAAPCAG ATAAAATGAA    180
GCAGGAATTA GAGGCCAAGA TGGATGAACA GAAAAATCAT CACCAGCAGC AAGTTGACAG    240
TATCATTAAG GAACACGAGG TATCTATCAA GAGGAACTCG AG                                282
  
```

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGATAGAGCT | CAAAAACATG | GCATGGATGA | ATTTATCTCT | 60 |
| TCCAACCCCT | GTAACCTTGA | CCACGCTTCC | CTCTTTGAGA | TGGTACAACG | CCTTACTTTG | 120 |
| GATCACAGAC | TTAATGATTC | CTATTCTTGC | CTGGGCTGGT | TCAGTCCTGG | CCAGGTGTTT | 180 |
| GTACTAGACG | AGTATTGCGC | CCGAAATGGA | GTCCGGGGGT | GTCACCGACA | TCTCTGCTAC | 240 |
| CTCAGAGACT | TGCTTGAACG | GGCAGAAAAT | GGCGCCATGA | TCGACCCAC | CCTTCTTCAC | 300 |
| TACAGCTTTG | CCTTCTGTGC | ATCCCATGTC | CATGGGAACA | GTCAACAAAT | GCATGTGTAC | 360 |
| CTTAGTGGGC | TGCCACCAAA | TACAGACCAC | GGTCTTCCC | TATAGTGAGT | CGTATTAATT | 420 |
| TCAGAGGAGT | ATTTAGAAGA | GAAGCTGAAG | CTGTCGAG | | | 458 |

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATGGGACT | CCAAGCCTGC | CTCCTAGGGC | TCTTTGCCCT | CATCCTCTCT | GGCAAATGCA | 60 |
| GTTACAGCCC | GGAGCCAGAG | GAGCGGAGGA | CGCTGCCCCC | AGGCTGGGTG | TCCCTGGGCC | 120 |
| GTGCGGACCC | TGAGGAAGAG | CTGAGTCTCA | CCTTTGCCCT | GAGACAGCAG | AATGTGGAAA | 180 |
| GACTCTCGGA | GCTGGTGCGG | GCTGTGTCGG | ATCCCAGCTC | TCCTCAATAC | GGAAAATACC | 240 |
| TGACCTTAGA | GAATGTGGCT | GATCTGGTGA | GGCCATCCCC | ACTGACCCTC | CACCTCGAGG | 300 |
| TTCTCCCTAT | ACTGAGTCGT | ATTAATTTTC | AGAGGAGTAT | TTAGAAGAGA | AGCTGAAGCT | 360 |
| GTCGAG | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GGCGGTGGG | GGTTAATTAT | CTGAAACCTA | CTAAAACGGA | CTACAGTTAT | CTCTAGGCAA | 60 |
| TGCTGTTGGA | GTGTTTCCTG | CAAATGCATT | TCACTCATTT | TTTTGTGATT | ATTTTATAAG | 120 |
| TATACTGGGG | CAAAAATTTT | ACATTCTAAA | TTGTTCTTAT | TTATTATTTT | TATTATAGAT | 180 |
| ATATGAGGAT | ATTACTTACT | CTATTACACA | TATAATTTAT | CTTTTAAATT | TTCAAGTGAG | 240 |
| TTCTACAATT | AACTTTATCA | TCTAAATTCT | CATTACAGAT | AGCATTTTAA | TGTCCAGAAA | 300 |
| GAAAAAAAGG | TTTTTTATTG | TTATATGTGA | AACCATAAAA | ATATTACCAG | CTTGTGGCCG | 360 |
| GGCGTGGTGG | CTCACGCCCTA | TAATCCCAGC | ACTTTGGGAG | GCCGAATCAC | CTGAGGTCAG | 420 |
| GAGTTCAAGA | CCAGCCTGGC | CAACATGCGG | AAACCCCGTC | TCTACAAAAA | TGGAAAAATT | 480 |
| AGCCCGGCAT | GATGGCAGGT | GCCTGTAATC | CCAGCTACTC | GAG | | 523 |

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACCCAGATGA AACTTTTGGG GGGAGAGTGC CCAGACCAGC | 60 |
| CTTTGTCCAC TATGACAAGG AGGAGGCATC TGATGTGGAG ATCTCCTTGG AAAGTGA | 120 |
| TGATGACAGC GTGGTGATCG TGCCCGAGGG GCTTCCCCC CTGCCACCCC CACCACCCTC | 180 |
| AGGTGCCACA CCACCCCTA TAGCCCCAC TGGGCCACCA ACAGCCTCCC CTCCTGTGCC | 240 |
| AGCGAAGGAG GAGCCTGAAG AACTTCTGTC AGCCCCAGGG CCTCTCCCGC CACCCACC | 300 |
| TCCGCCGCGG CCTGTTCTCG GTCCCTGTGAC GCTCCCTCCA CCCCAGTTGG TCCCTGAAGG | 360 |
| GACTCCTGGT GGGGGAGGAC CCCCAGCCCT GGAAGAGGAT TTGACAGTTA TTAATATCAA | 420 |
| CAGCAGTGAT GAAGAGGAGG AGGAAGAGGA AGAAGAGGAA GAAGAAGAAG AGGAAGAAGA | 480 |
| GGAAGAGGAG GAAGACTTGT AGGAAGAGGA AGAGGATGAA GAGGAATATT TTGAAGGGGT | 540 |
| TACTCGAG | 548 |

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTTACTAGG AATTAAAAGA CGGATTTCCA AGGAGATTCA | 60 |
| GAGGCAGCAA GCACTACAGA AGTCAGAACT CCAGCACCAT CTGCTCCGTT TCTTGAAGTT | 120 |
| TGCTGAACGA GGACTCACAG CTGCAACGTG GGGTGATTGT ATTGATCAAA ACCCACTGGG | 180 |
| AAGGACAAAG AGTTTGCCGC CTTCGGGGA TCCAAGGGAC TGTGGCGACC GTGCCTCTGT | 240 |
| GCCAGCGTCC CAGGAAGGAA GCCAACCCCTG AGCGAGCCTG TCCTCTGTGG CAGGTCCACA | 300 |
| CGGTGTGGGT GGGCAGGGCT TGGACCCCGG TCTCCATGGC AGGTCCATAC AGCATGGGTG | 360 |
| GCAGGGTTTG GACCCGCCCA GCAGCACCAC GGACCCAGC CACTCTCGGG GGCAGACGTC | 420 |
| AGAATCCGTT CCTGAGCAGC TCCCGTGCCC TGGGGGCAGT CACAGAGCCC CCCAACACCC | 480 |
| CCGTGCTCTG CACCAGCCTC TCCCTCCACA CCCGAAGCAG GCGTCCATCT GTGCCTCCT | 540 |
| GGCAGCCCCCT CAAACACACA CCACCCATA TCTCGAG | 577 |

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACATCTTCAT TGCTGAGGTT GCAGCTGCTG TGGTGCCTT | 60 |
| GGTGTACACC ACAATGGCTG AGCACTTCCT GACGTTGCTG GTAGTGCCTG CCATCAAGAA | 120 |
| AGATTATGGT TCCCAGGAAG ACTTCACTCA AGTGTGGAAC ACCACCATGA AAGGGCTCAA | 180 |
| GTGCTGTGGC TTCACCAACT ATACGGATTT TGAGGACTCA CCCTACTTCA AAGAGAACAG | 240 |
| TGCTTTTCCC CCATTCTGTT GCAATGACAA CGTCACCAAC ACAGCCAATG AAACCTGCAC | 300 |

CAAGCAAAAG GCTCAGGACC AAAAAGTAGA GGGTTGCTTC AATCAGCTTT TGTATGACAT 360
CCGAACATAAT GCAGTCACCG TGGGTGGTGT GGCAGCTGGA ATTGGGGGCC TCGAG 415

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC TTCATGGCCT ACTAAAAGAT ACTTCAAAGT GACAAAAACG TGTCCTTCC 60
CCACTTAGAG ACAATGATTA ACAGGGCCCT ATATGTTCTT ACCACATACA GAGGATGCAT 120
TTATTTTTC TCTATGACAC TTGCAAAAAT CTCTACTGTA ATTAATTTGG GTCTATTATT 180
AACTCTCTGT TCCATCATAG AATGTGGCCA GGCCTTACAA TGGAGAGCCA GAGTTAAAC 240
TTCAAGTTGC ATCTGTTTTT GGGCTGAGTC ACCACCGGAC CTCGAG 286

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC AAAGAGGCCT AAAAATGAAA ACCTCTGCAC TTTAATTTTT TTCAGTAATT 60
TCCAGTATT TCTAGGTATA AAGAGCAGCT CGTTTCTCTT ATTTATTTTA GTCTCATGTG 120
TCAATACTTT CCGATGCTTT GCTTAATTCA TGTATGTGTG CAGTGCTGCA ATGCCAGAC 180
AAACGTGAGC ACACCCACCA ATCTCGAG 208

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 452 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC AAAGAGGCCT ATGATGAAGC TGGGCATTTA TAACTAGATT CATTAGGAA 60
TACAAAGAAA ATACTTAAAG GGATCAATAA TGGTGTCTTC TGGTTGCAGA ATGCGAAGTC 120
TGTGGTTTAT CATTGTAATC AGCTTCTTAC CAAATACAGA AGGTTTCAGC AGAGCAGCTT 180
TACCATTGG GCTGGTGAGG CGAGAATTAT CCTGTGAAGG TTATCTATA GATCTGCGAT 240
GCCCCGGCAG TGATGTCATC ATGATTGAGA GCGCTAACTA TGGTCGGACG GATGACAAGA 300
TTTGTGATGC TGACCCATT CAGATGGAGA ATACAGACTG CTACCTCCCC GATGCCTTCA 360
AAATTATGAC TCAAAGGTGC AACAAATCGAA CACAGTGTAT AGTAGTTACT GGGTCAGATG 420
TGTTTCCTGA TCCATGTCCT GGAACGCTCG AG 452

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

GAATTCGGCC AAAGAGGCCT ATCTTCCTGA AGAGCAATGG AGCCGCTTTT ACTTGGAAGA      60
GGACTAATCG TATATCTAAT GTTCCTCCTG TTAATAATTCT CAAAAGCAAT TGAAATACCA      120
TCTTCAGTTC AACAGGTTCC AACATCATA AAACAGTCAA AAGTCCAAGT TGCCTTTCCC      180
TTCGATGAGT ATTTCAAAT TGAATGTGAA GCTAAAGGAA ATCCAGAACC AACATTTTCG      240
TGGACTAAGG ATGGCAACCC TTTTATTTC ACTGACCATC GGATAATTCC ATCGAACAAT      300
TCAGGAACAT TCAGGATTCA CAAACTCGAG                                     330

```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

GAATTCGGCC TTCATGGCCT AAGCAAACCC AGAGGTGGAT GTTATGAACA GCTGTGTCTG      60
CCAAACACAT TTACCCTTTT GCCCCACTTT GAAGGGCAAG AAATGGCGTC TGCTCTGGTG      120
GCTTAAGTGA GCAGAACAGG TAGTATTACA CCACCGGCCC CCCCCCCCCA GACTCTTTTT      180
TTGAGTGACA GCTTCTGGG ATGTCACAGT CCAACCAGAA ACACCCCTCT GTCTAGGACT      240
GCAGTGTGGA GTTCACCTTG GAAGGGCGTT CTAGGTAGGA AGAGCCCGCA GGGCCATGCA      300
GACCTCATGC CCAGCTCTCT GACGCTTGTG ACAGTGCCTC TTCCAGTGAA CATTCCCAGC      360
CCAGCCCCAT CCTCGAG                                     377

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

GAATTCGGCC TTCATGGCCT AGGCAAGGTC TTCGGCTCGT GCCGTTCTAA GCCGGAGAAT      60
TCTCGCGGGA GCAGGGTTAC GTCCTCGTGG GATTCTGTGG CGGTGGCTGA GGTCTCCAG      120
CAGCCTGACC TGAGTGGGTT AGTGATCCAG AGAAACCAGC AGGCCAACTT GGTGAGGAAG      180
GTTCCGGGAAG CTGTTGGAGC AGTGTGGGGA ATTTCCACC AGGATGAGTA TGATTGGCTG      240
TGATTTTAGA TCGTAAAGCT GAAAATTGAA ATCATGAAAG TAGACAGGAC TAACTGAAG      300
AAGAACTCGA G                                     311

```

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

```
GCATTGATGG AAAAGCATAA TGTCTTAGAA AAAGGCTTTC TAAAAGAAAA AGAGCAAGAG      60
GCCATTCTCTT TTCAAGATAG ATACAAAGAA CTTCAAGGAAA AACATAAACA AGAATTGGAA      120
GACATGAGGA AAGCTGGTCA CGAAGCCCTC AGCATTATTG TGGATGAATA TAAGGCACTA      180
CTGCAGTCTT CAGTTAAGCA ACAAGTAGAA GCTATTGAAA AACAGTACAT TTCTGCAATT      240
GAGAAACAGG CACACAAGTG TGAGGAGTTG CTAAATGCTC AGCATCAGAG GTCCTTGAA      300
GTGCTAGATA CAGAGAAGGA ACTGTTAAAA GAAAAAATAA AGGAAGCCCA TCTCGAG      357
```

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```
GTTCTAGACC TGCCTCGAGC GTTAATGGTA TAAATCACTT GTTGTAAG TATTGTTTT      60
AAATATTGCC AGATTGATA TCTTAGTATT GTATTTTAT ATTTGTCTTC ATGTGTTTT      120
GTTTTCTCAT AAGTGCTGT ACCCCCTTT TTTTCTTT AAAGAGAAAT AATGAGAGAG      180
ATTGTCTGTC TTGAAGTTCT CAGTGCCTGT GCATTGCTGC CACTACACAG CTAGTATCAT      240
GACAGCAGCT TCAGAACAG AGCTGGCTTC CAGGCAAGGC TGGTGGGGA AGAAAGAGAA      300
AAACAAAAGA ATTATTCTC TATGCCGAGA CCAGCTCGGT CAGGGAGACC CTAACCTAGC      360
GGTGCTAGAG GAATTAAAG CATAGACACA GAAATATAGA GGTGTGAAGT GGGAAATCAG      420
GGGTCTCACA GCCTTCAGAG CTCAGCCACG AACAGAGATT TACCCACGTA TTTATTAACA      480
GCAAGACTCG AG                                         492
```

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```
GAATTCGGCC TTCATGGCCT ACTTCCCTCT AAGGTCCCCA AATGCCTCTC ACGTGCCTAG      60
CATTTAGCTG CTGACCGAG CATGCTCACT GACAACTTT TGGCCAAGAA GAGCCTTTTG      120
GTCTCTCTTG GTCAGATCTA GGAGGGCTTC AGGACTCTCC AAAACTCACC CACTCAGAGA      180
GCCTGCCAGG AACACTCAGC TGAGCGATGG CATTGTGGAG CCTGGGTTT CAGAAGGGAG      240
CCCATAGTGA GTGGTAGCAT AACCTTGTTA AGGTTGTATT TTCCTTAGAT ATAGAAACAA      300
ATCAAATGCT GCTAAATTGG TAAGGGATGG AGTTTTATA TCACGTCACA TTTTGCTGAG      360
CCGTAACCAG ACAGGGAAAA AGCAGAGACC TCGAG                                         395
```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

GAATTCGGCC TTCATGGCCT ACCAAGTTCT AACTGTAAAA TGGGGACATT TTACCTTTCT      60
TTCTTTGGAT AGGATCAGTT CTTAAGAGCA GCCCCGGTAA CTGGAGGAAT GGGAGCCGTT      120
TTGATGAGAA AAATGGGCTG GAGAGAAGGA GAAGGATTAG GAAAAACAA AGAAGGCAAT      180
AAGGAACCCA TCCTAGTTGA TTTAAGACA GACCGAAAAG GTCTTGTTC AGTAGGAGAA      240
AGAGCACAAA AGAGGCCTCG AG                                     262

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

GAATTCGGCC TTCATGGCCT ACCCATTTGT CAATTTTTC TTTGTTGCAA TTGCTTTTGG      60
TGCCTTTGTC ATGAAACCTT TGCCTACAGG TGCTGTTTAT TTACACCCTT GTCCCAACCT      120
CACCCACTC CCTTTCTTTT GCTGGTGGGA AGTCAGTAAG AACTGTGGGT GGGGTTCTGA      180
GGTAATCAAT ACAAAGAAGA AGGTAAGAAA TTGGAGGGGA CTCAGGGGAG ATGGCAATGC      240
TGACAAGGGG TTGGATGGAA TTTGTTCTGT AACTGGAAG CAGCTCGAG                     289

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

GCTCCTTCTG TATCCTTCCT TTCCCATCTG TCTGCTTCTA ACAAATAAGA CAAGCTAAGA      60
AGCAGCTTGT TTCATGATTC TATACTCACT TCCAAGCTTT CTCTGCATAG ACTTTCCTAG      120
TTTGCCACTT TATCTTTTCT CCATCCCTCC AGCCAGTCAT GAGATTCTAC TCCCCATTCA      180
TACATGCATT TATTTATCCA GACTTTACTG AAGGCTTACT CTTTGAAGTT TGCAAAATGC      240
CAGTGAGGCA AAGCATGCAT CCTGTACAGG AAAAAGCTCAG TCTAGAGGGG AGAGATAAGC      300
AAACAAGTGA TTACCACACC AGGCTCGAG                                     329

```

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

| | |
|--|-----|
| ATTGAATTCT AGACCTGCCT CGAGAGCTTT TGAGATTGTC TATTTTGTCT GAGTGAGTTT | 60 |
| TGGTACTTTA TTGTTTTCGA TTGGTCCATT TCTTCTACGT TGTCAGATCT CTGAGTGTCA | 120 |
| AGTTGTTTCAT AGTACTCCGT TATTATCTTT TTCATGACTG TAGGATCTGT GGTGATATTG | 180 |
| ATGATTGTG TCTTCACTCC TTTTGTGG CCTACACTCG AG | 222 |

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAACCTGCAG AAATGAAGAC TAGAGTACAC AGCACACTCA | 60 |
| GAGCCCAGAC AGACTTCGTC CCAGGACATC ATCTGTTCTT GATGCCCATC CTCTCTCCT | 120 |
| AAACATCATT TACTTTTTCC TCTAAAAGTG CCTGCAGACC CCCACTACTC TCTCCCATGG | 180 |
| AGAAGGGCAT ATAAGCTTCG AATCTCACGG GGTATTGGG CACTCTGTCT CTGTGTATGC | 240 |
| TCCTATGCAT GTAATAAATT TATGTGTCCT TTCTCCTATT AATTGGTCTA ATGTCCATTT | 300 |
| ATTCCATAGA TTCAATTATC AAACCTCAG AGGGCAGAGG GAAAAATTTT ACTCCCTTAT | 360 |
| ATCATCAGAA ATATAAATAA AAATAGCACA ACACTCAGTA AATGATTATG TTATTATTGT | 420 |
| TATGTTTGTA ATATCTTGGT GTCTGGTTAT TTAAATCAT ATCACTTAA GAAACAGTGT | 480 |
| TCCTTAGGCC ATGAAGGCCG AATTG | 505 |

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

| | |
|---|-----|
| GTATGAACAT TGAGGGCCCA GATCTCAATG TGGAAGGTCC GGAGGGAGGC TTGAAAGGTC | 60 |
| CCAAATTCAA GATGCCTGAC ATGAATATCA AAGCTCCCAA GATCTCCATG CCTGACATTG | 120 |
| ACTTAACTT GAAAGGCCCC AAGGTGAAAG GTGATGTGGA TATTTCTCTT CCCAAACTTG | 180 |
| AAGGGGATCT GAAAGGGCCA GAGGTGATA TCAAAGGCC TAAAGTGGAC ATCAATGCCC | 240 |
| CAGATGTGGA TGTTCATGGT CCAGACTGGC ATCTGAAGAT GCCCAAAGTG AAAATGCCCC | 300 |
| AGTTCAGCAT GCCTGGCTTC AAAGGAGAAG GCCCTGAAGT CGATGTTACC CTCCTAAAG | 360 |
| CTGACATTGA CATTCTGGT CCAATGTAG ACGTTGATGT TCCAGACGTG AATATTGAAG | 420 |
| GTCCAGATGC AAAGCTGAAG GGCCCCAAGT TCAAGATGCC TGAGATGAAC ATCAAAGCCC | 480 |
| CCAAGATCTC CATGCCTGAC TTTGACCTGA ACTTGAAGGG ACCCAAATG AAGGGTGTATG | 540 |
| TGGTTGTGTC TTTGCCCCAA GTGGAAGGTG ATCTAAAAG CCCTGAGGTG GACATCAAGG | 600 |
| CCCCAAAGT GGACATTGAC ACTCCTGACA TTAACATCAA GAGGCTCGAG | 650 |

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```

GAATTCGGCC TTCATGGCCT AGGGGCTGGA GGGTGGCCCG AAGCAGATGG GGCCGGCCTT      60
GCAGGCACTT CTAAGGCCTT GGGGTTTGCT TCCGAGGGAG TAGGGAAGGA GAGCGATGTC      120
ACCCTGTGAG GCTTGGTCAC ATACCCCAAT GGATTTGGTA GCACACGCCA CAGTGAAGGT      180
ATAAGCTACT GTCATCACAC GTAATTATTT CATGAAACAG AAAATTTTAA AATAAAAGAA      240
AATAGAAGTT TCCTATTTT CTTCTCCTGC ACTATTGGAT CATCCTGTTT AGCCCTCTTT      300
TAAGACAAAT GGACTTAGCA AACGAGTGTA AATAGGAATG AATGGTTTGG TGGGGTTTAT      360
TTTATTTTAT TTTATTTTAT TTTATTTTAT TTTATTTATT TTATTGAGAC AGAGTTTCAC      420
TCTTGTTGCC CAGGCTGGGC TCGAG                                         445

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

GCCTGCCTCC AGGCCTTTGC TCCCACTGTT GNCTCCACTT AGAATAACAT TCCACCCCAT      60
CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCCTTA AGGCCAGTTC TAACCCTAAC      120
TGACAACAAA TCATCTCTAC ATGATCTTTT CCTTCTGGGA ATGCCTGCAG CACTGTTTAA      180
TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA      240
TGCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

GAATTTGACA TCTTAGAACA TTCTGCAACC TTTTGCCTGG GAAATGGAAG CAGATCTAAT      60
CTTTACCACC CTCATGGCTC AAGGACCTCA TCTGGCAGCC TGGCTCATGT TTTTCAGCCA      120
AGTAGCTTCC AGCTTACAGC AGCCCTCAAA TTTGGACCTG CCACCAGCTC CAGAGCTTGA      180
CTGGATGGAG ACAGGACCAT CTCTGACATT CATTGGCCAT CAGGATATAC CAGGAGTTGG      240
TAACATCCAC TCAGGTGCCA CACCTCCCTG GATGATCCAA GATGAAGAAT ACATTGCTGG      300
GAACCAAGAA ATAGGACCAT CCTATGAAGA ATTTCTTAAA GAAAAGGAAA AACAGAAGTT      360
GAAAAAACTC CCCCAGACC GAGTTGGGGC CAACTTTGAT CACAGCTCCA AGGACCTCGA      420
G                                         421

```


(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

GAATTCGGCC TTCATGGCCT AAGCCAGTCA ACCAGCAGTA TTAGTGCTGT TTTCAAAGAT      60
TTAAGCTCTA TAAAATTGGG AAATTATCTA AGATCATTTT CCCTAAGCAT TGACACATAG      120
CTTCATCTGA GGTGAGATAT GGCAGCTGTT TGTATCTGCA CTGTGTCTGT CTACAAAAAG      180
TGAAAAATAC AGTGTTTACT TGAAATTTTA ACTTTGTAAC TGCAAGAATT CCAGTTCAGC      240
CGAGCCACTT CGAG                                         254

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

GCAAACAGAC AAGGCTTACA GGTTAGTTCA GGATCTGCGC CTTATCAAGC AAATTGTTTT      60
GCCTATCCAA CCTGCGGTGC CAAACCCATA TACTCTCCTA TCCTCAATAC CTCCTCCAC      120
AACCCTCCA TAACCCATTA TCGGTTCTG GATCTCAAAC ATGCTTTCTT TGCTATTCCT      180
TTGCATCCTT CATCCAGCC TCTCTTTGCT TTCACTTGGG CTGGCCCTGA CACCCATCAG      240
CCTCAGCAAC TTACCTGGGC TGTACTGCCA CAAGCCTTCA CGGACAGCCC CCATTACTTC      300
AGTAGCCCTC GAG                                         313

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```

GCCTGCCCCC ACCTTACAGG TCTGGGATGT ACCTTTCCAT CTGTTGCTGC TTTCTTCTAT      60
GGGCCCCGTC CCTCACTCTC AAGAACCCTCA ACTACTCCGT GCCGGAGGAG CAAGGGGCCG      120
GCACGGTGAT CGGGAACATC GGCAGGGATG CTCGACTGCA GCCTGGGCTT CCGCCTGCAG      180
AGCGCGGCGG CGGAGGGCGC AGCAAGTCGG GTAGCTACCG GGTGCTGGAG AACTCCGCAC      240
CGCACCTGCT GGACGTGGAC GCAGACAGCG GGCTCCTCTA CACCAAGCAG CGCATCGACC      300
GCGAGTCCCT GTGCCGCCAC AATGCCAAGT GCCAGCTGTC CCTCGAG      347

```

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

GAATTCGGCC TTCATGGCCT AGCAGATGAT TGACATTGCT ATCGATGGTT TCCTTTTGAC      60
TCCAGTGCAG AAGATCTGCA AGTATCCCTT ACAGTTGGCT GAGCTCCTAA AGTATACTGC      120
CCAAGACCAC AGTGACTACA GGTATGTGGC AGCTGCTTTG GCTGTCATGA GAAATGTGAC      180
TCAGCAGATC AACGAACGCA AGCGACGTTT AGAGAATATT GACAAGATTG CTCAGTGGCA      240
GGCTTCTGTC CTAGACTGGG AGGGCGAGGA CATCCTAGAC AGGAGCTCGG AGCTGATCTA      300
CACTGGGGAG ATGGCCTGGA TCTACCAGCC CTACGGCCGC AACCAGCAGC GGGTCTTCTT      360
CCTGTTTGAC CACCAGATGG TCCTCTGCAA GAAGGACCTA ATCCGGAGAG ACATCCTGTA      420
CTACAAAGGC CGCATTGACA TGGATGCTCG AG                                     452

```

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```

GATAACTTGA GATCAAATCA GTCATATTG ACTCTTCTCT TTTCACTCC TTTTATATCT      60
GATCAGTCAG CAGTTTTTTG AAACCCTGTT CGAAGCAGTT CTCAACACTT GTGCACCCAT      120
TCTTTCTCCT ACACCACTCA ATCTAGACCC TCACATGTGG CTGTCCTGCT TTCCTTCTCT      180
CCTACTTCTA AGCTATTCTG TGGAGAGATG TCAAAGTAAT CTTCACAAAA AATCTGATTG      240
CATCACTTCA CATCTCGAG                                     259

```

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

GAATTCGGCC AAAGAGGCCT AATTAGAAAT GGCTACTCCC CAGTCAATTT TCATCTTTGC      60
AATCTGCATT TTAATGATAA CAGAATTAAT TCTGGCCTCA AAAAGCTACT ATGATATCTT      120
AGGTGTGCCA AAATCGGCAT CAGAGCGCCA AATCAAGAAG GCCTTTCACA AGTTGGCCAT      180
GAAGTACCAC CCTGACAAAA ATAAGAGCCC AGATGCTGAA GCAAAATTCA GAGAGATTGC      240
AGAAGCATAT GAAACACTCT CAGATGCTAA TAGACGAAAA GAGTATGATA CACTTGGACA      300
CAGTGCTTTT ACTAGTGGTA ACGGGCTCGA G                                     331

```

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGAGCATTT ACCTGTCTGA CAATTGTATT TTTAATGATA | 60 |
| GTTTGCTTTT ACTTGGTCTT TATATATTCA ATTACAAATT ACTGATATTT TGTTTAAATC | 120 |
| TACCACATTT TTCCATTGA CTGTTTATTT TTATGTCCTT TCTTCTTTT AGATTAAAGTC | 180 |
| TTTTTCTTC TCACCCCTC ACCCTCCCC CCTGGTTATA CATTCTTTTA CTATTCTTTT | 240 |
| TGTTATTCCA TAGTTGCAGC AACTCGAG | 269 |

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACATTGAGGT AAGAGATATT TAAAAGGTTT TTAGGTGAAA | 60 |
| TTGAAGCAG GGATGAGATT GGGATTCCAC CTTTGTTC ATGCATACCT GTTGATAATC | 120 |
| AGTGTTCTT GTATCGACTC CGTGCAACT CCAGAGCAGG GGGTATCCTC CTGTAGTGCA | 180 |
| CCTTCTCTT TGGCCTGGAG GCAGCACTTT CTGTGCCTGG GCAGCAGAAA TGGGGAATGT | 240 |
| TCTTGGTCC GTTGAAAAA CGGGCCCCAA CATCTAGCCC TGTTGCATAA GGCATGGAAT | 300 |
| TGCCCAGTTG GGGAGGACCT GTGCTGAAA GGGATCATCA AACTCCATCT GCCCATCAG | 360 |
| ATGCCTGAAC TCTTGATACA ACTCCTGCCA TCCAAGCTAC TCGAG | 405 |

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACTCGTACTT ATTTATAAAA AAAGTTAACT GTAAAAACAGC | 60 |
| CTCAGGCAGG TCCTTCAGGA GGTACTCCAG AAGAAAGTAC TGTTATCATA GATGACAACT | 120 |
| CCATATGTGT TATTGCACCT GAAGACCTTT CACCTGGACA AGATGCCGAG GTGGAAGACA | 180 |
| GTGATACAGA TGATCCTGAG TATCTTAGTT TTTTGTGTTT TGTTGAGACG AAATCTCACT | 240 |
| CTTGCCCCCA GGCTGGAGTG CAATGGCAG ACCTCGGCTC ACTGCAACCT CTGCCTCCCG | 300 |
| GGTTCAAGCG ACTCTCCAAG CCTCGAG | 327 |

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGAATAATAC ACTAGTAAAA AAAAATGTAT GTCAGGCACT | 60 |
| GGGAAGGGCA GTAGGAATAT AGAAATGAGA AGCCGTGGAT TAGAGACTCA CAGTCTACTG | 120 |
| GGTAAAAGAA TACGAAAGCC AATGTATTAT ACTGTGGTAG CTGCTTTAGT AGATGTATGG | 180 |
| ATAGAAAAGT AACAAAGAGAA GAGAATGACT ATCTCTGCCT AACAGAAAGA TATTTTAAAA | 240 |
| GAAGGGTTT GGGGCTGGAT TTTGAAGGCT CAATAGGCTC CTACCATATA GAGAACTAGG | 300 |
| AAGCGAGTCC TCGAG | 315 |

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTATCCAGG TTTACATTTT AAGGCAGTCG AGACCTTATT | 60 |
| CACGTGGTAT ATAAACAACC ACATTTCTCT TTTATATGGA ACAACACTTT TCATTGCGG | 120 |
| CTGGCCTTCT CACTAGCTTA TGCTTTTTTT TTTAAGACC TTTCTTAGCA CTCGCTGAAC | 180 |
| TCCTCCCCCT CACAATCAAT CTCAGCAACT CAGCAGAGTC GCTTCAGTTC ACAGCTCTTA | 240 |
| ATCCTTCACT CCAGACTAAA GCTAATCTTA TGCTCTCAA CAGCTACAAC TCACTGTTAT | 300 |
| CACAGTTCG ACAGCAGAGA CTCGAG | 326 |

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

| | |
|--|-----|
| GAATTCGCCA AAGAGCCTAT AGAAATAATA CCACGACCTG CGCATTCAAA GCTGTTGTAT | 60 |
| CTGGATTGTG ACTGCGTGGA AGGTCCAGGC GGGAAGACAG GGGCTGTTGC TTTTCGTTAT | 120 |
| AAACTCTGCA TTAATTGATT TTTGCACTAC GTACATTTAC TTTGATAACA CTGGAAGAGAA | 180 |
| TAAATTGGCC ATGTAGTGTA GCTTCCAAAA AAAACTATTG CTTGGGTTTC AAGGTCAAGG | 240 |
| AAATTCATT CTCATCAGTT TCTTGGGAAA GAGGAAGTGG AATGATGTTG TCAGAAAGTG | 300 |
| AAACCATGGG TCATTTTCAG AACTACTCAG AGTAATAAAT ATTTTGTGTC AGTTTGTTC | 360 |
| TTACAAGTGA AATGGTCCCC TCGAG | 385 |

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AAGAGATTTT | TATTATGATT | TTGATTTCCT | TACTACAACA | 60 |
| TTGCATGTGT | CTGGAGTATA | GCCATTACAC | TTTATGAAAA | AGGCAAAATG | GTCATTTGGG | 120 |
| GTGTTTTAGG | AAGTTTGCCA | AAAGGCTCCT | TTGTCATTAT | AATCCTTCCT | AAGCTGCCAT | 180 |
| CCACGGGTTT | AGGTCATGGA | TATGAAAAGT | GAAAGGGTTT | AGAGATGAAG | TAGTGTCCCC | 240 |
| TGAGTGCTTA | CCAACCTGTT | AATCTTTTGT | AGATGTTAAT | TTTTTCATAT | AGAGCCCCCT | 300 |
| AAAATCTTGA | TGGCTCTAGA | TCAGTCAAGC | CTAAGAGAAG | ACGTATTTAT | GGAAAAAAC | 360 |
| AAAAAACAAA | AAAACCTTGC | TGGATTGCTA | GTAATATCTA | CTTCTTGAA | ATTAATACTT | 420 |
| CATATTTTTT | AAAAAATTA | TTGATGCATT | AGGACTCGAG | | | 460 |

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | AAAGNGGCCT | AGGAAAAACA | TGAAATACAT | AAATGGATTA | ATTTTGCAAA | 60 |
| TTAATCTNGC | AAATTAATCT | ATAGCTCTTA | ATGTTTCTTC | CAAATTAAAG | GAAAAATGGA | 120 |
| TAAAGGAAGTA | CTTTCTTGGC | AAACTGTAGA | TGAATACTGA | ATAAAAGTCA | TTCTTTCCTA | 180 |
| AAGAAGAAAA | GTGCATTTTA | GTTTTTTAGA | AAAAATGTAA | TTTGTAGAAAG | TCTCTTCTAT | 240 |
| GCAGATTTTA | GAAAGTCTTT | TCTATTTTGA | GAAAGTCTTC | TTGTATGCAG | ATTTTGTTC | 300 |
| ACTTCCCCAT | CTGTACTTAC | CAAAGGAAAA | ATAAACAGTT | TATAGAATAT | TAATAGAATA | 360 |
| ATTATGTGCN | ATGTAAAATA | TGTTGAATCT | CCCTAATTTA | TATTTACTAT | GTGAATATAA | 420 |
| ACTACAGAAT | AAAGAACTG | TTCTCCTTT | TATCCATTAT | TTTGTGAAA | ACAACTAAAG | 480 |
| AAATCTTACA | GATTAATGTT | CATATTAATA | GGACTCCTCG | AG | | 522 |

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGGTAGTTAT | CAAGAGATTT | TAAAACTTCA | ACCCTTTTTTC | 60 |
| TCTTATAGTT | AGTGAAGAGA | GTAGAATATC | TCCAGTTTTG | GCTGACATCT | CTACAACCTG | 120 |
| AACAATTGGC | TTAAACTTCA | CTTGGGATTC | CCGGTTGCTT | GTTTTAGCAT | GGCNAAATTT | 180 |
| GGCGTTTACA | GAATCCTTCT | TCTGGCTATT | TCTCTGACAA | ACTGTCTGGA | GAGTACAAAA | 240 |
| CTGCTGGCAG | ACCTTAAAAA | ATGTGGTGAC | TTGGAATGTG | AAGCTTTAAT | AAACAGAGTC | 300 |
| TCAGCCATGA | GAGATTATAG | AGGACCTGAC | TGCCGATACC | TGAACCTCAC | TAAGGGAGAA | 360 |
| GAGATATCTG | TTTATGTAA | ACTTGCAGGA | GAAAGGGAAG | ATTTGTGGGC | AGGAAGTAAA | 420 |
| GGAAAGGAGT | TTGGATATTT | TCCCAGAGAT | GCAGTCCAGA | TTGAAGAGGT | GTTTCATATCT | 480 |
| GAGGAAATTC | AGATGTCAAC | GAAAGAATCT | GACTTCTTTT | GTCTTCTTGG | AGTAAGTTAC | 540 |
| ACATTTGACA | ATGAAGATAG | TGAATTAAAC | GGTGAACCTG | AG | | 582 |

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

GAATTCGGCC AAAGAGGCCT ACTGATCAAG TGACCCATTA CTGCGGGAAA AAACCACACA      60
TACAAAAGCC TTTGACCCCA GTAATTTTGT ATTGGTATAT TTACCCTGAT CTTAAACTGC      120
AAGGAATGTC CGCAATTAGA GTTTTTCTTT GTTTTCTAAG TCTGAAACTT GATAATCCAT      180
TTCTGCCTTC CCATGACGAG TGGACATTCC TCCAGCCAGT GGTGAGTTCC TCTTTCCTTC      240
GCTCTCAGCA AGAGCATGGG TTGCCCTCCC ATCTCGTAAG CAGAGCCTAC CACAAACGCA      300
GCTCAAATCT CGAG                                     314
  
```

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

GAATTCGGCC AAAGAGGCCT ATTGGGTCCT ATTTACAAC TTAAGAATGG AGGCATACTT      60
CAGGAAAGAA AGCACCAGTG CAGTTCCAAT TTATTATTGT ATCTGCTGTC TTGAGAGTAC      120
AGGGTGTATG AGAGTGCACA GTGGTTTAGA ATCACTATGG AATTTAAAAA GACCCAGAGA      180
CATTACAAG AATCCACATT CTAAGTCGTC AGAATCCACA TTTCTGACCT TGTCTGCTGG      240
GGCCTGCTCT GTTTTGTATG GCTCAAAATA TAATTCTTTT ATTGAAATAC ATGTTCTCTCA      300
TCCTGTTTCA GGGCTTCTGC CTGGAATGTT CCTCCCCCTA GCATTGTAG GGCTGGCTCC      360
TTCCTGTCAT GCAGGTCTCA GCTCAGATGA CCCCATCTCA GAGAGGGCTT CCCTGACCAA      420
CCAATCTACA GCCCTTCCTA GTCACTTTTT TCCACATCAC CCTCTTTATG CATGGAGGCA      480
GATAGGTGTT TTACCCTGTT TATTTATTAT TATTATTTT TTGAGACAAA GTCTTGCTCT      540
GGCACCCAGG CTCGAG                                     556
  
```

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

GAATTCGGCC AAAGAGGCCT AGAAGTAACG GAAGCTACCT TGTATAAAGA CCTCAACACT      60
GCTGACCATG ATCAGCGCAG CCTGGAGCAT CTTCTCATC GGGACTAAAA TTGGGCTGTT      120
CCTTCAAGTA GCACCTCTAT CAGTTATGGC TAAATCCTGT CCATCTGTGT GTCGCTGCGA      180
TGCGGGTTTC ATTTACTGTA ATGATCGCTT TCTGACATCC ATTCCAACAG GAATACCAGA      240
GGATGCTACA ACTCTCTACC TTCAGAACAA CCAAATAAAT AATGCTGGGA TTCCTTCAGA      300
TTTGA AAAAC TTGCTGAAAG TAGAAAGAAT ATACCTATAC CACAACAGTT TAGATGAATT      360
TCCTACCAAC CTCCCAAAGT ATGTAAAAGA GTTACATTG CAAGAAAATA ACATAAGGCT      420
  
```

CGAG

424

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

| | |
|---|-----|
| GAATTCGGCC TAAGNGGCCT ACATAAAAGT AAGAAAATAT CTTACTAAAA TCTCTTTTCT | 60 |
| TATAACATTT AGNTTACGTA TATATTTTAT CTCCTTTTT TTGNAATATA TATAAATCAA | 120 |
| ATAACAGCTG AATAAACCTT TGGTCTTTT TTTTTTTTT TGTCTCAGGA TTGTCTTTAT | 180 |
| CTGGGACCCG AGATTAATTG CTTTCGTTTT GCTTTGGCAA AAGATTGTTT TTACAATTTT | 240 |
| TAGTCTTTTA AAGTTGACAC AGATTTGTTT AGTCTTGCTC ATTCTAAAAG CACACAAAAG | 300 |
| TTGAGCATAA AAATAGGATT AAATTTAGCA ATAAAGAATT ATAAAGACTA AAAGATACTG | 360 |
| AGTAAGTTGT TTGACAGAAA CCGATTATC CATGATGATT ATTTGCAGGC TTCTCGAG | 418 |

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAACTCCAG AGGCAAGTGT TATATGAATT ATGCATTGTA | 60 |
| TTCTACATGT TTATTAGACA TGTATGGCAG ATACATTTAT ATTTTACTAA TGGTTATGAT | 120 |
| GACTTTAATA ACTTTCAAAG GATTATGGGG ACTCGAG | 157 |

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ATGTTTTTAC TACTATTATT TTTTTTTACC CAAGGGAGAA | 60 |
| AGACAAAAAA ACGGTGGGAT TTATTTAACA TGATCTTGGC AAACGTCTTC TGCCTCTTCT | 120 |
| TCTTTCTAGA CGAGACCTC CGCTCTTTGG CCAGCCCTTC CTCCCTGCAG GGCCCCGAGC | 180 |
| TCCACGGCTG GCGCCCCCA GTGGACTGTG TCCGGGCCAA TGAGCTGTGT GCCGCCGAAT | 240 |
| CCAAGTGCAG CTCTCGCTAC CGCACTCTGC GGCAGTGCCT GGCAGGCCGC GACCGCAACA | 300 |
| CCATGCTGGC CAACAAGGAG TGCCAGGCGG CCTTGGAGGT CTTGCAGGAG AGCCCCGCTGT | 360 |
| ACGACTGCCG CTGCAAGCGG GGCATGAAGA AGGAGCTGCA GTGTCTGCAG ATCTACTGGA | 420 |
| GCATCCACCT GGGTCTCGAG | 440 |

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```

GAATTCGGCC AAAGAGGCAT AACATAGAG AAATTGGTGA TGTTAAACCT TCTGAATTTT    60
GTTTAAAGTG CACTGGGAAG TGATGGAAGG GTTTGTAGCA TAGCAGTAAT CTGATCTGAT    120
CTGATCCGGT GTGAATGTCT TTTTAGCAGA TGATTTTCATT TTACCAGCTC TCTNGAAAGT    180
TTAATCAATG TGATAGCCAT GACAGTTTAT TAACTACTT ATTTGAGAAA GTAAGTGCCT    240
GTGGGAATCC AGATTATTTG TTTACTTCAT TTTAGATGTT AGTGCTAGCA CCCTTGTTTA    300
ATATTTGTTT TAACACTTAT ATACTTAAAA GCAGGAAATC TCGAG                    345

```

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

GAATTCGGCC AAAGAGGCCT AAGAACTCAC AATAAAGTAT CATATTCCTC TCTTTTGACC    60
TAGAATTCAT AGCCCTAGTA ATCTCGTTTT GATTAGATGC TTTGATTGGC AGTTATACAT    120
CTTTGATAAC ATTTTCAATG TGAAATGAAT TATTCTTTTCG TTAAAGCCAT TTTAAGCAGA    180
ATGTCTATAA ATGAGGGCCC ACGAGAAGGA ATAACAAAGC AGGGGTGTTG GGGATGGTGG    240
CTGGGGAGCT TTGGTGTATT TATTAACCTG TGGTTGAGTT TTGCGATGTG TGCAAGTACA    300
CACAGCCCCG AACAACTCGA G                                         321

```

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

GAATTCGGCC AAAGAGGCCT AGTTTTAAAA CGTATTGTTT AATTTTCNAA CATTTAGGGA    60
TTTCCAGAT ATCTTNGTTG TNGGTTTCTA ATTTGATTCC ATTATGGTTA GAGACCATAC    120
TTGGTATGAT GAATTA AAAAATNTA GAGGTTTGTA TATGGCCTGA AACATTTTTT    180
AGGTGAGTGT TCAGTTTGTA ATAGGAAAGA TGTGTCCTGC TGCCGTTAGG TAAAGTGTTC    240
CATAAGTAAT AATTAGTCA AGTTGGTTGA TCGTGNTAAG GTCTGCTCTA TCCTTGCTGA    300
TTTCTGTCT GCTTGTCTA GTGATTACTG AGAAAGGAGT GTTGAAGTCN ACAACGATTG    360
TTATGGGTTT GTTCTCTTC TCCNTGAAAT TCTGTCTGNN TATGCGTCCT GTATTTTGAG    420
GACCCCTCGA G                                         431

```


(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

GAATTCGGGC TTCATGGCAT ANGACAGAGGT TCCGGGNCCA GNNCANGCNC GGGACAAGNT      60
CAGAGATGAN GTTGCCCAANA GTNATGNNGA ACTCCAGTNC CCGNTGTCCC CGGNTTTTCT      120
CTCTTGTTGGN ACATGGGGAN NTNTGGANTC CAGCTCCCAG NACTGGAGTG CTATTCAANT      180
GATCNAGGAN GGAAGTGACA NAAATGTTTT TTTTTTTNTT TTTTAAAAAA GNAGNNNCNN      240
GGGGATCNGA AGNAGATGAA TGCCCTCAAA GGCCATGNAT GTACTTCAAA NGAAGTGGNT      300
NNTGAAAACA GNTNNAANAA TGTAAANCGA NAGTNAAAAT NNATGTTGNG GANGAAGGAA      360
NTTGGTGGNN AGTNAAAAAA GAAGTAANCC GA                                     392

```

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

GAATTCGGCC TTCATGGCCT AGGTGTGCTT CCCTTTCCCC ATTTCCCAT ATTCCCAGCT      60
GTATAGTAGT GTAGTGA AAA TCACTTGAGA TGTGGAAGAG TAGTCTGGTC TAGGAAGAGA      120
GAGGGAAAAAG TAAGTTTCCC AGGATAAGAG GGGGAAAAAA GGCCCCAAAG CCTTCTCAAT      180
GAGGAATGGG GAAGGAGGTT TTGCTGCCAG GTTTTACTAA GTGCATTGA ATGAACCCTG      240
CTATTGTAGT CCTCTTTTAT TAATGCTTTC CTGACATTTA CCCTGTTAGT TGAGGCTACT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

GAATTCGGCC TTCATGGCCT AATCACNGNA GTGACTGACA TTATATATTA NGGATCAAAT      60
TATGTCCACA AGCAATATTA TATAATCTAC GTAGAAGTGT AATAACAAAC AAGAGTACAC      120
TTAAAATTAC TTAAAAGAT GTCTTTAGTT CATTCCAATA TAATTCTTGA TTTAAAATTAG      180
GATTATTTCT ACATTTTAGG ANNTACAAAG GATCACGGGT AACATGGATT GGGNCCANAT      240
ATTTTTTTAA AGTTTCGAAT TGGTATCTGT AGTAGTGGAA TGTATAGAT TTGAAGTAAC      300
TCTCCACGGA CAGTGCTGCT TCGTGTA GCAATTTAAT TGGAGAAGTG GCCATTCTTA      360
CTTCAGGGAT GCAAAGATGG TCTCATACCA TTTGGATAAA TGTGCTGGTA TCCATGCTTT      420
TTTTCAACTA ATAACATCAT CTCTTTCAT GACCAGTTAA TTGGGCTATT TGGCAGCCCA      480

```

STGAACCTAT GTACTAATGG CAAGTTAGGG GCAAATGGAA ATGGACACAT CCGATAAAGT 540
 TGAAATGTAT GTTTTAATCT TTCACAGAAG TCCCTCGAG 579

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTCGGCC TTTATGGCCT ACCTACGGTA CCTGAAAACA ACGATGGCAT GGAAAACACC 60
 TCCCATTTAC CTGTTGTTGC TGCTGTCTGT TTTCTGTGATT CACCAAGTTT CNTCTCAAGA 120
 TTTATCNCC TGTGCAGGGA GATGTGGGA AGGTATTCT ANAGATGCCA CCTGCAACTG 180
 TGATTATAAC TGTCAACACT ACATGGAGTG CTGCCCTGAT TTCAAGAGAG TCTGCACTGC 240
 GGAGCTTTCC TGTAAGAGG GCTGCTTTGA GTCCTTCGAG AGAGGGAGGG AGTGTGACTG 300
 CGACGCCCAA TGTAAGAAGT ATGACAAGTG CTGTCCCGAT TATGAGAGTT TCTGTGCAGA 360
 AGTAAAGAT AACAAGAAGA ACAGAACTAA AAAGATACCT ACCCCCAAAC CACCAGTTGT 420
 AGATGAAGCT GGAAGTGGAT TGGACAATGG TGACTTCAAG GTCACAACTC CTGACACGTC 480
 TACCACCAA CACAATAAAG TCAGCACATC TCCAAGATC ACNACAGCAA AACCAATAAA 540
 TCCAGGACC CTCGAG 556

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCGGCC TTCATGGCCT ATTATTTTGG CACCAGCGTC AAGACAAATA ATATCCTCTC 60
 CCATTATTTT CATAAGTAAC ACAGATTCCTC TGATTTTTAA AACTAAAAA TACAGCTAAA 120
 CCTTCTTAT GTATAAGTA TGCCTATCAT ATACAGGGAG AGGTGGGTAA TAACTTCCT 180
 GTAATGACAG TGTGTTGGCAT TTCTTTATGG ATGGAATTGG AACATGAACA AGACCATGTC 240
 CAGCGTTTTT ACTGTGAATG TAAATGGAAC AGCAGCCCAA AGCTGTTGTC TGTGCCCCAG 300
 AGGTGCTACC TGTAGACAGG GACCAACTCC ATGTGTGTGT GTTAAGTGT TGA CTCCAAT 360
 TAAGACTCCC AAGCAAATCC TGCATATTCC AAATGTAAAG AGTACTCAGT GGGAAAAAGG 420
 TTGTTACCTC AAAGTCATTG CTTCTTTCCT GGCTGGGTCA CAGGGTGAAG AGATGAAGGT 480
 GTCTGATGTA TATAGACAAT TAGGGAAAAA TGAGCGGCTT TCCTCGAG 528

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```

GAATTCGGCC TTCATGGCCT ACTGGAATCT GCAGCCCCCA CATGCATCTG TCTAACGCAT      60
GCCTCGTGT CGTTTTGCAA ACATGCCTGT GGTGGAGGGT GGTCAGTTGT AGCCCTGTGC      120
GTCTCAAGGC TGCCTTGTA GGCATTCCC AGTGCCTGCC CTTGAGCTCC TTACCACCCC      180
TTTTCTGCT CGGCCCTTA ATCCCTGACA GACCTGGACT GTGTGGCTGA AGGGGGACCT      240
GCAGCACTGC AGAAATGCCT CTGCGTGGTG CCATGAAGGA AAGAAACCTT GGCCTGTCT      300
CGAG                                                                    304

```

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs --
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

```

GAATTCGGCC TTCATGGCCT AGGGCAGGGG GAGGGGTGCA NAGTGGGACC CTCACCACAG      60
GGTACTGAGA CAGGTCATTG TAGGTCGCC CCGCAATGGT GTTGAGTTGC ATCAAGTACT      120
CGAAGTTGGA TATCTCAGC TGTACCCATT TCTGGGTAAG GCCTGAGGCA CGCACCATCT      180
CCTGGGGGGA GCGGCTGCTT AGGTAGCCAA GAGAGGGGGG CCGTAGGCGC AGGANCCACC      240
AGTACACCTG GCCCATCCC ACCCATCCC TCGAG                                                                    275

```

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

GAATTCGGCC TTCATGGCCT AACCAGCTTT AATTTCATT GAGGAATAAT AACCAACCCTA      60
GAGATTCATA GGAAAGAGCA TTGAAATACA TTTTGTGCAT AAAGATACCT AAAACCATCT      120
ACCCAGCTTA GGGTTGAACT GAATTTCTGT GAAATAAATT TGTTTTAAAT ACTAATTATT      180
TTAAACTAC TTAATCTTA AAAACAATGT CATCAGTTTC AAAAGTTTCA CTTGGGAGG      240
ATATTCCTTA AAAGGCATAC ATAGATGGTA AAGTATAAAA TATTTCTGAC AGAATTATTC      300
AGTATTATTC AACATTTACT TTCATGTTG TTATTGTACC ACAAAGATAG TGTCATTGTT      360
GGGTAAAAAT GTTGGCTGTT TTTGTTAATA TACTTAAAC TGTAACCACT GGCTCGAG      418

```

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT      60
GCTCAGCCAC CAGTTCAAGC GCCGGGAGGC CGACCAGACC CACGCACAGA ACTTCTCCTC      120

```

CGCCGTGAAG TCCCCGGTCC AGGTCATCCT GCTCCGTGCC CTCGCCTTCC TGGCNTGCGC 180
 CTTCTACTG ACCACCGCGC TGTATGGGGC CAGCGGACAC TTCGCCCCAG GCACCACTGT 240
 GCCCCTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CCTGACAATG GCACCAGGCT 300
 CGAG 304

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC 60
 ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCCCAGA 120
 ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA 180
 AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA 240
 GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA 300
 CTCTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
 CTTACCCATG GGAACCTGAG 380

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCGGCC AAAGAGGCCT AAACAAATGA GGGTAGTAAT TTTTATCTG CTAAACTTA 60
 TATTTATATC ACATACTTGT TGCAATGATT TCAGTGTCTA CATAAATGGT GGCTTAGCTG 120
 AGGCAGGTCT AGAATTCAAT CGAG 144

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

GAATTCGGCC AAAGAGGCCT ACTAGACGTT TGTACAACT ATTCCCTTGA GTTATTTTCT 60
 CTGGCTCTTC AGCTCCTTCC TCCCACCCCC TCCCCTGCAC CACCAATCCA TTCTTTTGCT 120
 TAATTTCTCT CCATCCTTCA GGTTCAGCT TTAAGAGGTC ACTTCTTTTA GGAGACATTC 180
 CCTGAATCCT CTCACCTCCA CCCACAAAAA AGGCCTCTCC AGATGCCCTT CTTTCTGCT 240
 CAAACCTCAT CTGCTTCCTT TATCATATGC TTATCGTTTT GGATTGTAAT TATTTATTTA 300
 ATTGCAATGTC TTTCTGCTAG TTTTGTGTT AGCAACAACA AGGATCTCGA G 351

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

GAATTCGGCC AAAGAGGCCT AGATGATGGC AGGAATGAAA ATCCAGCTTG TATGCATGCT      60
ACTCCTGGCT TTCAGCTCCT GGAGTCTGTG CTCAGATTCA GAAGAGGAAA TGAAAGCATT      120
AGAAGCAGAT TTCTTGACCA ATATGCATAC ATCAAAGATT AGTAAAGCAC ATGTTCCCTC      180
TTGGAAGATG ACTCTGCTAA ATGTTTGAGT TCTTGTAAT AATTTGAACA GCCCAGCTGA      240
GGAAACAGGA GAAGTTCATG AAGAGGAGCT TGTGCAAGA AGGAAACTTC CTACTGCTTT      300
AGATGGCTTT AGCTTGAAG CAATGTTGAC AATATACCAG CTCCACAAAA TCTGTCACAG      360
CAGGGCTTTT CAACACTGGG AGTTAATCCA GGAAGATATT CTTGATACTG GAAATGACAA      420
AAATGGAAGG GAAGAAGTCA TAAAGAGAAA AATTCCTTAT ATTCTGAAAC GGCAGCTGTA      480
TGAGAATAAA CCCAGAAGTC TCGAG                                     505

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

GAATTCGGCC AAAGAGGCCT AGTCGTAAGT TACCATAATA GGTGCTTGCA GTCATTGATA      60
TAATCCAGAA AGCTAACGAA ATGCAAATGA TCAGGCTCAG TATAACTATA TTAGTTATCA      120
TCTTTATATA TCTTTTGCAT ATATTGTCGT TAAGATCTGT CATGGAAAAT AAGGATATGA      180
GCTCCTGCGG GAAAGAATAT TTAGCGTTTC GGAGAGAAAAG TCATTTACGA TGTGAGCAAG      240
ACACTTGTTT AGAGGCAAAC ATAAATCCCA ACATATTCCA CCGACCAAAC AAGCATAAAA      300
ATCACAAAAA TTCAAACCTC TTCCGGAAAC TCCTACTGGC CCTCGAG                                     347

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

GAATTCGGCC AAAGAGGCCT ATCTTACTAT TTTTATGTCA TTGGTTTTTT CTCTTTTCTT      60
TCTTTCTTTT TTTTTTTTTT TTTTGTAGGC AGAGTCTCGC TCTGTGGGGA CACTGTTCCG      120
TTCAGAGGCC CCTCCAGGCC ATGGGGTGGG GGACAGTGGT GGGCGTGGGA ATCCAGCGA      180
GCATCTGGA GGGTGCGTCG TCTCCATGTA TTTTGCTCTT CCCCATCTTT TCCATGGGGT      240
CCCCTGCCAG GGTCAAGCAC TAATATGTGG TGAAGGCAGC AAACAGCGTC GGCGTCCCTT      300
TAGGGGTGGG GAGAGGGCTG TAGCACCAAG ACCCCCTCC CCGCCCAAG ACATCCCTGA      360

```

AAAGGAGACT AAAATAAAGC CCCGGCGCCT CGAG

394

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGGAAAAACA | GAGTAAAAAA | TTGCAAAAGA | AGAAGGAAAC | 60 |
| AATAACAGAG | TCAGCTGGTC | GACAACAGAA | AAAGAAAATA | GAGAGACAAG | AAGAGAAACT | 120 |
| GAAGAATAAC | AACAGAGA | TATCAATGGT | TCGAATGAAA | TCCATGTTTG | CTATTGGCTT | 180 |
| TTGTTTTACT | GCCCTAATGG | GAATGTTCAA | TTCCATATTT | GATGGTAGAG | TGGTGGCAAA | 240 |
| GCTTCCTTTT | ACCCCTCTTT | CTTACATCCA | AGGACTGTCT | CATCGAAATC | TGCTGGGAGA | 300 |
| TGACACCACA | GACTGTTCCC | TCGAG | | | | 325 |

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCN | AGGGTCACAG | GGTGGTTATC | TCACTTCGCA | GCTTTTCCTT | 60 |
| TCTGAGGCCA | GAAAAGGAAG | GGGTTTGCCT | TCCTCTAGTA | TTTATTCTTC | TGGACTACAT | 120 |
| CAAGTACTCT | AAGCCTGATG | TTAGGCAATA | ACTGCCCATT | AGCCATTGGC | TACATTTGCC | 180 |
| TCTTTCTTGT | TCCAACAATA | TTAGTGATCT | GTGGNACAGG | ACACACTCTT | TGTTTGCTAG | 240 |
| CTACAAATTC | TAACAAAGCT | AAGTTTTATT | CATGTAGNTA | TTCACAAATT | AANACAACAC | 300 |
| ACACACCACA | CACACACACA | CACACACACA | CACACACACA | CACACACATA | CCACAAAACC | 360 |
| CAGAGATCAC | CAATACTAT | ATAAATAAAC | AAGCCCAAAG | TCACAGATCA | GGGACACTCG | 420 |
| AG | | | | | | 422 |

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGACGTCCAA | GAAAAAACAT | TTGGTGAAAG | TCAGGATTTA | 60 |
| CCTTTGAAAT | CCGACTTGGG | CACCAGGGAA | GATAGTAGTG | TTGCATCTAG | TGATAGGAGT | 120 |
| AGTGTGGAGC | GAGAAGTGGC | AGAACACCTA | GCAAAAGGCT | TCTGGAGTGA | CATTGGGCAGC | 180 |
| ACGGGACTCT | CTTGCCAAAT | GCAGTTATCA | CCTGCTGTGG | CCAAAGATGG | CTCAGAACAG | 240 |
| ATCTCACAGA | AACGGTCTGA | GTGTCGGTGG | TTAGGTNTCA | GGATTAGTGA | GAGCCCAGAA | 300 |

CCAGGTCTCA CTCGAG

316

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```

GAATTCGGCC AAAGAGGCCT AGTCAGTCTG AGTTAGAAAA TCGACTCCAT CATCTAACAG      60
AGACTCTCAT CCAGAAACAG ACCATGCTGG AGAGTCTCAG CACAGAAAAG AACTCCCTGG      120
TCTTTCAACT GGAGCGCCTC GAACAGCAGA TGAAGTCCGC CTCTGGAAAGT AGTAGTAATG      180
GGTCTTCGAT TAATATGTCT GGAATTGACA ATGGTGAAGG CACTCGTCTG CGAAATGTTT      240
CTGTTCTTTT TAATGACACA GAAACTAATC TGGCAGGAAT GTACGGAAAA GTTCGCAAAG      300
CTGCTAGTTC AATTGATCAG TTTAGTATTC GCCTGGGAAT TTTCTCCGA AGATACCCCA      360
TAGCGCGAGT TTTTGTAAAT ATATATATGG CTTTGCTTCA CCTCTGGGTC ATGATTGTTT      420
TGTTGACTTA CACACCAGAA ATGCACCACG GCCTCGAG      458

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

GAATTCGGCC AAAGAGGCCT ATCGAGGTTT GGTGACTGA TGGAAGCTTT TATTTCTTTA      60
ACCATTTATG CATTTTCTCA ATTTGCTACA ATAAACATAG ATTGCACAGG GGTGAATACT      120
AAGGAAGTCG GAGGGTTAGG GTTAATTTCT GTGAAAGACC AAATATGTTT CTCTGGTTCT      180
CTCGAG      186

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

GAATTCGGCC AAAGAGGCCT AGCATTATGG TATATTTTAA ATTCATCAAG CTCATCTGTA      60
TGTGTCTTTT TGTCCTTTTA CTAAGTCTAG GATTGGGGCT GGGATCATGG CAGCCTGCTC      120
TGATGTATTT CTCTCCACTC TATTTTATTA TTTTTTAAA GAGTTCTAAC TTAAATACGT      180
GGACCAGCTA TTGGATAACT TTAATTCATA TATTTATCAT TCTTTCTATT CACTTTGCCA      240
CATACACACC ATGTGATGAT TTAAACCCG ATTTCTGTAT AGAGAATGTT AAAAGGATAG      300
CACTCGAG      308

```

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```

GACATGCTGT GGTTCACCG CGCACTCACC CTGCTCATCA TCCTCCGCCA CCTCACCAGG      60
AAGGACCCAC AGGGGCTGGG CGTGACGAGT GACGCCATCG CCGATGCCTG CCAGGCCCTG      120
GTGGGCCCCA CCGCCACAG CCGTTGCTGG TGATCTCCGG GATCCCCACC CACCTGGACG      180
AGGGCGTAGT CAGAGGCGCC ATCCGCAAGG CCTGCAACGC CCACGGCGGG GTCTTCAAAG      240
ACGAGATCTA CATCCCGCTG CAGGAAGAAG ACACCAAGAA GCCAAAAGAC AAGGCCGAGG      300
GCG                                                                    303

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```

GAATTCGGCC TTCATGGCCT ACACTTTAAT TGCTGTTATC ATGGGCCTAA TTACAGTCAC      60
TGCAGTGGCC ACCACTGCCG GAATGGCATT ACACCACTCC ATTCAAGCGG CTCATTTTGT      120
TAATGGTTGG CAAGCCAATT CCATCCAAAT GTGGAATTCT CAACAAGGCA TCGATCGAAA      180
ATTGGCAAAT CAAATTAGTG ATTTAAGACA GTCTGTATT TGGCTTGAG ATCAGGTAGT      240
GAGTCTCGAG                                                                    250

```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

```

GGTGACGCCT GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG      60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCCA CCCTGGGGCT CCTCATGGCC      120
CGGCTCCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAG CATCCCGAGG GTTCTTCGCA      180
GCTGCCATCC TCTTCCTATC ACAGTCCCAC GTGGCGCGGG CCACCCCGGG CTCAGACCAG      240
GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCATCTGGG CCGACCTGCA GGAGCTCTGG      300
TTCCTCGAG                                                                    309

```

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

```
GAATTCGGCC TTCATGGCCT AATGAAGAAA AGCAGAAATTC CAAATTCAAA CTGTTGGAGT   60
GAGCCAAGTG GACAGACCCT CCATGAGTGC ACTTTCTTCC AAGAAATCCC CAGATTTACC   120
CCATAGAGGT CTGGGATTAC CTGGAATATA ATATGAAAAA CATTTTITAG GCTGGGTGTG   180
GGGCTCACAC CTGTAATCCC AGCACTTTGG GAGGCTGAGG CGGGCGGATC ACCTGAGGTT   240
GGGAGCTCGA G                                     251
```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```
GAATTCGGAA CAATGGGGGT TTCAAAACAT AAAAGTGAAA GTCCTTGTA ATCTCCTTAT   60
CCAAATGAGA AAGACAAGGA AAAAAATAAG TCAAAATCTT CAGGCAAAGA AAAAGGCAGT   120
GATTCATTTA AATCTGAGAA GATGGATAAA ATCTCCTCCG GTGGCAAAAA GGAGTCCAGG   180
CATGATAAAG AAAAGATAGA AAAGAAAGAG AAACGGGACC TCGAG                                     225
```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```
CTCGAGGCGT GTGGGATCAT GAGGCAAAGA AAGTCCAACG AGGGAGAGAG GAGAGTGAGG   60
GATGAGAGGG GACACTTGCT CCATCCTAGT CCCACGCGG CCCAGCTGGC TTCCTTTTCC   120
AGAATATCTC CTTGCTATAA CCTGGCAGCA GGGGAGCCAA GGTCTTCTC CATCCTTACA   180
GGCACTGAAC CAGGATGTAG GCGCACACTG CTGTGTTCTC TCTGGCCCAT CCTCTCTAAT   240
TGTCTTTCCC TTCCCAGGTC ACAGGATGCT TATTCTCATC TCCAGGCCCTT TGCACGGGCC   300
GGGCTGTCTG CCAATCCCCG CACTCTCCCC TTCTTAGGGC CAGGCTAACT CTTCCCCATC   360
CCCGGGGCTC AAGCGTTCAG GTCTCTTCCA AAAGCAGTCT TGGTGGTCCC TGCCACGCGT   420
TACCCTCTC TCAAGTCACC CGGGAGGTGG AGGTTGCTGT AAGCCAAGAT CGCAGTGAGC   480
TGAGATTGCA CCATTGCACT CCAGCCTAGG CCATGAAGGC CGAATTC                                     527
```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

| | |
|---|-----|
| GCACTCATAA AAATCTTACT CAGAAATCTT CAGAGGTTTG CTAAGGATAC AATTGATTG | 60 |
| TTACACATT AATGCTCACC AGCTGCTTAG GCCCACACCA TTTATCCACC CTGATTGCT | 120 |
| ACTGCTCTTT GAAATACAAC CAGTGTTTCA GCCAGACTGT TTTCTGCTT CTGCTCCCCT | 180 |
| TCTCCTCCTC CCAGCACATC TGTGAATTCT TTGACTGGTT TACCACTCCC AAATCCTCC | 240 |
| CCAGCAATGC AGATCTTCTA CACCCTTTAG GATCTAAGCT AAGTCTGCTT CCCAGATATC | 300 |
| CTCCCGAACA GCTCGAG | 317 |

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

| | |
|--|-----|
| GGTCATTCTT TCCATCGCTG CGGACACGGG AGTCAGAAGT GAAACAGTCC TGTCCTCGTG | 60 |
| GGGCTTACGT TCCAGGCGCA AGAGCCACAG GTAGTCGAAT TGGGAAACCG CCTCGGATGT | 120 |
| CACATAAGCG CCCAGGGAGG ACAGGGCAGG ACAGGGCCTC CCTGGGGAGG TGACTTGAGT | 180 |
| CAAGACTCAA AAGAGGGAAG CGAGGGAACA AGCCATGCGA GGAACCTAACG AAGGAACATT | 240 |
| CCAGAAAGAT TTCACATCCC AAGCCTAAGG TCCAGGGGCA GCAGGCATTG AGGCGGATGT | 300 |
| GGCTGGAGTG GAGAGAAAGA GGAATTAAAA GGATGGCATG AGCTCGAG | 348 |

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC | 60 |
| TTATGTGCCT GTCCCTGTGC ACAGCCTTTG CCTTGAGCAA ACCACAGAA AAGAAGGACC | 120 |
| GTGTACATCA TGAGCCTCAG CTCAGTGACA AGGTTACAA TGATGCTCAG AGTTTTGATT | 180 |
| ATGACCATGA TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG | 240 |
| AAGAGAGCAA GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGGCTGGCTC GAG | 293 |

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AATAAATTGC CAGCATANTA AAAAACTGCC TTACTACTCAA | 60 |
| TTGCTACACC TTTTCACAGG CAAAAGGTTT TATTCTCTCC TAAATTAATT TTATCCCGTT | 120 |
| TTTTTTTACC ACCTAACTTT TGCCTTTTAT TCAGAATAA TGTATTTTTT TCTTATTGTC | 180 |
| GTTTTTTTTT TCAAAATTCC CTCCTCGGTG GAAAGTAAAG GAGTAGGAAC ATACTATTAT | 240 |
| TCAACCAACA TGCAGCAACC CTTACGTACG GTCCTCGAG | 279 |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAATC TTTAAGTGGA TTGTGAGTAG | 60 |
| ATTTTTTTAA GGAGCATTTT TATAATATT TTCTGAATC CTTGCATATT TGACAGTGTC | 120 |
| TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTTGTT | 180 |
| TTTGTTTTGT GAGACACAGT CTCACCCTAT CACCCAGGCT GGAGTGCACT GGCACATCT | 240 |
| CGGCTTACTG CAGCCTTGAC CTCCCAGACT CAAGTGATCC TCCCACCTGC CTCGAG | 296 |

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

| | |
|--|-----|
| GAATTCGGCC TNCATGGCCT ATGTTTTTTA TATATGGATT TATTTTTGCT TTTTATAGCT | 60 |
| GATTCAGTGT GAAAATGAGG TAGGGAAATT GTTGTATTATC ACAGAAATCC CAGAATTAAT | 120 |
| ACTGGAAGAC CCCAGTGAAG CCAAAGAGAA CCTCATTCTG CAAGAAACAT CTGTGATAGA | 180 |
| GTCGCTGGCT GCAGATGGGA GCCCAGGGCT AAAATCAGTG CTATCTACAA GCCGAAATTT | 240 |
| AAGCAACAAC TGTGACACAG GAGAGAAGCC AGTGGTTACC TTCAAAGAAA ACATTAAGAC | 300 |
| ACGAGAAGTG AACAGAGACC AAGGAAGAAG TTTTCCTCCC AAAGAGGTGA GAAGGGACTA | 360 |
| TAGCAAAGGA CTCGAG | 376 |

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAAGATTGG CAAGATGCTT ATTTTGGTG CCATATTGG | 60 |
| CTGCCCTTGAC CCAGTGGCAA CACTAGCTGC AGTTATGACA GAGAAGTCTC CTTTACCAC | 120 |
| ACCAATTGGT CGAAAAGATG AAGCAGATCT TGCAAAATCA GCTTTGGCCA TGGCGGATTC | 180 |
| AGACCACCTG ACGATCTACA ATGCATATCT AGGATGGAAG AAAGCACGAC AAGAAGGAGG | 240 |
| TTATCGTTCT GAAATCACAT ACTGCCGGAG GCTACTCGAG | 280 |

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS: ..

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCAGTAAGC CAGGATTGCA CCACTGCACT CCAGCCTGAG | 60 |
| TGACAGAGTG AGACTCTGTT TCAAAACAAA AAAAAAACT TTACAGCAAT CCTGGTCCCT | 120 |
| ACCATGGAGC ATGTGTTACA GGAAAACAGC CAGTCCACTC TGCAACCAAT TTGGACATGG | 180 |
| CCCTGAAAAT CCTTTTTCGA CAGAAAGGGG AAAATAAGAG TACTGGCAGA AAGTCAGATG | 240 |
| CTGGGGATGC CTCACCCTCT AGTCTCATGA CTATCACACA TGAGACGGTG TTCCGCTGTA | 300 |
| ACTTTTCCCC CCCCCCCCC CGTTTGTGGA TCTGAATCTG GAAAAGAGCT TGGAGAGATT | 360 |
| TACAGGCCTC CTCTTCTGCA ATCAGTAAGA GTACCATGTG GAGGCAGAGA GCCAGAATAG | 420 |
| GTGTGGGGC TTCTCGAG | 438 |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGAACAGCTC TCCAATTCAC ACTTATCTGT ACAATGTACA | 60 |
| TTAATAACTA ATTTGTTAGA TGATTAATAC CAATAATTAA CTTGCTAGAG GACCCAGGAA | 120 |
| ACAGAATATC TGCAAGGCC AGAGTAGATC ATAAATAAAT AGGAATGCAG ACATAAGATG | 180 |
| TTCAGTTTGT GAACAGTAAA GCTATAATGA GTTTCTTTA AAATCAAACA ATTGTACAAT | 240 |
| GCATTATAGT CTACAACTTA TTCTGTAGTT CAAATAAATA AAACCTTCCC CTGTTACAGA | 300 |
| AAGACAGCCC TCCTCCAGC AACATTTCAG ACTGGATGGA TTGATTCTCT ACCTGACATA | 360 |
| ACTCTAAAAT CCTCACTGAA GAAGCCAGGA AGTCAAACCTG AGGCTGAAGA CCTGAAAGTA | 420 |
| CAGGGGACTA AAGCCAGAAA GCAGTAGGCC ATGAG | 455 |

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACATGGACCT CCTGCACAAG AACATGAAAC ACCTGTGGTT | 60 |
| CTTCCTCCTC CTGGTGGCAG CTCCCAGATG GGTCTGTCC CAGGTGCAGC TACATCAGTG | 120 |
| GGGCACAGGA CTGTTGAAGC CTTCCGAGAC CCTGTCCCTC ACCTGCGCTG TGAATGGTGA | 180 |
| GCCCTTCAGT GGTATTCTTCT GGACCTGGAT CCGCCAGNCC CCCGGGAAGG GCCTGGAGTG | 240 |
| GATTGGGCAA ATCAATTATG ATGGAACCAC CAAGCACAAAC CCCTCCCTCG AG | 292 |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs ..
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGGGTGGGC TTTAATGGCA GCTGGGGTAA AAGGAAACAA | 60 |
| AAACAGTAAT TCTGAAGAGC ACAGGGAACA GGCAGCCAGG ACCAGCCTGG CCCATTCCAG | 120 |
| GCCAGCTGAG CTGAAATGCT GATTCTGTCC AGGGGGCTGC TGTATGTGTA GACTGGTGGC | 180 |
| AGTCTTGGGG ACTGAGGCCT CTTGGAGAGA AGGGAAGACT GTCGGCTCAG AAGTCCATGG | 240 |
| AGCTGTGGGC CAGGTAGTCC TTGCGACCGA TGTGCTGAC CTGCTTGGTC TGCATAGCCT | 300 |
| CGAG | 304 |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCAGCTCTC TTCTAAAAGA GAAGTGGGTG GGCACACTGA | 60 |
| ACTGTTTGGT GGCCCAACC ACAGGAAGCT GCAATTCTCT GGCTTAGGGT GATACTTTTG | 120 |
| CCCTCCTTGT GCCCTCTCT GGACGCTCTG CACCAACCCC AGGCTACTGA GCCACCTTCC | 180 |
| CTCCTCATGC CTTCCCTGAG CTTTGGTGCA TCTCATCTGG ACTATGGGTT GTACTGTGAC | 240 |
| CATCCCAACA CCTCACCTC TGTCTACAAG GAAATGGGAG GTGGAGCCTC CTGGCTGAGA | 300 |
| AATTGTTTTG CAAATGGATC TCGAG | 325 |

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCTCATCA ACGAGAAGCT CATCAGAACC AAGGGGCTGT | 60 |
| GGGGCCCCGT CCATGAGCTG GGCCGCAACC AGCAGCGGCA GGAGTGGGAG TTCCACCAC | 120 |

| | |
|---|-----|
| ACACCACCGA GGCCACCTGC AACCTGTGGT GTGTGTATGT GCATGAGACG GTCTTGGGCA | 180 |
| TTCCTCGAAG CCGTGCCAAT ATTGCTCTGT GGCCCCCAGT TCGGGAGAAG AGAGTCAGAA | 240 |
| TCTACCTGAG CAAGGGTCCC AATGTGAAAA ACTGGAATGC ATGGACCGCA CTGGAAACTC | 300 |
| GAG | 303 |

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTTGTTTCA AATCCACACA GCTCTGAATT ACCAACGCTG | 60 |
| AATTTCCAAG ATACTGTAAA CACCCTGACC AACAGTCCAG CCATCCCATT GGAAACATCT | 120 |
| GCATGTCAGG ACATACCCAC TTCTGCCAAT GTACAAAATG CAGAGGGTAC CAAATGGGGA | 180 |
| GAGGAGGCAT TGAAAATGGA TCTTGACAAT AACTTTTATT CAACTGAGGT GTCAGTTTCT | 240 |
| TCCACTGAAA ATGCTGTCTG TTCTGACCTC CGGGCAGGGG ATGTACCTGT TTTATCTTTG | 300 |
| AGTAATAGCA GTGAGAATGC CGCCTCTGTG ATCAGCTCGA G | 341 |

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAATC TTAAAGTGA TTGTGAGTAG | 60 |
| ATTTTTTTAA GGAGCATTIT TATAATATTT TTCCTGAATC CTTGCATATT TGACAGTGTG | 120 |
| TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTITTTTGT | 180 |
| TTTGTITTTGT GAGACACAGT CTCACCTAT CACCCAGGCT GGAGTGCAT GGCATATCT | 240 |
| CGGCTTACTG CAGCCTTGAC CTCCAGACT CAAGTGATCC TCCCACCTGC CTCGAG | 296 |

(2) INFORMATION FOR SEQ ID NO:480:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC | 60 |
| ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCC TTTGCCGAGA | 120 |
| ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA | 180 |
| AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA | 240 |
| GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTC AAC GATGGCTTCC AATAACATGA | 300 |

CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
CTTACCCATG GGAACCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAATC TTAAAGTGA TTGTGAGTAG 60
ATTTTTTTAA GGAGCATTTT TATAATATTT TTCTGAATC CTTGCATATT TGACAGTGTC 120
TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTTGTT 180
TTTGTTTTGT GAGACACAGT CTCACCCTAT CACCCAGGCT GGAGTGCAT GGCATATCT 240
CGGCTTACTG CAGCCTTGAC CTCCCAGACT CAAGTGATCC TCCCACCTGC CTCGAG 296

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC 60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATA ATCAGTTCCC TTGCGGAGA 120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA 180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA 240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA 300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
CTTACCCATG GGAACCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAATTCGGCC TTCATGGCCT AGGCTGGACA GACTTTCTAA TGAACCCAAT GGTTATGATG 60
ATGGTTCTTC CTTTATTGAT ATTGTGCTT CTGCCTAAAG TGGTCAACAC AAGTGATCCT 120
GACATGAGAC GGGAAATGGA GCAGTCAATG AATATGCTGA ATTCCAACCA TGAGTTGCCT 180
GATGTTTCTG AGTTCATGAC AAGACTCTTC TCTTCAAAAT CATCTGGCAA ATCTAGCAAC 240
GGACAGCTCG AG 252

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```

GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT      60
GCTCAGCCAC CAGTTCAAGC GCCGGGAGGC CGACCAGACC CACGCACAGA ACTTCTCCTC      120
CGCCGTGAAG TCCCCGGTCC AGGTCATCCT GTCCTCGTGCC CTCGCCTTCC TGGCCTGCGC      180
CTTCCTACTG ACCACCGCGC TGTATGGGCG CAGCGGACAC TTCGCCCCAG GCACCACTGT      240
GCCCTTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CCTGACAATG GCACCAGGCT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                     380

```

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                     380

```


(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

GAATTCGGCC TTCATGGCCT AGGTTTACAG GCATACCTCA TTTTATTGCA CTTCACTTTA      60
TTGTGCTTTG CAGATAATTG TGCTTTTAC AAATTGAAGG TTAGTGGCAA CCCTGTGTTG      120
AGCAAGTTCA TTGGCAACAT TTTTCCAACA GCATGTACTC ACTGTCTCT ATGTCACATC      180
TTGATAATTT TCATATTTCC AACTTTTTC TATCATGAT GATGATTAGT GATCTTTGTT      240
ACTGTNGTAG TTGTTTTGTG GGCACCACAC TGTATGCAGN AAAGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```
GCTACCTTAA AAAATAGATA CTCCACTAGA GGCTGTGCTT AATTCAAATC CATGTGTGTG      60
CCTGCATTAC ATGTGTGAAC ACGTGTCTTCT GTCGTGTGTG TCATGCACAT CTGTGTGTTG      120
CATAGCATAA GCCAAATGAA AATCATTTGT TCATGGGATT CATATGAGGA ACAAATTTAA      180
ATTTGAATAC AGTCAGATAA CTGCCACGCA GGGCATTGTT GGAACCATCC CCGAATGCCC      240
TGATGTGATT TCCCTCAGAA AATCCTTGT ATTAGAGGAG AAGGTCTGGG CAGGGGCAGC      300
AGCATCTCAG ACATCAAGTC AACTTTATCA TCTACTACAT CAGCACTGAA GTCCAACGGC      360
ATCCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```
GAATTCGGCC TTCATGGCCT ATGCTTTTTT CTTTATTCTT TGTAGTTGTT TAGGAGTGGG      60
GGGCCTCGCA GAACACCTAG TCCAGCCCAC TGCCAGAGC AGGTGTGTCC CTTTCATACT      120
TCAGTCCACT TTAACACAGC CTCCCCCAC CCCCTTCTAT GGTAGCAGTT CTCCTCGGGG      180
TCTCCATGGA CACCCTGTGC CCCAAGCCGA TGGCCCCACC CAGCAGCATC AGCAGAGCTG      240
CCCCCTTCT CCGCAGAGCA GGCTCTCCTT TACGGGACTC TCCTCTTCCC TCCCACCCC      300
CCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```
GGAATAAGAA GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC NGCTTCACAC      60
ACACAGATAC GGAGANCCA GAAGTGCCAG AGTCAGCATT CTGGAAGAAA ATCATAGCAT      120
ATCAACAGAA ACTTCTAAAC TATTTTGCTC GCAACTTTTA CAACATGAGA ATGTTAGCCT      180
TATTTGTCGC ATTTGCTATC AATTTCTCT TGCTCTTTTA TAAGGTCTCC ACTTCTCTG      240
TGTTGAAGG AAAGGAGCTC CCCACGAGGC TCGAG
```

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

| | |
|--|-----|
| GCCTTGGGCC CTCGAAAGT CTTGGAGAAG CAGTTTTACT TCCCTTCCTT CACTTAGACC | 60 |
| CCATTCTTTA GCATTTCTTC TGAAGCTCCC ACAAGACCCA AGAATGGCTG CTGCAGTGTC | 120 |
| TCCTCTTCAG TCAGGGACCC TGGTTGAGGT TTGTGTATTG TTCATTATTG CTCTGTTTTG | 180 |
| CAGTTGTTCA AAGTTGGAAG ACTTGCCTGC GGAGCAGTGG AACCATGCCA CAGTCCGCAA | 240 |
| TGCCTTAAAG GNACTGCTCA AAGAGATGAA CCAGAGCACA TTAGCCAAAG AAACCCCTCGA | 300 |
| G | 301 |

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

| | |
|---|-----|
| GGAAGATGTC TACAGAAAAG GTAGACCAAA AGGAGGAAGC TGGGGAAAAA AGAGTGTGCG | 60 |
| GAGACCAGAT CAAGGGACCG GACAAAGAGG AGGAACCACC AGCTGCTGCA TCCCATGGCC | 120 |
| AGGGGTGGCG TCCAGGTGGC AGAGCAGCTA GGAACGCAAG GCCTGAACCT GGGGCCAGAC | 180 |
| ACCCTGCTCT CCCGGCCATG GTCAACGACC CTCCAGTACC TGCCTTACTG TGGGCCCAGG | 240 |
| AGGTGGGCCA AGTCTTGGA GGGCGTGCC GCAGGCTGCT GCTGCAGTTT GGGGTGCTCT | 300 |
| TCTGCACCAT CCTCCTTTTG CTCTGGGTGT CTGTCTTCCT CTATGGCTCC TTCTACTATT | 360 |
| CCTATATGCC GACAGTCAGC GCACTCGAG | 389 |

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

| | |
|---|-----|
| GTGGCGATTG GTCCTGTCAT GGTATTATCA GCCATGTGGT GGATGGCTAC TTGTCTTCTA | 60 |
| AGCCACTTGC CTTCTGATCG CTGGACTGAC TCTCTGCCC TCTCTTGGTG CAGTCCTCAG | 120 |
| GAGGCTCGGT CACACTCTCC AAGAGCACAG CCATCATCTC CCACGGTACC ACAGGCCTGG | 180 |
| TCACATGGGA TGCCGCCCTC TACCTTGCA AATGGGCCAT CGAGAACCCG GCAGCCTTCA | 240 |
| TTAACAGGTG ACCTCGGGGC ACAGGGCAGG GCACCGAGGC AGGCTTACCC TGGTGCACTC | 300 |
| GAAAACACGG TCCCTTTTCC TCCCGCCAGG ACTGTCCTAG AGCTTGGCAG TGGTGCCGGC | 360 |
| CTCACAGGCC TTGCCATCTG CAAGANGTGC CGCCCCGGG CATACATCTT CAGCGACCCT | 420 |
| CACAGCCNGG TCCTCGAG | 438 |

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```
GAATTCGGCC TTCATGGCCT AGGTAAAATT TGTATAACAA AAAATTAACC GTTTAAACT      60
GAATAATTCA GTGAGATTTA GTGAATTCAC AATATTGTGC AACTGCCACC TCTTTCTACT      120
TCTAAACCAT TTTCTCTATA CCAAAAGTAA GCCCGTACC TATGATGCAG TCCCTTCCCG      180
TTTCTTCTC TCCTCAGTCC CTGGCAACCA TCACTCTGCT TTCTGTCTCT GTGGATTAC      240
TTATTCTAAT ATTTAATTC AGTGGGAATC CCTGCCTCGA G                                281
```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```
GAATTCGGCC TTCATGGCCT ACACTTAGAG AGGCAGTCGG GATGGAGGGT CGAGTTGAAG      60
ACAGGGAGGG GTGAGGAACG AGCAGAGGCC AGTTGTTTGG CCACTTGAGG GAGTTTGGAC      120
TTGTCCCGAG GGCCTAGGG AGCCGTGAAG GGCTTCAAGC CGGGGAGGAT CATGAACATT      180
TCCCCAGAGG AGCTCAAAAT GGAGTTGCCG GAGAGACAGC CCAGGTTCGT GGTTTACAGC      240
TACAAGTACG TGCATGACGA TGGCCGAGTG TCCTACCCTT TGTGTTTCAT CTTCTCCAGC      300
CCTGTGGGCT GCAAGCCGGA ACAACAGATG ATGTATGCAG GGAGTAAAAA CAGGCTGGTG      360
CAGACAGCAG AGCTCACAAA GGTGTTGCGA ATCCGCACCA CTGATGACCT CACTGAGGCC      420
TGGCTCCAAG AAAAGTTGTC TTTCTTTCGT TGATCTCTGG GCTGGGGACT GAATTCCTGA      480
TGTCTGAGTC CTCAAGGTGA CTGGGGACTT GGAACCCCTA GGACCTGAAC AACCAAGACT      540
TTAAATAAAT TTTAAATGC AAAACTCGAG                                570
```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```
GAATTCGGCC TTCATGGCCT AGGTGCATGC CATCAAATAC TCTAACGAGA CATTTTAAAT      60
GAAAGACTTA AACAGATAG GCCACAATGA ACCAAATTAG AAATCTGAAC ATGTCACCAC      120
TTGCAGCATA AAGGAATATA AAAGGGCAGA GCAAAGTCTT TTTTCTAAG GTGAATATT      180
CTAAGGTAAG TATTCATTG TAAAAGTTT TTTTCCAN CANGTCTGAA NNCTTTTAC      240
CANNNGNGA GNATTACAAC AAAACATCCC TNGGTTAAAA AAAAAAATA CCATCTTGCA      300
ATTCAGCACA CACNGCAGC TGGTGTGCTC ATCCAAACCN ATCAGTAGGC TAAGAGNATT      360
TNAATTCCA TACATATGAG TTTAGGTATT AATGCCGATT ACACAGTACA CAGTACAGAG      420
GGAGGTCCCT ATATCCACAC ACAACACAC CCCATCCAGC ATTTACACCN AAAGCCTTAC      480
CCTCGAG                                487
```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

GAATTCGGCC TTCATGGCCT AACAAATCAA AGAAACTTTT TTCTGAACCA TTTGAAATTT      60
GCCAGCCTGA TGTCCTCATCA CCCCCAAGT ATTTTAGCAT CTATGCAACA AAACATTTTC      120
TCTGACAAAA CCACATCAGA ACTCTCAAAT CAGGAAACAA ACATTGATAC ATGTCTATCA      180
ACTAATCCTG TCTTCAATGA CATTTTACCG ATTGTTCCAA TGATGTCAGC ATCACGGGTC      240
ACATTTAATA GTTGCCTCCT TCAGTCTCGA G
                                                                                   271

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

GCACCTCTGG ATGTTGGTTC TCTTTGTCAT TTTCAACAGT CTGCAGGGAC TTTATGTTTT      60
CATGGTTTAT TTCATTTTAC ACAACCAAAT GTGTTGCCCT ATGAAGGCCA GTTACACTGT      120
GGAAATGAAT GGGCATCCTG GACCCAGCAC AGCCTTTTTC ACGCCCGGGA GTGGAATGCC      180
TCCTGCTGGA GGGGAAATCA GCAAGTCCAC CCAGAATCTC ATCGGTGCTA TGGAGGAGGT      240
GCCACCTGAC TGGGAGAGAG CATCCTTCCA ACAGGGCAGT CAGGCCAGCC CTGATTAAAA      300
GCCACGTCCA CTCGAG
                                                                                   316

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

GACAAAGACC AGCAATGGAT CACTTGGAGT CTTTATTGTC TGAATGTGAT CGGAGAACTG      60
AGCTCGCCAA GAAGCGGCTG GCAGAAACAC AGGAGGAAAT CAGTGCGGAA GTTCTGCAA      120
AGGCAGGAAA AGTACATGAG TTAAATGAAG AAATAGGNAA ACTCCTTGCT AAAGCCGAAC      180
AGCTAGGGGC TGAAGGTAAT GTGGATGAAT CCCAGNAGAT TCTTATGGAA GTGGNAAAAG      240
TTCGTGCGGA GGAAAAAGGA GNACTCGAG
                                                                                   269

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

GAATTCGGCC TTCATGGCCT ACTTGTCTCA CTCTGCATCA TCCCTTAGTC TACAACAGGC      60
CTTTTCTGAA CTTAGACGTG CCCAAATGAC AGAAGGACCC AACACAGCAC CTCCAAACTT      120
TAGTCATACA GGACCAACAT TTCCAGTAGT ACCTCCTTTC TTAAGTAGCA TTGCTGGAGT      180
CCCAACCACA GCAGCAGCCA CAGCACCAGT CCCTGCAACA AGCAGCCCTC CTAATGACAT      240
TTCCACATCA GTAATTCAGT CTGAGGTTAC AGTGCCCACT GAAGAGGGGA TTGCTGGAGT      300
TGCCACCAGC ACAGGTGTGG TAACTTCAGG TGGTCTCCCC ATACCACCTG TGTCTGAATC      360
ACCACTACTT TCCAGCGTAG TTTCAAGTAT CACAATACTC GAG                          403

```

(2) INFORMATION FOR SEQ ID NO:503:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```

GTTTGGATGA TTGGTGGCGT GTACGCAGCT GCTATGGCCT GGGCCATCAT CCCCCACTAT      60
GGGTGGAGTT TTCAGATGGG TTCTGCCTAC CAGTTCCACA GCTGGAGGGT CTTCTGCCTC      120
GTCTGCGCCT TTCCTTCTGT GTTTGCCATT GGGGCTCTGA CCACGCAGCC TGAGAGCCCC      180
CGTTTCTTCC TAGAGAATGG AAAGCATGAT GAGGCCTGGA TGGTCTGAA GCAGGTCCAT      240
GATACCAACA TGCGAGCCAA AGGACATCCT GAGCGACTCG AG                          282

```

(2) INFORMATION FOR SEQ ID NO:504:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```

GAATTCGGCC TTCATGGCCT ACTGAGAAAA AAAATCAAAT CTAATTTTAA AATGAAGGTA      60
TTTAAAACCA TGGCACAAGG GAGCCTTATT TATGGAGCTG GTGGGAAGCC AGGATGTTTC      120
CAATCCGCTG CTCTTACAGG AGCCTGTGCC TCGCCAGTTC TGTGCTGCAG TGGGCAGCCA      180
ACTGAAGTGC ATGAGTCAAA TGCACGAAGC AGCAGACTCG AG                          222

```

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

| | |
|--|-----|
| GAATTCGGCC TTCATGCCCT AGTGGTGCAG TTTTTCAGGA TTGTAGAGAT GCTAACAAAT | 60 |
| TACAGGTTCT CTCATGCAAA CACTTTGCTA GGAATTATAT ATATCAAGTT TATATTTGGC | 120 |
| AATCAGGCTT TAGAAGCAGA AGGTCTAGCT ATCTCAAACCT ACCACCTACC TCCCTCACCA | 180 |
| AAGCCGCTCG AG | 192 |

(2) INFORMATION FOR SEQ ID NO:506: ..

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

| | |
|---|-----|
| GAATTCGGCC TTCNTGGCNT AGTAAAATTG TTAAAGTTGA CAGGATCAGT TTTGGAAGAT | 60 |
| GCTTGGAAGG AAAAAGGAAA GATGGATATG GAAGAAATTA TTCAGAGAAT TGAANACGTT | 120 |
| GTCCTAGATG CAAACTGCAG TAGAGATGTA AGACAGATGC TCTTGAAGCT TGTAAGACTC | 180 |
| CGGTCAAGTA ACTGGGNCAG AGTCCANGCA ACTTCAACAT ATAGAGGNGC NACACCAGAA | 240 |
| AATGATCCTA ACTACTTTAT GNATGNACCC ACATTTTATA CATCTGATGG TGTTCTTTTC | 300 |
| ACTGCAGCTG ATCCAGATTA CCANGAGAAA NTCCAAGAAN NACTTGAAAG AGANGATCCT | 360 |
| CGAG | 364 |

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

| | |
|---|-----|
| GAATTCGGCC TTCGATTGAA TTCTAGGACT TGACAGAATT CGAGTTATCC TTCTCAGAAC | 60 |
| ATGTGCAGAG TCTCTTTTGG CCTCACCATG TGGTCTGTG CTCTTTCAGG TGGGAGTTTT | 120 |
| GGGGCCTCCA GGGCAGCAGG CACCACCTCC ATATCCCGGC CCACATCCAG CTGGACCCCC | 180 |
| TGTCATACAG CAGCCAACAA CACCCATGTT TGTAGCTCCC CCCCAGAGAC CCAGCGGCTT | 240 |
| CTTCACTCAG AGGCCTACCT GAAATACATT GAAGGACTCA GTGCGGAGTC CAACAGCATT | 300 |
| AGCAAGTGGG ATCAGAGCAA TCTCGAG | 327 |

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

GAATTCAGTG AGTGGGCATG GCTGATCTTG TGCAAATTAA AAGTTATGGG GCATAAGAAT      60
AGCAAAAGTT GAACTTCTTT TAAAAAGGAA AGTACCCTGA GAGCCAGTAT TGGTTGAGGC      120
TCTTCAGTAT GCCCAGGTTG GCAGCACTGA GAACCGCAGG AACGGCCTGT TGTACAAAA      180
AGGAGATTGA CTCAGCTGCC CTTGGTGCAT CTGACTGACT ATGACTGCTG AGAGATTCCA      240
AGGACCCTTA ATGCCAGGGC TAACCTCTCC ATGTGCAGTG AGACCTCTGG AGGAAGTGTC      300
ATCCTCTGGC TTTGTGTGGT ACTCATTATG GTGCAGTGCG GGCATGAAAT GAAGACACAC      360
AAATAGGCTC GAG                                                              373

```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS: --

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```

GAATTCGGCC TTCATGGCCT ACTCTTCCTG GCTCCTTCTC AGCCTTGTTG CTGTAAGTGC      60
TGCTCAGTCC ACCATTGAGG AACAGGCCAA GACATTTTGG GACAAGTTTA ACCACGAAGC      120
CGAAGACCTG TTCTATCAAA GTTCATTGCG TTCTTGGAAT TATAACACCA ATATTACTGA      180
AGAGAATGTC CAAAACATGA ATAATGCTGG GGACAAATGG TCTGCCTTTT TAAAGGAACA      240
GTCCACACTT GCCCAAATGT ATCCACTACA AGAAATTCAG AATCTCACAG TCAAGTTCA      300
GTGCAGGCTC GAG                                                              313

```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```

GAATTCGGCC TTCATGGCCT ACTTGAACAA TTTAAATATA GGAGAAGACT ATTTTITAGA      60
AATGTTTTCC GTCGCCAACT TGTTAAAGCT TTATAGCACT TTGCATATTT TGGAGAATGT      120
CAACTATATT TTTATCAGAG CTGATTTGTT CCAGTGGAAC AACAGTGGCG TAGACATCGC      180
CCACAAGGTT CTGCATACTC GAG                                                              203

```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

GAATTCGGCC TTCATGGCCT ACGTGGTATT AAGGAGACAA TCTGAGGCAT TCCCACCACT      60
CAATTTGACA TGCAGTTGGC AAGGTTCTTC TTCCCTTCCC ACTTTAGATC GTGCCCTGTC      120

```


| | |
|---|-----|
| CCAGGTCAGA CCCGAAAGAT TCATAGGCAC ACTTACAGCC TTCATAGTCT CAGCCATAGT | 180 |
| CATCCTAGCA ACTGCTAGTG TGGCTGTAGC ATCTATTACT GAATCAGTAC AAACAGCTGC | 240 |
| TTTTGTAGAT AATTGGCCA GAAATGTTTC TAATGAACTT CTCTTACAGC AAGGTATAGA | 300 |
| TCAAAAGATT CTTGCACATC TGCAAGCCCT CGAG | 334 |

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

| | |
|---|-----|
| GAATTCGGNC TTCATGGCCN AAAGCTCTNG AAGGAGTATT AGAGTACAGA GTCTGAGNCT | 60 |
| NTGANAAATG GTGGTCAGAA GCCNTCTTCA TCAGATANAT TTCTCAGATG TGCCCCCTTCC | 120 |
| GCGGCAGAGG NGGATATTCA TCTCCTAGTT CATGTTTCTAGT AACATGTCAG TANGCAGATN | 180 |
| ANTCACTACC AGTATCTGCT TCTACTTTTC CTGCATGAGT CACTTATCCC TGCTTTTCTAGT | 240 |
| GAACNTAAGG AAAGATGTAG AAGCTGTAACT TGGCAGTCTT GCTAGTCAGA CATCCATTTC | 300 |
| TATTGGAATT TTACTTAGAA GTGCAGAACT GGCTCTTTTG CTCCATCCAG TGGATCAAGC | 360 |
| AAATACTCTT AAGTCTCCTG TTTCTGAAAG TGTGAGCCCA GTGGTACCTG ANTATTTGCC | 420 |
| TACAGAAAAT GGGGATTTTT TGNCCCTCAA AAGAAAACAA ATTAGTAGGG ATATAAATAG | 480 |
| AATTAGAAGT GTAAGTGTTA ATCATATGTC AGACAACAGA TCTATGAGTA TCTCGAG | 537 |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCA AGGTGCTTAA TATTAAAAA AAAAAAAGTA TATCCAACCA | 60 |
| CAGATATACA GTTCTGCCTT TTTTCTCTT TTACCTAAAT ATACTCCATA AACAGTTTCC | 120 |
| ATGTTGTGTA ATATCTTCAT GTTCTACTT TTCAGTGATT GCTTAAATGT CCATTGGGCT | 180 |
| GATAGGTCAC AGTTCGCTAA CCCATCTCAT TGTTGTTTAT TGGGATCTCC ACTTTCCTTC | 240 |
| GAG | 243 |

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAAA GATTATCCAC AAATGCAGTG | 60 |
| GNCCCTGGGA CAAGCCCTTT AAAGGAGTCA TNGAGAATCG TCTGTTGCTC ACAGCATCAA | 120 |

| | |
|---|-----|
| TCNGGTATTT AGTTCTCAAG CTTGAGGATT CTAGTTTTCG TCAGAGGGTC GGGTTCAGTC | 180 |
| TCTAAAAGAC GCTCTGAAAG CAGACCAGGC TGTTCCTTG GAGCTTTTCA GGTTAGATTC | 240 |
| TCATGTGTGT ATCTTCCATC TACCACGATT ATTTGGCTAC CAGATGCCTT AGCAAGCTGA | 300 |
| ACAGTGAGCT CAGAAGTGCC ACCATCTATA GTAACATTCT CGAG | 344 |

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGAGTATCC GCTTACAGAA AAGACACTTC ATCACCTAGC | 60 |
| ACTGATTTAT GCAGCTTTGG TTTCAATTGG GCTAAACTCT GAAGAACTGG ATGTAAAGCT | 120 |
| TATAATTGCC CCAGGAGTAG AAGCAACTGC CTGATAATT CGACAAATTG CTGACCACAG | 180 |
| TTTAATGACC TCAAAGAGAG ATCCTCATGA ATGGTTGGAT AAATCCTGGC TTAAAGTTTC | 240 |
| ACCATCTGAG GAAGAAATGT ACTTACTTGA TTTTCCATGT ATTAACCCAA TCGTGGCTCG | 300 |
| AG | 302 |

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AATCCATAAA | 60 |
| AGGCTTTTCA GATGTCTCTG CTGAAAATAA ATGGAGCTCT AGTAAATGTT AGAGTTTTTG | 120 |
| CTAGTAGAGT TTTGATGCTT TTTGTCTTTG TTCTACTACT GAGCTTGACAC CTAGGATGCC | 180 |
| TTCTTATAGT GCCATTCAAC ATGCAAGTTT CTTTTTCTGG GGCTGTGTGT CCAGGTGACT | 240 |
| TTATGAGTTA GGCTTTGGCA AATGCCAGAC TTGTTTCATCC TAACACTAGA ATGTAGGGAT | 300 |
| CCTGCATTCA GCATGACCCT CGAG | 324 |

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATAGGCCANG AAGGCCGGCC TTCATGGCCT ATAGGCCATG | 60 |
| AAGGGTTGGT TGTGTTTCC TAACAATGAA TAAGACAGAA ACCCTTGATA GCTAAATTCA | 120 |
| TCTGCAGTCA AACTAAGTTT TGCAGTGTCT TTTTAAGAGC CAGGCAATTC TACCACAAAA | 180 |
| TAAAATATAT TTTTAAATC CACATTACTA TACCACTGAC AAGTCTTTAC TTCAGAACTC | 240 |

| | |
|--|-----|
| ATCATTGAGA AATGTGTAGC TGCTTCCAGA GTGTGTCTAA TACTGTTGGA ACAGGCGTTT | 300 |
| CAGAAAAGAAA TGAGAGGCCC ACTCTCAGTA ACTCCATGAA GGGTGCCGAG CTCCTCTGTT | 360 |
| GAGGATTTGG CTTGTGAGAG GCAATGTTCC TATCATTGTC CAATTTGGCC TTTGTTATTC | 420 |
| CCACATTGGC TCGAG | 435 |

(2) INFORMATION FOR SEQ ID NO:518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACCAGGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAGG | 60 |
| TGATCTGCTC ACCTCGGCCT CTCAAAGTGT TGGGATTACA GGAGTGAGCC ACCGCACCGG | 120 |
| GCCAAAAAAT CCAATTTCTT AGAGATTAAA TAACCCTTCA GGATTATCAA AGGAAATAAT | 180 |
| TAGGGAAAGG TAGATGTTCT GTCCCAAGTAA GAGAAGAAAG TGGTCCAGAA ATTTTATCTC | 240 |
| CCATCAAATG ATCCATTTTA CTTAAGTATT AAACCAAGTG ACATTCTTCA GTTTAACTCT | 300 |
| GATAAATGAA TCATATTCCT CTTGAAAAAT AACTTTTGTA TTTCGTGCTC TAAAAAGAGA | 360 |
| ACCACCCCTC GAG | 373 |

(2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AAACAATTAA TTGTGGGTGT CTGAGGGGGA AGGTGCGCAGC | 60 |
| TTTGGGCAGC TTTGAGAAGC GGTACAAGAG TTCTGTGCCT GTGTGTCCAG CCTGGAGGCC | 120 |
| AGCCAGTGCA TTTATTTTAA GCTCTTAGAA GCAACTCCTT GGCCCAAGAA TCGGTGACCC | 180 |
| CTGAGATGGG TCACGCATC TCTTACACT TCCTTCTCTC CGTGGGATAC TGGACTCGTG | 240 |
| CCTCTGCGCC CATTCTCTTC TCACGCATAT CCATGAGCTT TAATTTCACT TTCTGATCAC | 300 |
| GGTACGTCCA TAAAGCCAGT ATTACACTTA AATGAAGTAT TCTTTTGTGT AATCGTTTTT | 360 |
| TTTAGAAGGT AAACAAATTT AATAAAGCTA TCTCGAG | 397 |

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCC ACATGAATCT NGTAATTTGT GTCCTACTTT TGTCCATTTG | 60 |
| GAAAAATAAT TGCATGACTA CAAACCAAAC CAATGGATCT TCTACTACAG GAGATAAAC | 120 |

| | |
|---|-----|
| TGTGGAATCA ATGCAGACAA AATTGAACTA CCTTAGAAGA AATCTACTCA TTTTAGTTGG | 180 |
| TATTATCATC ATGGTTTTTG TCTTTATCTG TTTTGTAT CTCCATTATA ATTGTCTGAG | 240 |
| CGATGATGCG TCCAAAGCAG GAATGGTCAA GAAAAAAGGC ATAGCAGCCA AGTCATCTAA | 300 |
| AACATCATTC AGTGAAGCCA AGACAGCCTC TCAATGCAGT CCAGAAACAC AATCCATGCT | 360 |
| ATCTACTGCA GACAAGTCAT CTGATTCATC GAGTCCAGAA AGGGCATCCG CACAATCCAG | 420 |
| CACAGAAAAA TTAATCAGAC CCTCAAGTCT ACAAAGGCCA TCCAACCTCG AG | 472 |

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs-
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACACCTCTTC TTAGGGCTGT TTTTAAAC ACAATGATAT | 60 |
| TCTAAGGAAC AAGAGGTTGG CTATGGACTT TTGTATACCC ATGCCTATCA TATTCGCTA | 120 |
| AATGTTGAT TATATAGAGA CATTCTTTG GAACTTTGAG CTGTGTGAAG ACAACACAAA | 180 |
| CCTGGCCATT CATGGCTGAC AGAAGGTTGG CCCTAACCT GCTCAGGCC ACACAGATTG | 240 |
| TGTAATATTC TTTGGATCTG GCTCTAGTCA GCAAAGTCTT GGTGTTGTAG GATACAGGTG | 300 |
| TCTTCATGCA TTCCATTTTA TACTCGAG | 328 |

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAAAAAGAA AAAGTAGCTG ATGAAGATGA TGTGGACAAT | 60 |
| GAGGAGGCTG CACTGCTGCA TGAAGAGGCT ACCATGACTA TTGAAGAGCT GCTGACACGC | 120 |
| TACGGGCAGA ACTGTCACAA GGGCCCTCCC CACAGCAAAT CTGGAGGTGG GACAGGCGAG | 180 |
| GAACCAGGGT CCCAGGGCCT CAATGGGGAG GCAGGACCTG AGGACTCAAC TAGGGAACT | 240 |
| CCTTCACAAG AAAATGGCCC CACAGCCAAG GCCTACACAG GCTTTTCCTC CAACTCGGAA | 300 |
| CGTGGAACTC GAG | 313 |

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

| | |
|---|-----|
| GAATTCGGCT TCATGGCCTA GCGTTGTGTG CATGCGAGCG CTCCTGCAGG CGTGTGCATG | 60 |
| GGGCCAGGTG TGCACGTGGA TGCCCGGTG AGTGTGTGTG CATGCACGTG TGTGCACGCA | 120 |

| | |
|---|-----|
| TGTGCACATG CCTCCAGCCC CACCTTCCAA CCCCTCAGTG CCCCAGGAC AGGGGCCCCCT | 180 |
| CTTAGCTATC AGGGTATGGC CGGACCGGCC CTTCCTGCCC AGCANGTTGC AAGCACTTGG | 240 |
| CCAGGCCGGC CCTCCAGGNT GCTGCTGCGT GGGGGCCCCG GTGCCCCCAG GTCCATGCAG | 300 |
| ACTGGGGATT CGGTGGGGAG GGGCGCTTCT AAGGAACCAA ACTGACGCTC ACTCTGGGCT | 360 |
| TCCAAGCAC CTTAGCACG GAGCCACCC CTAGCTCGAG | 400 |

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCCACCCTG TAGTCAACCC CACTCGTACT GTAGCGAGAC | 60 |
| AAAAACATGC CATTGTGAAG AAGGGTACAC TGAAGTCATG TCTTCTAACA GCACCCTTGA | 120 |
| GCAATGCACA CTTATCCCCG TGGTGGTATT ACCCACCATG GAGGACAAAA GAGGAGATGT | 180 |
| GAAAACCACT CGGGCTGTAC ATCCAACCCA ACCCTCCAGT AACCCAGCAG GACGGGGAAG | 240 |
| GACCTGGTTT CTACAGCCAT TTGGGCCAGA TGGGAGACTA AAGACCTGGG TTACGGTGT | 300 |
| AGCAGCTGGG GCATTGTGT TACTCATCTT TATTGTCTCC ATGATTATC TAGCTTGCAA | 360 |
| AAAGCCAAAG AAACCCCT GCCTCGAG | 388 |

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATTGAATTC TAGACCTGCG TCGACCGAAC CGAGTTGTAC | 60 |
| ATTTTTTTTG TGATGGGTTA TTTTATTAT TAATTATTAT TGTGTTTTTG GTTTTTTTTT | 120 |
| GGTTGGTTTT NGATTTATGA CAATNCCACT CTTGGCCCCA GTTGTCGTCC TGTCACCTCC | 180 |
| TCCCCTGTCC ATCACCCTGG CTCCCAGACC AGGCTCAGCA ACACATTGAG TCTTGGGTTT | 240 |
| CAGGAACCTT GCCAACCTCA ACCCTCCAGC CCGTGTCCA CTGGCTATGG CTCAGACCAA | 300 |
| GGGCTCCTCC TCTCCNTCT TGCCCTATGG AACAGCCCGG GTGCTCCAAG GGGGCCAGGA | 360 |
| GGGCATGGCT TGGCTCCAA GATAAGGGGT CCGGGGCCAG GACACCCAGG CAAGGTGGCC | 420 |
| CCTCCCTGCC TAGCCCCCTT CCCCCACCC AAAGTCGAG | 459 |

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

```

GAATTCGGCC TTCATGGCCT ACAACCTGGA AAATTCTCTG ACTTAGAAAT TTAAACAAAA    60
CCCTCCCCTT TCATTGAATC TCCATTGTCT GGAGTTTGCT TGTTTTAATC TAGCCTGTTC    120
CTCCACTATG GGCTCCCTTT CAAACTATGC CCTGCTTCAA CTAACCCCTTA CTGCTTTTTT    180
GACAATTCTA GTACAACCTC AGCACCTGCT TGCTCCAGTT TTCCGGACAC TATCTATCTT    240
GACTAATCAG TCTAATTGCT GGTATGTGA ACATCTAGAT AATGCAGAAC AACCCGAACA    300
CCTCGAG                                         307

```

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS: --
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

```

GAATTCGGCC TTCATGGCCT ACCAATACTA AGCTTATTTT ATTGTAATAC AGTTATTTGT    60
ACCACCTTAG AGCAATCTTT TGAAGAACAA GAAACACATA TTGAGCCACC ACGCCCAGCC    120
TTTTTTCAGT TTATTTTAA TCTTTTGCTG TTCATTGGCT CATTCTGTGT ATAAGCATGT    180
TAAATTTACC CAAATATGAA AATAGCCTCC CCTTGGCCCT GAACTCCTCT ACAAGCAACT    240
ACCTCATGAT TTTATCTCTT TATCCTCAA TTCTTTGGAA TATAATTTAT ACTTGTTTCA    300
TCCCTACCAC CCTCGAG                                         317

```

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

```

GAATTCGGCC TTCATGGCCT ACAGCAGTGT GCTTTCATCC AGTTTGCCAC ACGGCAGGCT    60
GCAGAAGTGG CTGTGAGAAG TCCTTTAATA AGTNGATTGT AAATGGCCGC AGACTGTATG    120
TGAAATGGGG AAGATCCAG GCAGCCAGAG GAAAAGAAAA AGAGAAGGAT GGNACTACAG    180
ACTCTGGGAT CAAACTAGAA CCTGTTCCAG GATTGCCAGG AGCTCTCCT CCTCCTCCTG    240
CAGCAGAAGA AGAAGCCTCT GCCAACTACT TCAACTTGCC CCCAAGTGGT CCTCCAGCTG    300
TGGTGAACAT TGAATNGCCA CCGCCCNCTG GCATTGCTNC ACCCCCACCC CCAGNTTTTG    360
GGCCACACAT GTTNCACCCA ATGGGACCAC CCCCTNNNAC TCGAG                                         405

```

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCAAGA    60

```

| | |
|---|-----|
| GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT | 120 |
| GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTGC CTTGGAAATA CACTGGAAGT | 190 |
| GGTACCAAAC AAATCTAATA AAATGATGTT AAAGAGATTG GCAGTAATTT TTATCAACTT | 240 |
| TCAGTTTGCA AACTTTTATA AAGATATGAA CGGGACACTC GAG | 283 |

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT TTCTATAAAT GAGTCTTTA TAAGAAGCTT GTATCATTCT | 60 |
| CACAAATTAA AAATAATAAT ATTTTAGCAA GCTATTTTTT AAATATAATT TAAGCCCACA | 120 |
| CTTCCACATT TGGGGTAAGT GATAATTTTT TCCTCTGAAA GACAACAAAT ACTAACACAG | 180 |
| GCCCAGACTT GGCTTTTG TGAGTCAATTAG TGATCCGAAG GTGAGTGGTA TTTAAACGTA | 240 |
| TGATGAGGGT AAGATTTGAT TTATTTTACA TATATATCTT CTGGTATCTG TGTGTGTGTG | 300 |
| TGTGTGTGTG GAAGCTCGAG | 320 |

(2) INFORMATION FOR SEQ ID NO:531:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

| | |
|---|-----|
| GAATTCGGCT TCATGGCTTG GGGGTGACAG TTAATATATN CGGTCAATTT AGATTGCTTC | 60 |
| CACTAATATT GGTATATCCA TATTATAAAA TATTTTAGTG AGTATAAAAT TGTCTGCATT | 120 |
| CATAAAGATG CATAAAATTA ACTACAGAAC CAGCTTGAGT AATGCTTTTC TCTTCTTTTC | 180 |
| TTCTTGTCAT TCAGATATTA TCTTTATACA TTGTTTGA GTATACATCT ATCAAAATGC | 240 |
| AACATTGTTG AAGGATATGT AATTTATACA GCAAACGTGT AATGGATAAA AATGTGCAAA | 300 |
| AACAATCCTT AAAGTATTGT ATTTGAACNA AAACAATCTT AAACCACATA ATCTGAAAAA | 360 |
| AAGGGGTACA TATTTTACCA AATATACTAA TCCATACAAG ACTGCTTGAG AAAAAGAATA | 420 |
| TGCCACCTAC TCGAG | 435 |

(2) INFORMATION FOR SEQ ID NO:532:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCCATCAG ATTGAAATTA ATTTAGACAG GAAGAATCTA | 60 |
| TATAAATTTG ATGCATAGCA AACTCTGACA TAATTTGGTT TATTTTGAAG TCTGGCATAT | 120 |

| | |
|---|-----|
| TTTTCATCAC TTTTATTTT ACGGGTAAAT CATAATATAT CATATTTTCA ATAAAAGTAT | 180 |
| TTTCTTAAAA ATCTGCCATT TGCTTCACAG ATTTTAAATC TTCTAACAGA AAAAGAACTA | 240 |
| AATATGTTT TGCCAACACA GTCCATTGTT CCAAGAACTT TTGTGCTTAA ACCAGGAATG | 300 |
| GTTCTGTTTT TGGGTGCTAT AGGCCGCATA GCCCTCGAG | 339 |

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATGTGCTCC AGGAGGCGCT GGGGGATGGT GACCTCCCAA | 60 |
| GGCGGGCAGA NACTTCTGC CGTCAGGGTC GCCTGCTGCT GAGCCTGGGG GATGAGGCGG | 120 |
| CGGCCGAGG GTCTGGATCC CCTGTGCCGT CGCCTCTTCC TTTTTCGACG CCTCCGCCGC | 180 |
| CGCCTGAGGA GCGGAGCTAG CCGGGAGTTA CACCGCCACC GCCAGGATGG ATAGAATGAC | 240 |
| AGAAGATGCT CTTGCTTGA ATCTGTTGAA GCGGAGCTTG GACCCAGCAG ATGAGCGAGA | 300 |
| TGATGTCCTG GCAAAGCGAC TCAAATGGA GGGGCATGAG GCCATGGAAC GTCTGAAAAT | 360 |
| GTTGGCATTG CTCNAAAGGA AGGANTTGGC AAATCTTGAG GTGCCACATG ANTTACCCAC | 420 |
| CNAACAGGAT GGCAGTGGTG TCAAGGGCCA TGAAGAAAAA CTTAACGGGA ACAACTCGAG | 480 |

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATATGTATTT TTAATCTATG ATGGTTTATG TGAATAGGAT | 60 |
| TTTCTCAGTT GTCAGCCTGG GCGACAGAGC GATACTCCAT CTAAAAAATAA GNAAAAAATAA | 120 |
| GAGGTGACTA GGCCATGAAG GCTCTGTCCT CACAGATGGA TTAATGCCAT TGTTGTGGGA | 180 |
| GTGGTTTTCT CATTGAAGGA TGAGCTTGAG CTTGGCCCCC TTCCTTCTCC CGCCTCATTC | 240 |
| CCCTCTATGT NGCCCCTATG ATGCCTAANG CCATGTTATG ATGTGGCAAA AAGGCCCTCG | 300 |
| CCAGATGCCA GCCCCTTGAC CNTGGAATTC CCAGCATCNA GAACTGTGGA CCNAATGNAT | 360 |
| GTTTTTTCCT TATAAANTAA CCNGCCACNG GTATTTTGT AAAGCNGCAC CNAGCAGACT | 420 |
| CGAG | 424 |

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACGTTGACTT AATCAGAGGG TCAACATTTG CCAAAGCAAA | 60 |
| ACCTGAAATT CCATGGACAT CTCTGACTCG GAAGGGGCTT GTTCGAGTTG TATTTTTC | 120 |
| ATTGTTTCAGC AATTGGTGA TACAGGTTAC CTCTTTAAGA ATCTTTGTTT GGCTGTTACT | 180 |
| ACTTTATTTT ATGCAAGTTA TAGCAATTGT CTTATATTTG ATGATGCCTA TTGTGAACAT | 240 |
| AAGTGAAGTA CTTGGACCTT TGTGCCTTAT GCTACTCATG GGAAGTGTCC ACTGTCNAAT | 300 |
| TGTGTCTACT CAGATAACAA GACNTCAGG AAACCTCGAG | 340 |

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGGCGCTCGC TGAGGCAAAA GGAGGCGCTC GGCCCGCGGC | 60 |
| CTGACAGGGA CTTAGCCCGC AGAGATCGAC CCCGCGCGCG TGACCCACACA CCCACCCACT | 120 |
| CATCCATCTA TCCACTCCCT GCGCCGCTC CTCCACCCCT GAGCAGAGCC GCGGAGGATG | 180 |
| ATAAACACCC AGGACAGTAT TTTGCCTTTG AGTAACTGTC CCCAGCTCCA GTGCTGCAGG | 240 |
| CACATTGTTT CAGGGCTCT GTGGTGCTCC TGATGCCCCC CACCCACTGT CGAAGATCCC | 300 |
| CGGTGGGCGA GGGGGCGGCA GGGATCCTTC TCTCTCAGCT CTAATATATA AGGACGAGAA | 360 |
| GCTCACTGTG ACCCAGGACC TCCCTGTGAA TGATGAAAA CCTCACATCG TCCACTTCCA | 420 |
| GTATGAGGTC ACCGAGGGTA CTCGAG | 446 |

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

| | |
|---|-----|
| GGCAAATTAC ATCACCAAAT CAGCATATTC TCCACTGGAA AGGAGAGGCC CACATAGCCA | 60 |
| AATTATAATC TGCAGGTTT TGAGCCAGTG TTAAATCTGA ACAGAGAAAA GATTTTTC | 120 |
| TCAATTGGCA AATTTTAATG ACATCACTCA TTGATACCCC AAAATCTCCA GTTCTTACCA | 180 |
| AGCTTGGCCT TGCCCAAGTG TTCTCTGTT CCCTCAACAA TGTTTCATGG NATCTAACAA | 240 |
| CTTCCCTACC CACTAACCTT CTCAGCTTTC ATGGTGAACC AAGCCTCCTC TGTGCGACTA | 300 |
| ACCTTCCCAG CTTTCATGGT GAACCAAGCC TCCTCTGTCC CGCTATTCTC GAG | 353 |

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGAAGGAGN AGCAAGCGGA TTTCAGAGAG GTTGTCTTC | 60 |
| AGAAAAAAT GGTTATTTCT TTGAACTCAT GCCTGAGCTT TATTGTTTA TTGTTATGCC | 120 |
| ACTGGATTGG GACAGCATCA CCTCTGAATC TTGAAGACCC TAATGTGTGT AGCCACTGGG | 180 |
| AAAGCTACTC AGTGACTGTG CAAGACTCAT ACCCAGATCC CTTACTCGAG | 230 |

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

| | |
|---|-----|
| GNGAACCAGA GATCCCCATA GATGGAACAG AATTATCCCA CTACCGTCAG CGTGCCCTCC | 60 |
| TGCAATCACA GCCAGTTCGC CGGACGCCTC TCCTCCACAA TTTCCTGCAC ATGCTGTCCT | 120 |
| CCCGCTCTTC TGGCATCCAG GTGGGAGAGC AAAGCACAGT GCAAGATTCT GNTACCCCT | 180 |
| CACCCCAACC GCCTCCCCCT CAGCCCTCCA CGGAGCGCCC CAGGACTTCC GCTTACATCA | 240 |
| GGCTCCGACA GCGGGTCAGT TACCCACAG CTGAGTGCTG CCAGCACCTT GGGATCCTGT | 300 |
| GCCTTTCAG CCGCTGCTCT GGCCTCGAG | 330 |

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTCCGACTT TCGTTCTTGA TTAATGAAAA CATTCTTGGC | 60 |
| AAATGCTTTC GCTCTGGTCC GTCTTGC GCCG GGTCCAAGAA TTTCACCTAG TTACCCCTCTA | 120 |
| GAATTATTGC ATTGGGGCCA GGTGGTGTCT AGTACAGTTT TTTACTTTGG AGAATTTATT | 180 |
| GAAATTTTCT TTGGCTGAGA ATGCCTTCAG TGTTTGTGGT TATTCCTTGG ATACTTGCAA | 240 |
| ATCGATTGTA TTTTCTCTGG GACACGGGGT TTCAGATAGA TCAGTTAAAT GAAGCTTGAT | 300 |
| TATATCGTAT TTCACGTCGC ATGCCATGTG TCTTGTCTGT TGGACTGTCA GGTCTCAAGA | 360 |
| GACGGGCTTG GGTTCCTCTG TGTGGCTGCT GCCTTGCCCC TTCCCCGATC CACTCTCGAG | 420 |

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

| | |
|---|-----|
| GTGGGCAAAG AAATGAAGTA CATTAAGGAG GCCTTTTTTT TCCTCCAATG GCTGTAGAT | 60 |
| TGTGTATTGC AACCAGGAGT TGTCAAGCTC CTGATCCTAA TCCAAGCTGG GGACTGTGGT | 120 |
| ACAGTGTGGC CAGCTGCCTT GCCAGCTGCC TTACCAGGCA GGTCTCGCAT CTGCCATTGT | 180 |

| | | |
|--|------------|-----|
| CATCCCATTG GAATCAAGTT GCAAGCCAGT GAACTTGCTG GGGTGTGCC | AGGTCAGAAC | 240 |
| AGTTACAGCT TAAAAGCCTT TGCTGCCCTT TTTCAGATCC TGTCCTGGG | AGAGTCTCCC | 300 |
| ACACTAAGTT CAGTGTGGGT ACCAGCTGTG GTGAGGGTGT GCTGCCACTG | CAGCTGCTGT | 360 |
| CTGGGCATCT GTGTTAGGGC CAATACTTCA AGAAGTGTGA GTCATTGTGA | AGTGACTGTA | 420 |
| GGCAGCTGGG AAATAACAGC TGTGAACAGA GAACAACCTG AG | | 462 |

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

| | | |
|--|------------|-----|
| GAATTCGGCC TTCATGGCCT ATGGGAGATA GGGGACTTAA TTATTTGTG | GTTTTTTCT | 60 |
| TTTTTAGGTC TTAGGAAGGT CTTTGTCCA TAGGTATCTG TATAATACAA | TTTTATTAGG | 120 |
| TGTAATAGAG ACAGTTTTGT GGAACAGAA TGCTGACACT GATTAAAATT | AAGGTGTATA | 180 |
| TATGTTTAGT CTTTGAGATG ATCTGTATGC TACATGTAGG TGTACATTGT | AATTTTCTGG | 240 |
| CTTGTAATTT TTTGTATCAT ACTCTGTTTC GGAATTTC AAATGCCTAT | GACCAGCCTA | 300 |
| TGACATCTGA ACCATACCAA CTGACCTTAG AAACAACGAC ACTCGAG | | 347 |

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

| | | |
|--|------------|-----|
| GAATTCGGCC GCCTAGCAAA AGTGAAAAA TAAATAAAAC AAGCCACAGA | TTGGGACAAA | 60 |
| ATATTTGTGA AGGATATATC TGATTAAGAA GTTATATCCA GAATATATGA | AGAACTTTCA | 120 |
| AAACTAAAGA AAACAATTCA TTTTTTTAAT TGGGCAAAAG ATTTAAACAA | ATATTTTACT | 180 |
| AAAGAAGATA TCCAGATAGC AAATAAACAC ATGATATTCA CCGAAATTAT | TAATTAGGAA | 240 |
| AATGCAAATT AAGATGAATA TCATTATATA CCTACTAGAA TGGCTATATT | TTAAAAGTTT | 300 |
| GAACTGCCA ATTACTGGTA AAGATGCAAA TCAGCGGAAG CTCGAG | | 346 |

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

| | | |
|--|-------------|-----|
| GAATTCGGCC TTCATGGCCT ACTTCTTCC TACATTAGTG GCATACTCTG | AATGACCTAG | 60 |
| TGAACAGACT GAGAAGAGGC CTCTGAATTG CAGAGTCTCG TCTGTAGGAG | AAGGTTTCAGG | 120 |
| AGAGTATTGA ATTTTAGGGA CTAGAATCCA TCTTACCTAT GCTGTTGCAA | TCGCATGCTG | 180 |

| | |
|---|-----|
| ACTGGAAGTG TGGGAAAGAG ACTTACAAGT AAGGACATGG GTTGTGTTTG TTTTGTGTTT | 240 |
| TTTGTGACAG AGTGAGACCC TGTCTCGNAA AAGGAAAAAA AGTAATAGAA CATTAAATAC | 300 |
| AGTATCACAC CATTATGTTT TAAAAAAGNA AAAAGACAAG AACTATATG AAGTGAGTGT | 360 |
| CTTTTAAAGT TTAATAAATT AAATGAAAAC AAACCTCGAG | 399 |

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

| | |
|---|-----|
| GAATTCGGCC GCCTCCATCT CCCTGGCCAT GTTCTTCTTG AAGACCCTGA CAGTGGCTTC | 60 |
| TTCTTTGTGG CAGCTGGCCA ACAGCCAGAC CCTGACAGCC AGCCCCAAG CACCTGGGTC | 120 |
| CCCAGAGGAT TCTGAGGGTG TCCCCCTCAT CAGCCTGCCC CGCGTGCCAC AGGGAGGGAG | 180 |
| TCAGCCTGGG CCCAGCCGGG GATTAACTCT CATGTCCAGT CAGGGCAGTG TGGACTCAGA | 240 |
| CCACCTAGGT TATGATGGTG GCAGCAGTGG CTCAGACAGT GAGGGTCCCA ATGACACCCT | 300 |
| TGGTGAGAAG GCCCCCTTCA CATTGCGGAC TCCACCTGGG CCAGCACCTC CACAGACTTC | 360 |
| ACTCGAG | 367 |

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AACCGCGGNC GCTCTACAAC TAGTGGATCC CCCGGGCTGC | 60 |
| AGGAATTCGA TATCAAGCTT AATTAAGAAT TCGGCCAAAG AGGCCTAAGC GAGAAGAGTC | 120 |
| CCCGCTCCGT GCCCTACCAC TACTTTGAGA AGGGCCGGCT AGATGAGTGT CAGATGTACC | 180 |
| GTTTGATGTA GCAGGCTCCA AGGAGCGCCC ATCGCTTCAT TACCGAGAAC CCTGTGTCT | 240 |
| CCCGCTGGGC CAAGAAGCGA CCCATCGTGT TCGCCACCC GTCTGGAGG GCCAAGTAGT | 300 |
| TCCTGTGGCC AGTGACTGCC AGGCCTCAGC CAGGCCTGTG ACCCATTCCA GGCCAACAGC | 360 |
| GCTCTAATGT GAGCATTAT GACTCACCTT CTACCTGACA CCAGGTAGAA CATGAAGTCT | 420 |
| CTATTACCCA AACTGGGTA CACTCGGAGG TCGAG | 455 |

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

| | |
|---|----|
| GAATTCGGCC TTCATGGCCT AGTCATTTTG TCAGCTTTCA CACAAGAATC TTTGATCCTA | 60 |
|---|----|

| | |
|---|-----|
| TTGTAATAGT TAATAAGGAA GTTCTTCTCT TGCTCAAAGA AGTCATCTAC CTCCTTAACT | 120 |
| CCAGTAAAAA GGACTTCATC AGCACTTTTC ACCACACTTT TGAAGAAGCC ACCAAACATT | 180 |
| TCTTTAGTAT TTTTCCGCCT AACACTTAGA TCCTGATCAT ATTCCAGGAA AACATGAAAG | 240 |
| TTGCGATCTT TACTGAGAAC AGGGTGAGAA GAAAGCCGCT GAAGAAAGAC TTCATGGGAG | 300 |
| GACACACTCT TCTTAAACAC AGCGAGATAC TCAGCTTCCA GTTCTTGTTT CATCTGGGCT | 360 |
| TATTATTCCA CCTTCTCCA GTTCTGTCAT CTCTCTCGA G | 401 |

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAAGCCCCT CTTACCTCTC TGGATGCTTT CTTTAACT | 60 |
| AACTCACCAC TGTGCTTCCC TGCAGACACC CAGAGCTCAG GACTGGGCAA GGCCAGGGA | 120 |
| TTCTCAGCCC TTCCCAGCT GGGAGGAGCT TGCCTGCCTG GCCACAGACA GTGTATCTTC | 180 |
| TAATTGGCTA AGTGGGCCTT GCCCAGAGTC CAGCTGTGTG GCTTTTATCA TGCATGACAA | 240 |
| ACCCCTGGCT TTCTGCCAG ATGGTAGGAC ATGGACCTTG ACCTGGGAAA GCCATTACTC | 300 |
| TTGTGTCTGC TACTGCCCTC CCACAGTCAC CCCAATATTA CAAGCACTGC CCCATTGGCT | 360 |
| CGAG | 364 |

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATGCTTTTCT TTGCAGCACT TAGCACAAAT AGTAATTTT | 60 |
| ATTTTACTTT TATAGATGTA TTTTATGTCC CTCCACCAGA CTGTATACTC CATGAGGACA | 120 |
| AGGATATTGA TGTTTATGTT AACTCTTGTA CACTCAGTGC CTGGCACCAT GCCTGACCCA | 180 |
| GAAGAGGGAC TCGAG | 195 |

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AACATAATGC GCTAGCAGAC TTGGGAATTA GGGGCAGAAT | 60 |
| GCTGCTCTAA ATTCAGGAAA TCATGGCAGC GTTTCATATT GAACATGGTC TATCCTACC | 120 |
| ACTAGCGCTT TCCTGGCTGA TTTCTTCTCC AGCTGGAGAC TTCTTTCTGG TTTTCCAATT | 180 |

| | |
|---|-----|
| TATGCTCCAC CCTCACCCCA ACCCACCCAT AAACCACTGG CTGCCGGAAG CAGTATCTTT | 240 |
| CATAGTGGTG AGTTCTGGAT TTTCAGCAGT AATGGCCGAG AGTCAGGGAC CAGATGAGTG | 300 |
| TGTGTGAGCT GGTGAGAAAA GGTAGATTCC CTCGA | 335 |

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

| | |
|--|-----|
| GCCAAACATG TCTCACCNAA NNCCAAATGT CCCNNGGGG AGCAAAATCT CCCCTGGACA | 60 |
| ACTGTGGAAT CACTGTNNGG AAGTGTTTAC TTGAGTGGTT TNCTGGCCTG GGCCTCATAC | 120 |
| TCTGAATTTT TGAAGTAAAT GGTCTGGGGG TGCTGGGGGT GGAGAGCAGA GCACTGGTAT | 180 |
| TTTTAGGAGA TCCCCCTGTC ATTCTAAAGC ATATCCAGGG TTAAGCACCA TTAATCTGAN | 240 |
| GATCTNCGT CTGATCTGCG GGCCCCCTTT CATCTANGTG CAGTATTTT CTCTATGCTT | 300 |
| TTTAAATAA TGAAAGTTTC TNGAACTCCA TCTGGACTTG AAATATAGCC TGCCACACAG | 360 |
| TTAGCAAATA TAGCAAGAAT AACAAGTGTT CTAAATGGAT TTTTAATTTA TTATGGCAAT | 420 |
| AGTACATTCC AANAGGGTGG CATTTTTTAA AATGAGATT TTCTTTTGGG CCTAAGATTA | 480 |
| CAGTCACATG GTTCCAAAT CAGAGGGTTC AAAAGGACAC AGAAAAGCCT GCTTCCCACT | 540 |
| TGNGCCCACT GGCCTCCCCCT TTTTTCGCAT AAATGGCAGT ATATAGCTTT GTCTGTTCTT | 600 |
| TGTTTNNNGA GCTTAATACC TTAGAGACAG ATTTTNGTAT ATCTGTACCT ACAGAACTCG | 660 |
| AG | 662 |

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

| | |
|---|-----|
| GCTGTTTTAA AAGAGTTGGG GGAAGAGGTA GAAATGAATC TTTTGGTTTA GTTTTTTAAT | 60 |
| TCTCTAAGGA CAACATTGGG GAAGTGAGCT TTAGAGTTAT ATTTGCAGTA TTTATTTTAA | 120 |
| TCATGAAATA TTCAAGTCTA GGCCCTTGGT GAATTGAGGC CTGGTGAGTA TTTCTGCTTT | 180 |
| CCCCCTGGAG AGATTGAGAT GGTTCCTGAT TGGGAGCTTT AATTCTGTGG GCATTTGTGG | 240 |
| GACTTACCAA AGAGGTATCT AGAGTTCCTT TAAAACCCCC GCCCTGTCCC TGCCACAAAA | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

```

GTCAAAAGAG GAGCTAGGAC CAGATCTCTA AGTCTTACNG TCCAGGTCAA AAAACAAGTA      60
CTTTCCTATC TGGTTATACA GAAATCTGGA AACAGTCACT CCCAGCCTCA CAATTAAAAA      120
AAGTTGGACA TACAGAAAGT TCATAGTTTT CTTGAACTC ATGATAGTGC TGAGATTTC      180
CGGCAACCAA CTGGCCCAGA TACTCCAGAG TCAAAGACAC TGTAAAGGAGA GTTGACATNT      240
GAGCATTAGA CAAGACACAG ATGGTANGAG TTAAGCTAGG GTTACTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

```

GAATTCGGCC TTCATGGCCT ACTCTATGGG GATGAGGTAG AGGAGAGCAA GATATTTCCG      60
CAGCAGGGAA AAGGGTAGAA CAGAAATAGGG TGACACAATT TACACTTGAT ACTGCATTAA      120
CATCTGGTAG AGTGTCTAGG GCAAAGGTTA GCCAAATAT AGCTGGATGG TTGAGGGATT      180
TAGAAGGAGT TGGGATGAAT CCATAGTCTC AATGAATGGA GAAAAAGTAA CTCAGGAAAG      240
TAAATGCTGG TGACTTATCA GCGGGTGGCT GGTGATGTTT GGTTTGGATT GTGAAAGCTG      300
CTTAGACCAA GATGGGCTGA GGAAGGGGA GGAGAGTGAG CATGTAGAGG TTGAGGCACT      360
TGGTCTCGAG      370

```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

```

GAATTCGGCC AAAGAGGCCT AATTGCCAAT CAACAACCTT TCCTAATCCA CCTTGATCCT      60
CAATCATAAT ACTCAAAAAC TGCCAAAAAC AAAATCTTCC TGACAAAAAT ACAGGCCAAA      120
CTTCCTCATC TGCTTCCAG GTCTTCTGTA ATCTTATCCC AGCTTATTTA CAGTCCTCCA      180
TTTACTAAGA AAACCCAAAA TAATCTTTTC CTGCCCCAAA TTCATGTTCT TCCCTTTCTC      240
TTTGTTTATA CTACCATACA TATCTAGAAA TGATACTCAA ATATTCATCC TCAGCACCCCT      300
CGAG      304

```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

```

GAATTCGGCC TTCATGGCCT AGAGGGGAAA GCATATCACT AGGACTGTGA CCCCTGTGCC      60
TACCCATCTT ACTCTCTACC TCTTAGGAAA GTTCACTGT GTTACTTGG GACTTCTGGA      120

```

CTAGCTGCCG TTTGCAACAG TGGACTTACC AGTTTGCCAC TACTCTGCTA CTTTCTACT 180
 GGTGCACACA CCTTAGTAAG GCAGTTTGAT TACTAAATGC AGCTGTCTCC AGAAATGGAA 240
 TGATGCTATA GGCCACTTAC TAAATGAATG ATCAGGAGTC TCGAG 285

(2) INFORMATION FOR SEQ ID NO:557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC TTCATGGCCT AGCTGGATCT GCCCACTGTG CACTCCATCA TCAGCAAAAT 60
 GATCATTAAT GAGGAGCTGA TGGCCTCCCT GGACCAGCCA ACACAGACAG TGGTGATGCA 120
 CCGCACTGAG CCCACTGCCC AGCAGAACCT GGCTCTGCAG CTGGCCGAGA AGCTGGGCAG 180
 CCTGGTGGAG AACCAACGAAC GGGTGTGTA CCACAAGCAG GGCACCTACG GGGGCTACTT 240
 CCGAGACCAG AAGGACGGCT ACCGCAAAAA CGAGGGCTAC ATGCGCCGCG GTGGCTACCG 300
 CCAGCAGCAG TCTCAGACGG CCTACTGAGC TCTCCACTCT GTTCCCGCC TGGGCCATCC 360
 AACCTTGAAG TCCTAAACCA CACCTCAGTC ACTAAAGGTC TGTCTCGAG 409

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GAATTCGGCC TTCATGGCCT AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGNGGTACC 60
 AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGGAG AAATCCTATA TACTCACTAA 120
 TAGATAAGAA GAAACAATTT AGAAGCAGAG GATCTGGCTT CCCATTTTTA GAATCAGAGA 180
 ATGAAAAAAA CGCACCTTGG AGAAAAATTT TAACGTTTGA GCAAGCTGTT GCAAGAGGAT 240
 TTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACCG TCTCGAG 287

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC TTCATGGCCT ACTTCTCAAA AATAGATGTA CTTGACTACT CTTTTCTTGA 60
 TTCTTCTGGG AGTAACCATC TCTTTGGAGA TGGTTGTTAG TAAGGTTATA AAAATAACCT 120
 TACTGAGGAA CTCCCATGCA ATCCTCTGAA AATAATAAAA ATTTCCTTAT TTCAAGAACC 180
 CTTATTTAAC AAAGTAATTG TTAGGGTTGA ATACTCTAGG GGCAATGAT TTATTGTGCC 240
 TTTTGTAATA GTCAACACTT GGCAGGTGTG TGTTTGACAC TGGCTGATGC TGGGCTTATT 300

TCTCTAAGAG TATGGTAATT CTAGTAAAGT AAAGAAAATT GTTTATCAGA TATTAGGAAC 360
TGTACATAGG CCCCCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GAATTCGGCC TTCATGGCCT AAAATTGTTC ACGAGGGATT ACGTGGTTTA CTGTCTGTG 60
GTCCAGATAG CTTTATATTC TTTAAGATTC AGCTCGGATT CTTATCCTAT TTTTGCCATT 120
AACTTTCATT ATGATTTTGG CAAAGCCATT TTGTTTGCTT ACATTTTCA CTTTAAATGT 180
GGTGTCTGGC CTCCCCCCA CACTCGAG 208

(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GAATTCGGCC TTCATGGCCT ACAACANTT TTTACTGNGT TATAAATAAA AACAGCGACA 60
CATCCTAAAT GTGCACCTGT GCCGTGGCTG AGCCGCTGCA GTGAGGGCTA GTGTGCAACA 120
CCGATGCTGT GCTGGACGCG TGCCCGAGCCG GGTCCCCTGA CAGGAGGCAN CCGGGGCCGG 180
TGCGTGTGTT TGCATGTTGC AGTCATGGGG CGGGGNCGGC AGANGCCTGT GTGATNGTNG 240
CGTCCCTGGA AAAAGAAGNN GGNAGGCCCT CTCNCACNTG TANCCAGCC TGCAGANGGG 300
GNGTTNTGTG GGTCTTCCC CGTGCATATG CGTGTGATNT CACCCATCCC GTGTGGGTGC 360
GCAGGAGGGG CCGAGGGAGG AGGGTGTGG AGGGCGGAAG TTACCTCTGA CTGGAGGAGA 420
NACCCGGCCC GTGTNACCAG CANAGGTGTG NTGTTCTAA AACTGGGAAA AATTTGTTCT 480
TAATTTTAAAC CACAGTCCCC TCGAG 505

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GAATTCGGCC TTCATTTAAA AGATAAGTTA GAAAAGTCAA AGCGAGAACG GCATAACGAG 60
ATGGAGGAGG CAGTAGGTAC AATAAAGAT AAATACGAAC GAGAAAGAGC GATGCTGTTT 120
GATGAAAACA AGAAGCTAAC TGCTGAAAAT GAAAAGCTCT GTTCCTTTGT GGATAAACTC 180
ACAGCTCAAA ATAGACAGCT GGAGGATGAG CTGCAGGATC TGGCAGCCAA GAAGGAGTCA 240
GTGGCCCACT GGGAAGCTCA GATTGCGGAA ATCATTCAGT GGGTCAGTGA CGAGAAAGAT 300

GCCCCGGGGTT ACCTTCAAGC TCTTGCTTCC NAGATGACCG AAGAGCTCGA G

351

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAAAACTGT CCATGGCATG AAAGACTTGG ACCGCCATCT | 60 |
| CAGAATCCAC ACGGGAGACA AACCGCACAA GTGTGAGTTC TGTGACAAGT GCTTCAGCCG | 120 |
| GAAGGACAAC CTGACCATGC ACATGCGGTG CCACACCAGT GTGAAGCCAC ACAAGTGTC | 180 |
| CCTGTGTGAC TACGCTGCCG TGGACAGCAG TAGCCTCAAG AAGCACCTGC GGATCCACTC | 240 |
| TGATGAGCGG CCGTACAAAT GCCAGCTCTG CCCCTATGCC AGCCGCAACT CCAGCCAGCT | 300 |
| CACCGTCCAC CTGCGATCTC ACACGGGTGA GTCCCTGACC AGGGGTCCTC GAG | 353 |

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATAGAATTCC TAGACTTTAC AGACTAATAG TTTGACATCT | 60 |
| ATCTCTGGCA AAATTCGAAA CTTAAACATT AAACAAGGGA AAATGAGGGG TGGAGGNAAA | 120 |
| GACTGCGGAT TTCTAGGAAC TAACAATTTG CTAAGNATCA TTCATTTTAA AACTAATGTT | 180 |
| ATTACTTTT GTGGTAGATC AGGGNATATG CAAGATCTTT ACTTTTCAGC AAGACATTTT | 240 |
| TCTCATAATG TCCTTATGGA GAAGACTGCT CTATGGACTA GNATAGTTTG ATAAGAAAGG | 300 |
| GCTGAGTCCA GCGNATTCAT TAGTTCAAGC AAAATCTACT GGAGGCCAAC TAGATTTCCA | 360 |
| GCCATTATCG TACTTGGCAC TTTCNATACT TTGAATTTTA ACCACCACAC CTCGAG | 416 |

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGACGGGGT TTCACCATGT TAGCCAGGAT GGTCTCGATC | 60 |
| TCCTGACCTC GTGATCCTCC CGCCTCAGCC TTCCGAAGTG CTGGGATTAC AGGCGTGAAC | 120 |
| CACCACGCCC AGCCATATAT CAGGAACTTG AGCATCCATG GAGTTTGGTG TCCAAGGGAG | 180 |
| GTCTTGGAAC CAATCCGCCA TGGATACTGA GGGATGACTA TAATATGAAC CTTGTATGTA | 240 |
| TGTAATTTAC CATTTTCTAG TTAGCCACAT TAAAAAAGGA AAAAGAAACA GGTGAAAAAT | 300 |
| ATTAAAAAAA TACGTTAACA CAATATATCC AGAACATGAT TTCACATTGA AATCAATATA | 360 |

AAAATTACTG AAATAGTTTA CAGTCTGGTG TGCATTTTAG ACTTAAAGCA TATCCCTTTG 420
GGCATGGTGG CCCATGCCTG TAGTCCTAGC CACTGAAGGC TCGAG 465

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GAATTCGGCC TTCATGGCCT ACAGCGAGAA GGAGTGATG AGTGTGAGTG TGTGTGCATG 60
GAAGTTGGGC ACTGGGCGTC TGANTCCTTC CCCACCCAAG AGAGGAAGGA CCCCTCACCA 120
CCCCCACTGG CGAGACAGTT TACTTTGCCG ACTTGCCATG TTTTGGCCAA AACCAAGATT 180
TTGAAGGAAA TGAGTGGCCA GCGCCAGGGC CCAGGCCATG TGGCCTGCCC AGCCTCAATG 240
TNACTTGGTG GCGGGGTGGG GTGGGGTGG GCAGCAGCAT CCCAGCCTTG AGATGCTTCA 300
CTTTCCTTCT CTGTAACCAG ACTTTGAAAA ATTGTTTCGT TCATCAGGCA TCTCGAG 357

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GAATTCGGCC TTCATGGCCT ATCTGCACTG AATTAGAACA AAATTTAGGA GACTTCTAAT 60
TTGAAGCCAG AGGTGCTGAC TTTTGAGTCT TTGGAGATTG CCTGTTGGAA ATATTCTGT 120
TGAGGGCCAA TGTCCCAATG GGCTCTGAAG ATGAGAAGGA TCCCTGCCCT ATGTGGATGC 180
CACTGGATCT GGAATCATTT CTGTGGCTCA GATTCTGTGA CACATTCTGC CAGGACAGGA 240
GCAGCCGTAT TGGGAAAAGA AGGGGGACAA TAACTAGAAA CGAACTAAGA TGTGGCCCTT 300
GCTTTTGTAC TTTTAATTTA ATGGGAAACA CTCGAG 336

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC TTCATGGNCT ACCTGGACCT TGGGTGGCAG GCCTGGGGCC TTCAGTCCTT 60
AATTCAGGAG GTAGCCAGTC GCTGGAAC TAAGTGAAC TCACTGTGTG TTGCCATAGC 120
TGGAGGGAAG AGGGAAAGGA GCGTGCAGG GGAGCAGAGA CCTCACCCCTT CCTCTGCCGA 180
CATCAGGCTG CCGGTGCTGG ACGGGGCCCT GGCAACCGTG GCAGGAGTGG TGATGTCCGA 240
TGATGGTAAC AAGGGCTTCC TGAGGACCCC GAGCTGTCTT AAGGGCTCTT TACCTGGAGT 300
AAGTATCCCC TTTAATCCTC CCAACAACAC TGTGAAATTG ATTCTGTTGT TATTCCCAT 360

| | |
|---|-----|
| TCACCGATGA GGAACCCACA GCCCAGAGAT GTTAAGTAAC CTGCCCCAAGC CTCCTCTGA | 420 |
| GCATGGCAGA GGGAGGGTCC GAATGCGGAA AGTCTGGCTT CAGTGCCCCC ATCCTCTCGA | 480 |
| G | 481 |

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTCATCATT TGGAAAATAC TTGATGGCAG GAGAACTTGC | 60 |
| TTAAACTAA AGGTGGAGAA AGAGTTAACT TCCAGGACAA CCCATTATAG CTCACCTTCTT | 120 |
| ACCAACAAAG CAGTTTTTAT ACAGCACCTT AGGACTCATT TCTAATGTCA ACCCAGATGG | 180 |
| CCAGTAAAGG CAAGGGAAGA GGCTAAGTGA CTCACAAAAA TCTCTGATAT TGAGGTCTAA | 240 |
| TGTGAAGGCT ATAGATAGGA ATTCCCCACA AACTTCTAAT GAGGACTAAT ATGAACAGCA | 300 |
| AATTGGAGAA GACACCAAGG ACCTAATTTT AGTTTCACTA GCCGTGGGAC CTTAGAAAAA | 360 |
| AGACCATTTG CTCTGGACTT TTGTTTCCCA AGCCATAAAA TGTGGAAGAA TCTTCACAAT | 420 |
| TTCAAGTTGG TCATGTATAT TTCCCTTTTA CAGAGAAAGC TGAAGCCTCG AG | 472 |

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAAAGGATC AAGCTGATCA GAAGCGGGAG CTGCATTGAG | 60 |
| GGAAAAATAT GGCCAGAGAA GGCCTCACTG AGGAGGTGAC GTTGGTGATG CTGGAGCTCA | 120 |
| GATCTGAAGG GGAAGAAGGA AGCAGCCACA TATAGAAGTG AGGGAGGGGG CTTAGGCAAA | 180 |
| AGGAACAGCA AGCGGAGAGG CCCTGAGAAA GGAAAGGCTT GGCTCGCTCA CCTGCAAGGG | 240 |
| CCCCCTGGCT TGACATAGTG AGAAAGGTGT GAAGATGAAT TTGGAGAAAG GCAGGGACAG | 300 |
| ACCACAGGAG ACCTTAGATT TGATTCTGAG GCGCATGGGA TCCCTTGAGA GGATGCTGAG | 360 |
| CAGGGGAGAG ATGTGATCTC CTTTTCATT TAACATGATC GCTGCAGCTG CTGCTGGAGA | 420 |
| ATGGTTGCAG GAGCGAGAGT AGAGACTGGG AAGGTCTGTG CATCCTCTAA GCNACAGGCG | 480 |
| TCTCGAG | 487 |

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```

GAATTCGGCC TTCATGGCCT AGAATAAATT GTGATACAAA AAAAAAAAAA AAAAAAGACT      60
GTACACTATG AATGGGTTGG TCGTTTTCTT CCTGGCTTTT TTTCTTTTTC TTCAGAGTTA      120
GGAAATACTT TTATTTTTTA AAGGAAAATT CATCATAAAT TTGCGCTGGT ACTTTTTGAC      180
ACAGGATTCT TTCAGTGAAG CTTTGCCGGC CGGAAATCTC CATGGCCGGC CTGCGCTCTG      240
CCCGGTCTTC ACTGAAGCCT GCTGGGCTCT CTCCACCTAC TTGGTCCATC AGTCTGTGCT      300
TGGCTCATCC TAGCAACCTG GATCCCGCAG CCGCTATGGC ACCGTGCTTG GCTGGAGGCT      360
GGTCCGAGCG TCCGTGACTA GCTTCCACCT TCGGCGCCAG CTTTGGACA AGGGGAACGC      420
AGTGGCACCC AAAAACTCGG AGACATGAGA CTCGAG                                456

```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

GAATTCTAGA CCTGCCTCGA GATGCCCGAC TACTACAAAC CTCAGTACCT GCTGGACTTT      60
GAAGACCGCC TTCCAGCTC GGTCCACGGC TCAGACAGTC TGTCCCTCAA CTCTTTCAAC      120
TCCGTACACT CCACCAACCT GGAGTGGGAT GACAGTGGCA TTGCCCCATC TAGTGAGGAT      180
GGAGACCTCA CAGACACGGT CAGTGGTCCC CGCTCCACAG CCTCCGACCT GACCAGCAGC      240
AAGGCCTCCA CCAGGAGCCC CACCCAGCGC CAGAACCCCT TCAACGAGGA GCCGGCAGAG      300
ACTGTGTCTT CCTCTGACAC CACCCCGTGT CACACCACCT CTCAGGAGAA GGAGGAGGCC      360
CAGGCCCTGG ACCCGCCGGA TGCCTGCACG GAGCTCGAG                                399

```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```

GAATTCGGCC TTCATGGCCT AGATTGGGT TAGTGTTTTT CTTTAGCAT GTTGAAATG      60
TCACCCAAC TTTTCTGGG TTCCTTTGAA AAGCCAGCTG TCTGTCTGTC TGGTTGTCAT      120
GTCTGAAGGT GATGTGCTT TACCTCTGGC TGCTTTAAGT ATCTTTTGCC TTTTCCCTT      180
TTGTGAATGT TTTTGCTGAA GTGTAACATA TACACAAAAG AGTGTGCAA TCATCAATGC      240
TTGATGGATT CTCGAG                                256

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

| | |
|---|-----|
| GAATTCGGCT TCATGGCCTA GAATCATGCA TTTCTTTTC TTTTTTTTTT TCCCGTTGGC | 60 |
| TTTGTCTATG CTGGTGGCAT CCAGGGCATT GCTTTGTCTC CCTGATTATG CCCAGGATTC | 120 |
| AAGGTCTTCT TATTTGTGGG GAGGCAGGCT GCCCACTGGG ACGGTTTTTA GTGTGTTTNC | 180 |
| CATTCCTGGC TCCCTCGAG | 199 |

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

| | |
|---|-----|
| GAATTCGGCC TTCATGJCCT AGGATTGAA GAAGTTGGGA AAGCATTATG TAGATTAATA | 60 |
| TACTGGTTGG TTCCCTATCT ATGTGGAAGG TCATATTAGC TGCAATTATT TAATTTGCTG | 120 |
| TGTTATTTTG TGTTATATAA CACAAATATA TTTGTATATT AACTTCATTT TTACTGTCAT | 180 |
| TTTTCTGTG GTATACAAA TGAACAAATC TTGTAATTAT TTTCAAATAT AGAAGTATAT | 240 |
| ACATTAGATG GATTCCAAG ATTTTGTAA NAAATCTTAA ATCAGTGTTT TGAGTTATTT | 300 |
| AATTTTAA TTAATCTACA AATTATGCAC NACAACTAG CAACTCGAG | 349 |

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACAAATTTTG CTCACTTTCA TTAATCAGTT GCTCAGATAG | 60 |
| AAGGAAATGA CATCTGGTTC TGTCTTCTC TACATCTTAA TTTTGGAAA ATATTTTCT | 120 |
| CATGGGGTGG ACAGGATGTC AAGTGCTCCC TTGGCTATTT CCCCTGTGGG AACATCACAA | 180 |
| AGTGCTTGCC TCAGCTCCTG CACTGTAACG GTGTGGACGA CTGCGGGAAT CAGGCCGATG | 240 |
| AGGACAACCTG TGGAGACAAC AATGGATGGT CTCTGCAATT TGACAAATAT TTTGCCAGTT | 300 |
| ACTACAAAAT GACTTCCCAA TATCCTTTTG AGGCAGAAAC ACCTGAATGT TTGGTCGGTT | 360 |
| CTGTGCCAGT GCAATGTCTT TGCCAAGGTC TGGAGCTTGA CTGTGATGAA ACCAATTTAC | 420 |
| GAGCTGTTCC ATCGGTTTCT TCAAATGTGA CTGCAATGTC ACTTCAGTGG AACTTAATAA | 480 |
| GAAAGCCCCT CGAG | 494 |

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

| | |
|---|----|
| GAATTCGGCC TTCATGGCCT AGGCACGTGA AATTTTAAAA GTTANAAAAA GAAAGATGCT | 60 |
|---|----|

| | |
|--|-----|
| TTTTGCAGCA GTTCCAGGGT AAACGGCCCC ATGCAACACA AACCCCTCGG AAGGGCATT | 120 |
| CAGCCTTGCA GTGGGCCACG GAGTGCACCA CGCGGCGCTC AGCCCCCAG GGAAGCGATG | 180 |
| CCCCACATCG GGCCAGAAAC AAAAGGGGGT GAGATAAAGC ATGCTCGAG | 229 |

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGGAGTTTG AGATATATTT AGGAAGCAGA GCCTATAAGA | 60 |
| CATGCTGATC ACTTGCATAC ATAACTGAG AGAACTAGAG GTATAGAAGA CTCTAGAAC | 120 |
| TTGGAGAAAT TGGATGAATG GATGTATTGT TATTGATGTA ATGAACCTTA GAGGTGGGTG | 180 |
| GGATCAGAAA GATCTATTG CTTTCAAAGG AAATGGGGAG TGGACAGGTA TGTGGCAGC | 240 |
| ATAAGAACTG GAATAACAGC ACATCTCATT CATGCCCTTA AAGAACGTGA AACTTTGAAT | 300 |
| GTACAGCAAT GGTATTCAAT AGGTATGACT TTGCCCTTAA AGGACATAGA CACCAGGGAT | 360 |
| GTTGCTAAAT ATCCTCCAAT GCACAACACA ACCCCTCGAG | 400 |

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACGAGGACGA GGACGTCAAG GATAACTGGG ATGACGATGA | 60 |
| TGATGAAAAA AAAGAGGAAG CAGAAGTAAA ACCAGAGGTA AAAATTTTCA AAAAGAAAAA | 120 |
| AATAGCAGAG AAGATAAAAG AGAAAGAACG GCAACAGAAG AAAAGGCAAG AAGAAATTAA | 180 |
| AAAGAGGTTA GAAGAACCCG AAGAACCTAA AGTGCTAACA CCAGAAGAAC AATTAGCAGA | 240 |
| TAAACTGCGG CTAAGAAAT TACAGGAAGA GTCAGACCTC GAATTAGCAA AGGAACTTT | 300 |
| TGGTGTTAAT CTCGAG | 316 |

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCGAGGCC TGAGCCTCTG CGTCTAGGAT CAAAATGGTT | 60 |
| TCAATCCCAG AATACTATGA AGGCAAGAAC GTCCTCCTCA CAGGAGCTAC CGGTTTTCTA | 120 |
| GGGAAGGTGC TTCTGGAAAA GTTGCTGAGG TCTTGCTCTA AGGTGAATTC AGTATATGTT | 180 |
| TTGGTGAGGC AGAAAGCTGG ACAGACACCA CAAGAGCGAG TGAAGAAGT CCTTAGTGGC | 240 |

AAGCTTTTGG ACAGATTGAG AGATGAAAAT CCAGATTTTA GAGAGNAAAT TATAGCAATC 300
AACAGCGAAC TCACCCAGAC TCGAG 325

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear --

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAATTCGNCC TTCATGNCCT ANGAGAAGNA CCCAGACCCC CCCAAGAAGG AGGAGGANCN 60
CCNNGAGNC NCTNCTCCAG NCGGANGAGG AGCGCAAGGC CAAGTNGGCC AAGATNGAGG 120
CGGAGCNCGA GGCCNTGNNC CAGGGCATCC GAGACAAGTA CGGCATCAAG AAGAAGGAGG 180
AGCGCGAGGC CGAGACCCAG ACGCCGCCAA GAAGGAGGAG GAGCGGCAGG AGGCGCTGCG 240
CCAGGCGGAG GAGGAGCGCA AGGCCAAGTA CGCCAAGATG GAGGCGGAGC GCGAGGCCGT 300
GCGCCAGGGC ATCCGAGACA AGTACGGCAT CAAGAAGAAG AAGAACGCTC GAG 353

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GARWYKCSS YYTTNANGGC TAGTCAGTGG CAGGGCCACC CAGAAGCCCC GCAGATGACG 60
GAGCTGAGAA CAGGGAATTN ACCTNCACGT GTTGCCATTT CCTCANTGGA AAGTCCTTGG 120
GAGGTGGCTG GGCTCAGCCT GAGCTCAGGG CTTTTCGGTG GGGTTGGGGC AGGGGCAGGG 180
CGGGCNNTTG CAGGTGGCAC AGGCTTCATC AAGGCAGGAC ACGGGNTTCA TCAAGGCAGG 240
AGCCACAGCG CCCGAGCCCT GGCAGGGGAG GTAAGGCCCA GGATGGGGCA GGGCCGTGTG 300
CTCCTGGNAC GGACATCCTT NTCTGCCAGA GACCTGCTCC CCAAGCCCTG TCCCTCCCAA 360
TCCCAGGCA GCCCACTCTG CCCTCCATAG ATGAATCTAA TATTGAATT CTAGACCTGC 420
CTCGAG 426

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC TTCATGGCCT AAGAAAAGAA AGTAAGATTA TCTCCAGCCA AAATGTCAAC 60
CAAGAATTCT ACAGATCTAG TTGAATATGT TGACAAGAGT CATGCTTTTC TCCCATCAT 120
TCCAAACACC CAGAGAGGTC AGCTAGAAGA CAGACTGAAC AACCAGGCAC GTACCATAGC 180
TTTCCTTCTT GAACAAGCCT TCCGCATCAA GGAGGACATC TCTGCTTGCC TGCAGGGGAC 240

CCATGGCTTT CGAAAAGAGG AATCGCTCGC CAGGAAGTTA CTGGAAAGCC ACATCCAGAC 300
 CATCACCAGC ATCGTCAAAA AACTCAGCCA AAATATTGAG ATTTTAGAAG ACCAAATAAG 360
 AGCTCGAG 368

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear --

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GGAATTCGGC CAAAGAGGCC TAAACGACTC TTTGCCCTGT TTCTTCTTGG CTTCCCTTGC 60
 GTAACAAGGA TGAAGGAGGT GGTTTAACTT TATTTTGTG CTTTAACTTT TTAAAGTCTA 120
 AAGTAAGTGC TTGAATCGGG TGGGTTTCA TTTTGTGCT TTCTCACCCC TCAGGTGGC 180
 CCCTAACTTG GCCTCTCACC CTCGTGTCAG CTGTTAGACA CTGACTCAGT GGCTCAGAAT 240
 ATGAAAGGCT CAGGAAGTAG CATGCTGGCC CCACCTCCCT GTCCCCATAC CTTAGCAGAG 300
 CAGCTGCCCA GCAGGGCCTC CTTCTCTTTC CTAAGAGTTT ACTCCATCCA TGGTGGGTGT 360
 CTTGGTAGGC CCGAGATACG AGAGGGAGTG CTGCTGTTAC AAGAATTAC AGTTGTTCTC 420
 TTCGGCACAA GCTCGAG 437

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAATTCGGCC AAAGAGGCCT AGTGCAGAGT TGCAAGCAAG TTTATCAGAG ATACGCCATG 60
 AAGTTCGTCC CCTGCCTCCT GCTGGTGACC TTGTCTGACC TGGGGACTTT GGGTCAGGCC 120
 CCGAGGCAAA AGCAAGGAAG CACTGGGGAG GAATTCATT TCCAGACTGG AGGGAGAGAT 180
 TCCTGCNCTA TGGCTCCAG CAGCTTGGGG CAAGGTGCTG GAGAAGTCTG GCTTCGCGTC 240
 GACTGCCGCA ACACAGACCA GACCTACTGG TGTGAGTACA GGGGGCAGCC CAGCAATGTG 300
 CCAGGCTTTT GCTGCTGACC CCAAACCTTA CTGGAATCAA GCCCTGCAGG AGCTGAGGCG 360
 CNTTCACCAT GCGTGCCAGG GGGCCCCGGT GCTTAGGCCA TCCGTGTGCA GGGAGGCTGG 420
 ACCCCAGGCC CATATGCAGC AGGTGACTTC CAGCCTCAAG GGCAGCCCAG AGCCCAACCA 480
 GCAGCCTGAG GCTGGGACGC CATCTCTGAG GCCCAAGGCC ACAGTGAAAC TCACAGAAGC 540
 AACACAGCTG GGAAGGAATC TCGAG 565

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

GAATTCGGCC AAAGGGCCTA CAGAATAGCG GTACCATGAT AGAATACTGC AATTGTGGTC      60
AGAATTACAG TATGCACAAA GAATTAATTA GCATTATTAA AGAGTCCTCA CTAAACATTT      120
CATATGATCA CACTGAAGAA CTGTAACATT CCATAGAGTG AAGTGGTTCA AATTTCTCTT      180
GGAATTTTTA CTTTGTGGG CCTTATTTTA TGATCCTTTT CATATTTCTT TTGACTTAGA      240
GTATTAATAC ATGGCCAAAA TAATTTAGTT ACTACCTCAT ACAAACAATA TAATGGTTAC      300
TCGAG                                     305

```

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

GAATTCGGCC AAAGAGGCCT AGTTGTTTTT AATGGCACAG GACTCTTCCA CTTTGTGGTC      60
CTCCTCTAGC ACAATACTGG ATGGCTGGGG CAAAAGATTA AAGGAAGTCT TTTCCACATC      120
ATTTTCTGCG TGTCCTCAA ATCTTTTAC TAAATTTGAT ACAAATTCCT CTATTTCTTG      180
ATGATATTGC TTTGAAATAG CATTGTTTAT GAATAGAATC TGTAATATAG GTCCATCTAA      240
CTTAGTATCG TTCACCAATA TTCCACTCGG TCGAGTCAGA ATGTTCAATT TTCGTTTAAAG      300
TTCTTGATTG TCGGCGCGGA GCTGCTCGAT GGTCTCCACG CACTCGAG      348

```

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

```

GAATTCGGCC AAAGAGGCCT ACTCATGACA GGATGACAGT CACATTTGGT AGACACCATC      60
AACCAATGAT CTCTAATTG CGGCCCCCAA CAAGCAATGG GGTCTGTGG GCTACATCTG      120
GAATTGAAA TGTCTCATGG AAATCATGTT CTTACCCTGG AGAAGGTGG CTGCTTAGGT      180
GCTACTTAGG AAACAGTCT GGCAGACCAG ATCTTCCCCA ACTCAGGGGC TATGCGGGGA      240
GAAGTATTAG GAGCCCTGA GCAGGAAGGA TGTACTTAGG AAGGCTACCG GGGATGGGGA      300
AGGGTAAAAG AGCTTAGAAG CCTGGGTGAA GTTTGGGTAG ACCAAAAACA GGAGGGAGGG      360
AGGGAGGATG TTCCCTTGA ATACAACTA GAGAAAAGCT TAGGGGANCA AGTCTTTTAA      420
TTTGGGGACA GTGAAGAGTT TCCTAAAAAT TCCCTGGCCC CCAGGCCTTG GCTAAAAACC      480
CTCGAG                                     486

```

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC AAAGAGGCCT AATTGATTGT GATTAACCAA GATGTATGGA AAACACTTTT 60
 AAGTGTGTAG TGCATGTATC TCATAAGGTC CATTAAGACG TTCATTATTT TTCAATTGAT 120
 GCGTCTTAAG CCCCACTTGA TGTTTGTGT AGTGCATTTC CACAGAAGGA TTCTGCACTG 180
 TGGGATTGAG TTCATTTTGT TAATTGCATA ATACAACCCC ATCGTGTTTC ATAGAAAATA 240
 GTAAATACTC TTGCTTTTAT TCATTGGTAT TCTTTGATAT TACTGAAGAA ATACCAAAGA 300
 AGCAAAGGAG CAAAGAAATA CCAAAGAAGC AAAGGAGCAA GTGAATAGTT CTTCAAACCT 360
 TTACATATTA AGGGCACGAA TGTTTCTTGA AATGTGGACA CATACTCGAG 410

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS: --
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAATT GAATTCTAGA CCTGCCTCGA 60
 G 61

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCGGCC TTCATGGCCT ATCTAGACCC AAATATTTTG AATATGTTAT CTTGTCTCTT 60
 TTCTTTTGT TATATAGAGA GATTGATGCA TAAATCTGT GTTTGTATGA CTGTAATTCC 120
 AAGTTTAGCG AAATTGTCCC TAGGACAACA CACCAACGGC CATGAGCTGT CTCGGTCCCTG 180
 CAAGCTTAGT CTCGATCCT GCCCACTCGA G 211

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC TTCATGCCTA GCCGGACCTG GTGCTCCTTT CCTTGGTGCT GGGCTTCGTG 60
 GAGCATTTTC TGGCTGTCAA CCGCGTCATC CCTACCAACG TTCCCGAGCT CACCTTCCAG 120
 CCCAGCCCCG CCCCCGACCC GCCTGGCGGC CTCACCTACT TTCCCGTGGC CGACCTGTCT 180
 ATCATCGCCG CCCTCTATGC CCGCTTCACC GCCAGATCC GAGGCGCCGT CGACCTGTCC 240
 CTCTATCCTC GAG 253

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

```

GAATTCGGCC TTCATGGCCT AAAGAAATGA AATAATATCT CTGAATTTTA GTCCATGTTT    60
TCAATGATTT CTGACTTTAT TATATTAAGT CTTATTAATG ATCACAATTT ATTTTGTAAG    120
TTTTCAGGCC AAAGGGACAA TTTATTTTGT AAATTTGGGA TTCTATTTCG AAAATAGGGA    180
TCGACTCGAG                                     190

```

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```

GAATTCGGCN TTCATGGCCT ACGGGGAACA GAGGATGGCG GAGGAGGGAA CACACAAGCA    60
GGAGCCCATG CAGCTGGGAG CCACTGAGAT CCCAGCTGGA GGAAGAGTGC CCTGGCACTG    120
AGGTCTAATG GCTGTCCAGC TGCTGCCCCA GGATGTGAGG GCAGGTGGTA GGCCATGAAG    180
GCCGATTGAA TTCTAGACCT GCCTCGAG                                     208

```

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```

GAGCTATAAA ACAGAAATAC ATGCATAGCT GCAGAAACCA TGATAGGTAG AGGACTTTTC    60
TTTTGGTTTT GTTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTACAGAGAA GAGACTCGAG    120

```

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCANGA | 60 |
| GGCAATACTT ATAGTGATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT | 120 |
| GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTCC TTGGAAATAC ACTGGAAGTG | 180 |
| GTACCAACA AATCTAATAA AATGATGTTA AAGAGATTG CAGTAATTT TATCNACTTT | 240 |
| CAGTTTGCAA ACTTTTATAA AGATATGAAA NGGACACTCG AG | 282 |

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

| | |
|---|-----|
| GGCCTTCATG GCCTAGACAC ATACAAAGAT AAGGCTTTGA TAAAATTCAA GAGTTATTG | 60 |
| TATTTTGAGG AAAAGACTT TGTGGATAA GCAGAGAAGA GCCTGAAGCA GACTCCCAT | 120 |
| AGTGAGATAA TATTTTATAA AAATGGTGTC AATCAAGGTG TGGCTTACAA AGACATTTCT | 180 |
| CGAG | 184 |

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTTTGAGTT AAATAGAGAG TTGATTAAAT GCATATATTG | 60 |
| ACAGTTACTG ACTCAGTAAG CTTCATAATT CTAGGAATCA ATCACTGCTG ATTCATATGT | 120 |
| TTAGATATAT TCATTTCTGT CTTTCTGTTT CTTAGGCCAA AAAGAAAAA GAAAACCAAT | 180 |
| ATTTAAGAGA AGAGAAAAAT GAAGACGGGA CATTTTGAAA TAGTCACCAT GCTGCTGGCA | 240 |
| ACCATGATTC TAGTGGACAT TTTCCAGGTG AAGGCTGAAG TGTTAGACAT GGCAGATAAT | 300 |
| GCATTTGATG ATGAATACCT GAAATGTACG GACAGGATGG AAATTAAATA CGTTCCCCCA | 360 |
| ATCCCTCGAG | 370 |

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGACTCTTA GATCTAAAAG GAACTGACT TGCCACCTTG | 60 |
| CCAGAGGAAT TCTTGAAATG TTTCTGCAGC CACTTGGCCT TGAAAATAAA GGGTGCAACT | 120 |
| CTCAATCTT GTTCTAACCC GGCTGGAGGA ACCACAAGAC CCAATGAAAT AGCATTTTCT | 180 |
| CTCCTTTTCC CAGCACTAGT ATATAACCTA TGAGGAACCC TTGTCTCTGA ATCTGCTCAG | 240 |

| | |
|---|-----|
| CTTGAAATTT TGTCTCTGAA GGAAGAGAAT GATCTCAGCC CTAGTCTGAC AGTCCTAGAT | 300 |
| TTCTGTGAAA TAAGAGTATT CTTCAACTTA GTGCTCACAC TCACATACCA TGAGGGTTCT | 360 |
| CTGCAGAGGA CTCGAG | 376 |

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AAGTCACTAT TTGGTAGCTG ACTTTGTGCC CTGATTAGAA | 60 |
| ACGTGGCTCC TTTC...TGGT AGTTGTTCTT AGAACCTATC AACCTGCAGA GATTTTATT | 120 |
| TTCATGGAAG GGAAGTGAAG GTTCTTTTCT TTGCTTCAGA CGGTACATC TTTAGATCCT | 180 |
| GAAGGGAGAG ATGCAGCTTG CTCTCTCCAG AGTCCAAATG CAGCAACAGA TTTTGCTTCC | 240 |
| ANGCAAGCAA GATATGCTAT AAAAACCTGC NACATTCTT CACCAGCTCC TCTCTTTGAA | 300 |
| TTTTCGATGC CTCGATGGTC ATTTTCGAGAT GACAGCTTGT AGTGAGATAG CTGTGGCATT | 360 |
| GGAAGGGGGG AAGCATGCAC CATTTTCCCT AGGGCCTTCC TGCTTTTGCT TGATAAGCAA | 420 |
| TTCCTTGAAT GGCATGTTCT CCACCTCTAG CCACTTTGTT TGTAGTCCCT ACTCTCGAG | 479 |

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

| | |
|---|-----|
| GAATTCGGCT TCATGGCCTA CACAGGCATA ACAGTCAGTC GGGAAAAGGT CACTGAAGTT | 60 |
| GCCCTTAAAG GTGAAGGGAC AGAAGAAGCT GAATGTAAAA AGGATGATGC TCTTGAAGT | 120 |
| CAGAGTCACG CTAAGTCTCC TCCATCCCCC GTGGAGAGAG AGATGGTAGT TCAAGTCGAA | 180 |
| AGGGAGAAAA CAGAAGCAGA GCCAACCCAT GTGAATGAAG AGAAGCTTGA GCACGAAACA | 240 |
| GCTGTTACCG NATCTGAAGA GGTCAGTAAG CAGCTCCTCC AGACAGTGAA TGTGCCCATC | 300 |
| ATAGATGGGG CAAAGGAAGT CAGCAGTTTG GAAGGAAGCC CTCCTCCCTG CCTAGGTCAA | 360 |
| GAGGAGGCAG TATGCACCAA AATTCAAGTT CAGAGCTCTG AGGCATCATT CACTCTAACA | 420 |
| GCGGCTGCAG AGGAGGAAAA GGTCTTAGGA GAACTGCCA ACATTTTAGA AACAGGTCTC | 480 |
| GAG | 483 |

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GGGCCGTGCA GGCAGTGAAT CGGAAAGTGG AGATGATGAA TGAAAAGAAC TTGGAGAAAG 60
 GACTGGGCGT GGACAGTGTG GACAAGGATG CCATGAACGC GGCCATCCAG CAGGCCATCA 120
 AGGCCCAGCC GTCCATGTCT CCCAAGAAGG CGCCCCCAGC GCCTGCAAAG GAGGCCAGGA 180
 ATGTCGTGGC CGTGGGTACT GGTGGCCGTG GGACCCACGA CCGAGACCCG AGTGAGAAAC 240
 CACCCCGGCT CCAGTGGTTT GAACAGCAGG CGAAGAAGTT GGCAAAGCTA CTCGAG 296

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC TTCATGGCCT AGAACTTTTT CATCTTTCCA AACAGAAATT CTATACCCAT 60
 TAAACAGTAA CTCTCCCTTC ACCACTCTCC CCAACCCCGG AGACCTCTAT TCTATTTTCT 120
 GTCTCTATAA ATTTGCCTAT TTAGGTACC TCACATAAGT GAAATCATAT ATTTGCCCTT 180
 TTGCATCTGG CTTATTTCAC TTAGCATGAT GTCTTCAAGG TTCATCCATG TGGTAGTAGC 240
 AGAATTTACT TCCTTTTAA GACTAGCATA CTCACACTGT TTTTGTGTT GTTTGTTTGT 300
 TTGTTTGTGTT TTGGGATGGA GTCTCACTCT GTTGCCCGAG CTGTGGTGCG GTGGTGCCAT 360
 CTCGGCTCAC TCGGCCTCT GCCTCCCGGG TTCAAGTGAT TCTCATACCT CAGCCATCCC 420
 TCGG 424

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GCGATTCGAT GTCCGTGCCC ACCTGGACCA CATCCCGAC TACACCCCCC CCTCTGCTCA 60
 CCACCATCTC CCCAGAACAG GAGTCGGACG AACGGAAGTG TAACTACGAG CGCTACAGAG 120
 GCCTGGTGCA GAACGACTTT GCCGGCATCT CAGAGGAGCA GTGCCTGTAC CAGATCTACA 180
 TTGATGAGTT GTACGGAGGC CTCCAGAGAC CCAGCGAAGA TGAGAAGAAG AAGCTGGCAG 240
 AGAAGAAGGC TTCCATCGGT TATACCTACG AGGACAGCAC GGTGGCCGAG GTAGAGAAGG 300
 CACTCGAG 308

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GGATGCTACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG 60

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TGGTTGCTCC | CATAACAACG | GGCTATACGG | TGAAAATCAG | TAATTATGGA | TGGGATCAGT | 120 |
| CAGATAAGTT | TGTGAAAATC | TACATTACCT | TAAGTGGAGT | TCATCAAGTT | CCCACTGAGA | 180 |
| ATGTGCAGGT | GCATTTTACA | GAGAGGTCAT | TTGATCTTTT | GGTAAAGAAT | CTAAATGGGA | 240 |
| AGAGTTACTC | CATGATTGTG | AACAATCTCT | TGAAACCCAT | CTCTGTGGAA | GGCAGTTCAA | 300 |
| AAAAAGTCAA | GACTGATACA | GTTCTTATAT | TGTGTAGAAA | GAAAGTGGAA | AACACAAGGT | 360 |
| GGGATTACCT | GACCCAGGTT | GAAAAGGAGT | GCAAGAAAAA | AGAGAAGCCC | TCCTATGACA | 420 |
| CTGAAACAGA | TCCTAGTGAG | GGATTGATGA | ATGTTCTAAA | GAAAATTTAT | GAAGATGGAG | 480 |
| ACGATGATAT | GAAGCGAACC | CTCGAG | | | | 506 |

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|-----|
| GGTGGAATGA | AAGATATACC | TAGAACGCCA | TCTAGAGGGA | GAAGCGAATG | TGATTCTTCC | 60 |
| CCAGAACCGA | AAGCTTTGCC | TCAGACTCCT | AGGCCGAGGA | GTCGTTCTCC | ATCATCCCCA | 120 |
| GAGCTCAACA | ACAAGTGTCT | TACCCCCCAG | AGAGAAAGAA | GCGGGTCAGA | ATCATCAGTT | 180 |
| GATCAGAAAA | CTGTGGCTCG | GACTCCCCCTG | GGGCAGAGAA | GTCGTTCCGGG | ATCCTCTCAA | 240 |
| GAACCTGATG | TGAAACCCAG | TGCATCCCCCT | CAGGAAAGAA | GTGAGTCAGA | CTCTTCTCCA | 300 |
| GATTCTAAAG | CCAAGACACG | AACCCCACTT | CGGCAGAGGA | GTCGGTCTGG | ATCATCTCCA | 360 |
| GAGGTTGACA | GCAAATCTCG | ACTATCCCCCT | CGGCGCAGTA | GGTCTGGTTC | CTCCCCCTGAA | 420 |
| GTGAAAGATA | AGCCAAGAGC | AGCACCCAGG | GCACAGAGTG | GTTCTGATTC | CTCTCCTGAA | 480 |
| CCTAAAGCTC | CAGCCCCTCG | GGCCCTTCCC | AGACAACTCG | AG | | 522 |

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TCATGGCCT | AGGCGCACCA | AGAGCAGGGC | TGTGTGTGGG | AGGCTGCAGC | 60 |
| CAGGATTGCC | TCAGCTCCTC | CCCCTCAGGC | TGGGAGGATA | GCACAGGCTA | GGGGCTCGGG | 120 |
| GTGGAGGGTC | TCAGCTCTGC | TGCCCCACCC | CCAGTACTAG | CCTAGCTTCC | CAAGCTGTGG | 180 |
| CTTAGAGGAT | AGTTGGCTTC | CTGCCCTCTCT | CCTCTAAAAT | AGCAAGTCTG | GGAATCCTG | 240 |
| GGGTGAGTGG | AGTCACCCCA | CTCCAGTTG | CTGGCAGAGA | CTGAGACTAA | AGCATCACTT | 300 |
| AATAAACCCC | CCAGCTCGAG | | | | | 320 |

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:608:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTTGTGTAT TCTTTTCTCT GTATCATATG TGATAGTGGG | 60 |
| GTAGTGCCAA ACATTGTTAA CTCTGATGAA TAATGTCTCT TTTGGTTAGA TCATTCTTAC | 120 |
| CTTACTGGTA TCTCTTACTG TTTCTTACC TAGTTATGCT GTTATTGCCT ATGGCTGTGC | 180 |
| CAGCTGCCCG AAGCTAACTT GTGAGAGGGA AGGTTGCCAG ACTGAGTTCT GCTACCACTG | 240 |
| CAAGCAGATA TGGCATCCAA ATCAGACATG CGATCTACTC GAG | 283 |

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACACATGAGT GTGACCTCTG CCATGGGGAA ACACACACAG | 60 |
| AGATATCTAT ACATATATAC ATACATACAA ACATAGGCTA TCTTGCCACA CTAAATGCTA | 120 |
| AGCACTGTCT TAAGAGGTAG AGCTGGTGTG AGTGAAATTA ATGTTACATT TTCCAGCTGT | 180 |
| AAACAGACAT CTGCATTTCC TAGTGAGCTG CCAGGAGCCA GATTGGGGAA CCGTAACTGA | 240 |
| TGTGCCAGGA ATGGTGCATT GATTCCAGT TCCAGGGATC TCTCGAG | 287 |

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

| | |
|---|-----|
| GAATGATAGG TCCTAGGTTT AACAGGGCCC TATTGACCC CCTGCTTGTG GTGCTGCTGG | 60 |
| CTCTTCAACT TCTTGTGGTG GCTGGTCTGG TCGGGCTCA GACCTGCCCT TCTGTGTGCT | 120 |
| CCTGCAGCAA CCAGTTCAGC AAGGTGATT GTGTTCCGAA AAACCTGCGT GAGGTTCCGG | 180 |
| ATGGCATCTC CACCAACACA CGGCTGCTGA ACCTCCATGA GAACCAAATC CAGATCATCA | 240 |
| AAGTGAACAG CTTCAAGCAC TTGAGACACT TGGAAATCCT ACAGTTGAGT AGGAACCATA | 300 |
| TCAGAACCAT TGAAATTGGG GCTTTCAATG GTCTGGCGAA CCTCAACACT CTCGAG | 356 |

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

| | |
|---|----|
| GAATTCGCCT TCATGGCCTA ACCACATGAT CCTTCGTGTT TCTGCCTTC CATTCCCTT | 60 |
|---|----|

GGGTGGATGG TTGGGTAGGT GGGGTTTCCT GGTTCGGGCT TTCTCAGACA AGGGCCCTCT 120
 AGGGAGGGTG CCCTGGACCC CCCACCACTC CTGGGCTGAG GAGCGTGTCA CATGATGCCG 180
 TTGGTGAGGT ACTGGAAGCC GTCATAGAGT TTGGTGGTGA TAGACCGCAT ACTGCCATCC 240
 ACCATCTGCT CCACCAGCAG CTGCAGCTGC TCCTCAGTCA TGCTCATGTG GAACCTCTCT 300
 TTGAGGTTNC GAATGGTGCT GGAGCCATGG AAGCAAGGAA GCTGAGAACC TTGTCCATGT 360
 GTTCCGAGC GGCAATCAGC CCTTGACGCA TCA 393

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs --
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GAATTCGGCC TTCATGGCCT AGGCGGGTTA AAGTCACATT TTTAAAAAGG CTAAACTCTA 60
 AATTGCTGTA TTGCTCTCT CTGGAGATTA ACAAAGTGCT TGGTTGCAG ATTTGCTGGT 120
 ACGGTGATCT CAATGATATG ACCGAGGGTG GGAGGGATGT GAGGAGGGAA ATCGGCAAAA 180
 CCCTGGCCAG CCAGCCAGCC AAGGTGACAC ACAGCCAGAG GGGGCTCCCC TCTCCTCTG 240
 CCGTCCGGCC ACGGCTCACC ACGCTGTCCA CTGGGAACGC GGCCCCGCGG CCCGCAGAGT 300
 CAGGCGTGAG CTTGCCCTT TTCTGAAAGG GCCTCCGCCT GGGCAGGCGC CGGGGGGCAG 360
 TCCTCGGGTC CCATGGCTTA GGAGCACAGC ACTGACGGCT GCAGTGGCTC GAAAGGCTGA 420
 AATTCCACAT TGCTCTCTAG CGATCCCGCA CTGCTGCGAC GCCCTCGCTT CCCGGCTTCC 480
 GAGAGGTCCC GCAGGGAGCT GCTGAGGGCG CTGCGCTTGA GGCCCTCACC GCTGGCATAG 540
 CTGTCGTCCA GGCAGGCCCG GCTCAGTGT TCCGTGCCC GACTCCTTTT TGAGGCTAGA 600
 GCACTGGGAC ATGCTGGGCC GCACGACGCC TTTCTGCTTC TCSAG 645

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GCGATTGAAT TCTAGACCTG CCTCGCACCA CCCCAAATCC CACATCCTGC ACCCCTGCCT 60
 CAGGCTTCTT GCCCTCAACC CCAATATTCT GAGCCTTCTC TTTTTTTTGG TTGTTTTTTT 120
 GAGACAGAGT CTTGCTCTGT CTGTCGCACA GGCTGGAGAG CAGTGGCGCG ATCTCAACTC 180
 ACTGCAACCT TCACCTCCCA GGTTCAGCA ATTCTCCTGT CTCAAGTGCC TAGATACCTT 240
 GGTAATGATT CCATTGGCCC CACCATGCCC TGTCCTGCCT TCCTGGCTGT GCCCAAGCTT 300
 GGTCCCTGCC TGCCTGCCTC ACTCTCTGGG TCTCGAG 337

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

GAATTCGGCC TTCATGGCCT AGGTTTTAGA ATTTTATATG AAGTATCTTA TTTGATTTTC      60
ATAATAACCA TAGAAGATAG ATACTATTAT TATCCTTGGA TTATAGATGA AATTGAAGAT      120
TGCTTCGCAG GTAGAGTTAA GATCCAGAAT GGTGACAAGA AGTATAATGT CTGCTTTTAT      180
GCCATAATAT ATCAGACTAT TCTGACTCAT TTAGATTACT TCAGGGCTAT CACTGAAGCT      240
TACAGTATTA TCACTACTGT GATACCCCTG CTCACACAAT TTGGTAAGTG TTTTGTATC      300
TTTTAGAACT TATACATTAG GCAGCAGCTA TCTGTTTGGT CAGCTGAAAG ACGGCCACAG      360
GATTTGCTTC TGGGTGGCCA TTAGCACCTT TCACCCATGC ACCAGAGAGA TACTTCCAGC      420
ACGAACTCGA G                                     --                          431

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

GAATTCGGCC TTCATGGCCT ACCAAAATTG TGCATACCCT TGGGATGAAA ATCATTGTAA      60
AGAAAAGAAA AAAGCAGGAN TATTTGAACA AATCACTAAA ACTCATGGAA CAATTTTGG      120
CATTACTTCA GGGATTGTCT TGGTCCTTCT CATTATTTCT ATTTTAGTAC AAGTGAAACA      180
GCCTCGAAAA AAGGTCATGG CTGCAAAAC CGCTTTTAAT AAAACCGGGT TCCAAGAAGT      240
GTTTGATCCT CCTCATTATG AACTGTTTTT ACTAAGGGAC AAAGAGATT CTGCAGACCT      300
GGCAGACTTG TCGGAAGAAT TGGACAATA CCAGAAGATG CGGCGCTCCT CCACCGCCTC      360
CCGCTGCATC CACGACCACC ACTGTGGGTC GCAGGCCTCC AGCGTCAAAC AAAGCAGGAC      420
CAACCTCAGT TCCATGGAAC TTCCTTTCCG AAATGACTTT GCACAACCAC AGCCAATGCT      480
CGAG                                     /                          484

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

GAATTCGGCC TTCATGGCCT AGCGTTCCTG GTTCCGTCCT TGTACATAAT ATTGTACAGC      60
ATTCAACCAC TTTTGTGAT CAGCAAAGTA GTCTCCAATG GCATTGTTGG CTTGTTCCAG      120
GAGACTGTCA TCTGCATCAC CAGATCCAGT TTTCAGGAGC TGGAGTACTC TAAACCAATC      180
CCCCAATTTC AGCCGGAGGC CAATAGCAAG ATCCCTTCTG TCCATCTCGA G                          231

```

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ANAATGCTTC | ATGAACTNGC | NGACAGGACT | GACACAGCTN | 60 |
| AGCTTTCTCTG | ACTGATTCCG | GGCCATGCAG | TCTACCAAAG | GGCTAGCTGT | TGAGACAATG | 120 |
| AGGATCAGGG | ACATTGCCCC | TCGTTCTGAA | TGTCCCCAGC | CACAGTACNT | ACATNGTTCT | 180 |
| TACATGTACC | TTCCCCCTCG | GTGACATTTT | ATATTTTCCA | AGNTGGCCAC | ANCNGTTCCC | 240 |
| TTCCCTTTCT | NNTNGNGNNG | NACACTCACA | CCCGTCTCTG | NGAGGTGAGG | CCACATATTC | 300 |
| TCTTTTCTGG | AATTTGGGTG | GGCCTGTGAC | AATGGCAGGA | CAATGCTGAG | TGGCTATGTC | 360 |
| ATAAAGGCAA | TACCCCTTCC | ATCCAATTCT | CTTGGGATGC | TCATGTTTGT | AATCCAGCCA | 420 |
| CCATGTTGTG | AGGAAGCCCA | CGTCACCTAT | GAAGACCTAC | ACAGAAAAGA | CTCAAGGCCC | 480 |
| CAGGCACTTG | AGCTGAAGGA | TGAAAAGAG | TTAGTCAGCA | GGGGAATG | GGGAAAGGTT | 540 |
| ATCTGGTAGA | AAGAAGGAAC | AGCTTGTGCA | GAGGTNCAGA | GGCAAGAGAG | AATTGGCAT | 600 |
| ATTGGGAAG | CTGCAAAAGA | TCTCGAG | | | | 627 |

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

| | | | | | | |
|------------|------------|------------|------------|------------|-----------|-----|
| GAATTCGGCC | TTCATGGCCT | ACGACTTCAA | AAATATGGGA | ACACAGTTAG | TTATTTTAC | 60 |
| ACAGTTCTTT | TTGTTTTGT | GTGTGTGTGC | TGTCGCTTGT | CGACAACAGC | TTTTTGT | 120 |
| CCTCAATGAG | | | | | | 130 |

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTGGGGGAG | GGGAAGGATG | TGGTTGNAG | AGNGGAAGCA | 60 |
| GAGTTTGAA | ACGCATGAGA | GCAGAGCTTC | GTGTGTTCCC | ACCCTCANTG | AGGANGTGTG | 120 |
| AGTGGGTGAG | CATGTGAGAG | TTGGGTGTTC | CTACCCTCAG | TGAGGAGGTG | TGAGTGGGGG | 180 |
| TGCATATAGA | GGCAGTGCCT | GCTGTGGGGT | CACAACTGGT | GCATGCCAGC | GCCAAAGGGA | 240 |
| CCTGTCTTTA | GGGGTCATTT | CAGCCAGCTC | CTCCCATCAC | AGATGACAGC | TCCAAGCCTA | 300 |
| GAAGGGGCTC | AGTGACAGGG | CCAGGACAAG | CCCTCAGGAC | TGTGGCCTCC | TGGCCCTTGG | 360 |
| TTCCCCTGCC | CCACAACATG | GTCTCCACAT | GGCTGGCTGG | CTGGCTGTCC | CTGTGTGTGT | 420 |
| GTGACACACC | GTGTGAGTGC | AGGGCTGTGC | CCGGGGTGGG | AGGGTGTCTA | TGTGGCACTG | 480 |
| ACTATCGAGC | TCGAG | | | | | 495 |

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCTGATGAT TCCAAACATT TNGTAAATTA ATTTTCTCT | 60 |
| CTTTACCTTT CAGCTTGGAA GGAAGACAGA AGCCTTAACC TCCAGGGTAA CATGTTGCAA | 120 |
| TTTGTTCACT TATTAATCTA ACAAGAATGC ACTGAGGTGC TCATTAAATG TCAGACCTTG | 180 |
| TGTGAGGTG AGGAAATCCA AAAGCAAAGG AGGCATGAAC CTCCATGCCC ATTCAGAAGG | 240 |
| GCACCAGGCC TTTTAAGAAG GGTGGATATG CACAAATTGA AAATAACTGA TAGTCCTGAC | 300 |
| TTATCTTTGC AATTAATAAG GCAATTCAT ACAATTCTTA TACTCGAG | 348 |

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCAGGATGG CACCGGACCC CTGGTTCTCC ACATACGATT | 60 |
| CTACTTGTC AATTGCCCAA GAAATTGCTG AGAAAATTCA ACAACGAAAT CAATATGAAC | 120 |
| GAAAGGTGA AAAGGCACCA AAGCTTACCG TGACAATCAG AGCTTTGTTG CAGAACCTGA | 180 |
| AGGAAAAGAT CGCCCTTTTG AAGGACTTAT TGCTAAGAGC TGTGTCAACA CATCAGATAA | 240 |
| CACAGCTTGA AGGGGACCGA AGACAGAACC TCTTGGATGA TCTGTAACT CGAG | 294 |

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTCAAGGG ACAATGAAAA TGTGACCCTT ACCAACGACA | 60 |
| GAAACTCCCA GGAAGCCACA ATTAATCAAA GACCACCAGG ATATTTGGGG AAGTTTATCC | 120 |
| TTCTGGAAAC CAGAATTTCT GATTGTGGA AAATTCTATA GATATTCTCT GCCAGACTCC | 180 |
| AGCCTATTTG TGTGAGACAT CTGGGGAGGC TCCCCTTTT TTCACCATTG GAGGACTGAA | 240 |
| AGTAAATTTA GCTTCCTCAG CAGAAAGAAA AGAAGCTGTT TTGGAGGTTA GGAAGAAGCT | 300 |
| CGAG | 304 |

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

| | |
|--|-----|
| GAATTCGGCC NTCATGGCCN ACTCTATTGG TGCAAAGTAA GATTTACATC TGTGTTTCAGA | 60 |
| ATCTTTGAGA TAATACCCCT TTTCTACATT TCTGCATTTT TTTTCTGTGA NCCCCACTAG | 120 |
| TATTNCNCCA TTTTNACCTT TTCATTTAAC TTATCCTCAC ATTATAAGAG ATGGATGACC | 180 |
| TATACAGACT TGGCCTTTGG GCTTTGGCTT CATTCAATAT CATCTTGGGT ACCACTGAAT | 240 |
| ACCGTTCAAT CTAGAGCTGG GTGGTAGGTT GAGATGTATA TTTCTAGCC CAGATCCCAG | 300 |
| AATCTAGAAG AAGTTAAATC TGATATGACT TTGATAAATA AGACAGTATG TTCTTCTAAC | 360 |
| CCCATCTCCC GTTCTCTGAC ACTGAACATA TATATGAAGT ATATATAACA TATACCGAGT | 420 |
| ATTTAAAATT TTAGAATAAA AATGTGCATT ACTGCACATC TTCCTGTCTT TCATTCTCTG | 480 |
| GTTGAGTTTC CCTCGAG | 497 |

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAGCAAGCA GAGGTGGCCT GCGTGTGTAT GTGCTCATGT | 60 |
| GTATGTGTGC ACATGCATGT CTGTGTGTGG ATGCCCATGC GTGTAACATC TGATGTGGCA | 120 |
| CATGATACAA CATAATTTAT TTATTATAGA AACCTGCAAG TAAAGATTCA AGAGGAATCG | 180 |
| CAGATCCCAA TCAAAGTGCC AAGTGGTAGG TTACCCTGAC AGATAGTACC TCCCTTTTTT | 240 |
| ATTTTTCAAA TGCTGGCATA GTTTTGTGTT CTTTACCAAC TCATTGATTT ACTGGGGACA | 300 |
| TCCTCTGTAC TTATCACAAC AGGTTCTCGA G | 331 |

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

| | |
|---|-----|
| GAAGTGCAT TACACCTTCT CTTCTGAAGT AAACACTAAA AATATCAGGT AACTTCTGCA | 60 |
| TTAAATTTTC TGCCATCTGA AGTGCTCCCA CTTACTATCT TCAGGTCTTG GCTTGACAGC | 120 |
| ATGGAAGCAA TGTGACTTGA AACAGCATGA TTTTTCAGAA CATCCTTCAG AAGTTCAGCA | 180 |
| TCCGCAAAAT AAATTATCCT AAGAATTGCT CTAAGGCACT TATGTCTGAC CGCAGGTCCT | 240 |
| GCTGAGGAAC TATACACTTC ATAAAGAACA CCAAATAATG TCTTAATAAA AGACTTAGCC | 300 |
| AGTTCCGGAT CCTCTTTCAT AAGCTGTGCT CGAG | 334 |

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTCGGATTCC CAGTGGAAC TTTAGTAGTA CTCAGATCCT | 60 |
| CCTTTGTTTG GTGCGTAGTA TATTAACAAG TAAACCTGCC TGTATGCTCA CCAGAAAGGA | 120 |
| AACAGAGCAT GTCAGTGCTT TGATCCTGAG AGCCTTTTGG CTTACAATTC CAGAAAATGC | 180 |
| TGAAGGCCAC ATCATTTTAG GAAAGAGTTT AATTGTACCT TTAAAAGGTC AAAGAGTTAT | 240 |
| AGATTCCACT GTATTACCTG GGATACTCAT TGAAATGTCA GAAGTTCAAT TAATGAGGCT | 300 |
| ATTACCTATC AAAAAATCAA CTGCCCTCAA GGTGGCACTC TTTGTACAA CTTTATCCGG | 360 |
| AGACTCTCGA G | 371 |

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

| | |
|---|-----|
| GAATTCGCCT TCATGGCCTA GATGTTTCAA TTTCGAAGTA CTTTGAAGT TTAGTAATGT | 60 |
| CAGAGTTGAA CATTTTCTGT AGCATGACTA TCGACTTGTC TTTTCAAGGC AGCCTGCAAA | 120 |
| GCCATTGAAC AAGCAAAGAC TCAAAACATC AATAAACTGG TTCTGTATAC AGACAGTATG | 180 |
| TTTACGATAA ATGGTAAGCT TTCACATTG ATTTCTTCTG TTTTCCAGT AACTGTGAAG | 240 |
| GGAAATTGGT AGGAGGTGTT GTAACAGGGC AGGACCCAAA TGGGAACGGG GGGATGACAT | 300 |
| TGTTTTGTCA GGTACCGAGC AAAGAGTGAG GATTTTGGAG TCTCCCTTCT GCTGCTCTGA | 360 |
| TGTTTTCCAC ATGCTTATTT CTTTGCCAGG CACTGGAGAT GCAGTCAGAA GTGGAAGTGG | 420 |
| CTCTTACTTC TAGTCTGTGT GTGTATAAGT CACTTAAGAT GGCGTGTTGA CTGCTTCTTT | 480 |
| GGGAAATGCC CTGAATAGGA GCATGTAGGG GATGTGCTCG AG | 522 |

(2) INFORMATION FOR SEQ ID NO:628:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAAATATC TGTGGGAAGG TGAGCTACTT AGCATTCAAC | 60 |
| AATGCAAAGT TTCAAAGCAT TTTGCAAATT TTAAATATAC GCTATAATTC TTCTGTAATT | 120 |
| GGTGTCTTTG GTACTTTTGG GTTAAATTGG AGTTATTCCA AAATAATTAT ATTTTATAGC | 180 |
| ACTTTTGACA CCATAACACT TAGCATCTCG AG | 212 |

(2) INFORMATION FOR SEQ ID NO:629:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

| | | | | | | |
|------------|------------|------------|------------|------------|--------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTCCTTCCG | CGCGAGTCTC | TGGAGAAGCC | GCAGCGCGAG | 60 |
| TTGCCGCCG | TGCTGCCCGG | GGCCGGCTTG | CCTTGCGCCA | TGGACTGGCA | GCCAGACGAG | 120 |
| CAGGGCCTGC | AGCAGGTCCT | GCAGCTGCTC | AAAGACTCAC | AGTCGCCCAA | CACAGCCACT | 180 |
| CAGCGCATCG | TGCAGGATTA | ACTCAAACAA | CTCAATCAGT | TTCCTGACTT | CAACAACACTAC | 240 |
| CTGATTTTCG | TCCTGACCAG | ACTCAAGTCA | GAAGATGAGC | CAACGCGCTC | TCTCAGTGGC | 300 |
| CTCATCCTCA | AGAACAACGT | GAAGGCACAC | TATCAGAGCT | TCCCACCCCC | CGCTCGAG | 358 |

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs --
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| AAGAGAACAA | TAAATAGGC | AGTCTCCTAC | CTCTTGTCTT | ACTCTAATAT | AAACTCCATG | 60 |
| AAGATAAGTA | TTGTATCCAT | ACTGTTTCATG | CTGCACAGCA | GTGCGCCTTA | TCTGCAGGGC | 120 |
| GACGCATCCC | AAGACCCCCA | GTGGATGCTT | GAAACTGCAG | AACTCGAG | | 168 |

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACATAACTGC | ATTCTGACCT | CCTTCTTGCA | GTGCCAAGAG | 60 |
| AAATGATGGT | GAACATAAGT | CGGGGTGTGG | GGTCGTTCTC | AAAATGCGGT | CATTGCTACA | 120 |
| GAAC TAGGGT | TTTTGGTTAG | TTACATNCTT | TGTGGAAGGA | CAGGGTGGTG | GGTACAGGTC | 180 |
| CCTGAGAAGC | AGACATGTGG | AATTGTTTGA | GACAATCCTA | CTCCCTGTGG | TACTCTCTCT | 240 |
| ATGTATATAT | TCCAATGAAG | GTAATTTACC | TCATGCTTTC | CTAAATACAT | AAATCTTTAC | 300 |
| ATTTCAAATG | CCTTGTTAGA | CTGTACTCAA | GATTCCAGAG | ACATTTTAAA | ATAATTCATT | 360 |
| TTCAAATCAT | AAATTTGGGA | AANGGGGCCC | TGGGATAAGC | AAGTTGACTG | GGCCACTGCT | 420 |
| TATGCCATTC | CCTGCACAA | TCTGGGCATG | GAGCAGCTCT | CCCAGAGCCC | ACTCGAG | 477 |

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTGCCTCCT | GATGAAGTCC | CTACTGTTCA | CCCTTGNAGT | 60 |
| TTTTATGCTC | CTGGCCCAAT | TGGTCTCAGG | TAATTGGTAT | GTGAAAAAGT | GTCTAAACGA | 120 |
| CGTTGGAATT | TGCAAGAAGA | AGTGCAAACC | TGAAGAGATG | CATACAAAGA | CTACAAGAT | 180 |

TTCAACAGTA ACAGCAACAA CAGTCAACAA CAACTTTGAT GATGACTACT GCTTCGATGT 240
 CTTCCGATGGC TCCTACCCGT TTCTCCCACT GGTGGAACAT TCCCAGCCTC NCTCTCCTGC 300
 TCTAGGATCC CCGACCCATT AAGACTCGAG 330

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GAATTCGGCC TTCATGGCCT AGGAGAAGGC CCTGCAGGCC GCATATGGCG CCAGCGCCCC 60
 CAGTGTGACC TCGGCTGCCC TCCGGTGGAT GTACCACCAC TCACAGCTGC AGGTAACCAG 120
 CGACCCTGGG TGCTCAGCTT CTTCCCTTCC AGGGGGACCA GCGTCACCTT TAGGTGAAGC 180
 CCAAAGCATT TGATTTCTGA ATTCTCTGA AATTTTCTT TCTTCCAATT CTCATAAGCA 240
 CTCTTCCCAC TGGTCTTTGA TGGTATCTGA GTGGAGGCTT TGTAGTGAGG GATTTTCATT 300
 ACAGGGATTT TCTTATTCCT TAGGCTTTCT GAAGTATGAT TATCCAGTG TTATTGATGA 360
 GGAAACCGAG GTTCACCCAG CTATTCTCGA G 391

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GAATTCGGCC TTCATGGCCT AAGTACAAAT ACCTATTATG TTGGTTGGGA ATAAGAAAGA 60
 CCTGCATATG GAAAGGGTGA TCAGTTATGA AGAAGGGAAA GCTTTGGCAG AATCTTGAA 120
 TGCAGCTTTT TNGGAATCTT CTGCTAAAGA AAATCAGACT GCTGTGGATG TTTTTCGAAG 180
 GATAATTTTG GAGGCAGAAA AAATGGACGG GGCAGCTTCA CAAGGCAAGT-CTTCATGCTC 240
 GGTGATGTGA TTCTGCTGCA AAGCCTGAGG AACTGGGAA TATATTWAC CTGAAGAAGC 300
 AAATGCCCCG TTCTCCTTGA AGATAAACTA TGCTTCTTTT TTCTTCTGTT AACCTGAAAG 360
 ATATCATTTG GGTGAGAGCT CCCCTCCCTT CAGATTATGT TAACTCTGAG TCTGTCCAAA 420
 TGAGTTCACT TCCATTTTCA AATTTTAAGC AATCATATTT TCAATTATA TATTGTATT 480
 CTTAATATTA TGACCAAGAC TCGAG 505

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GAATTCGGCC TTCATGCCTA CAAATATGTC CTCTGTCAAG ACCCCTGAAA CAGTTGTCCC 60

```

CACAGCCCCT GAGCTCCAGA TTTCCACCTC CACAGACCAA CCTGTCACCC CTAAGCCCAC      120
ATCTCGGACC ACTAGGAGCA GGACAAATAT GTCCTCTGTG AAGAACCCTG AATCAACTGT      180
CCCTATAGCC CCTGAGCTCC CACCTTCCAC CTCCACAGAG CAGCCTGTCA CCCCTGAGCC      240
CACATCTCGG GCTACTAGGG GAAGAAAAAA TAGATCCTCT GGCAAGACCC CTGAAACACT      300
TGTCCCCACA GCCCCTAAGC TCGAG                                           325

```

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

```

GAATTGGCCT TCATGGCCTA GCTTCCTCTT CAAAAATGTG TCTACCTAAG ATACTATTAT      60
TTAAGCCTCT GTGTACTTTT AACCGTAGAA CTGATTTTAT AGGAAGACGA AACTTGTCGG      120
CTTTCAAGAC ATGGAGTGTG TGCCTTGTGG AGACCTCCTT CCTCCTTACG AACCGCACTC      180
TCATCCACAA AGAACCTCGA G                                           201

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

```

GAATTCGGCC TTCATGGCCT AGGCAAAGCC TGAAAGTCCT TGGACTTCTC TGACCAGAAA      60
GGGAATTGTT CGAGTTGTAT TTTTCCCCTT TTTCTTCCGG TGGTGGTTAC AAGTAACATC      120
AAAGGTCATC TTTTCTGGC TCTTGTCTT TTATCTTCTT CAAGTTGCTG CAATAGTATT      180
ATTCTGCTCC ACTTCTAGCC CACACAGCAT ACCTCTGACA GAGGTGATTG GGCCGATATG      240
GCTGATGCTG CTCCTGGGAA CTGTGCATTG CCAGATTGTT TCCACAAGAA CACCCAAACC      300
TCCTCTAAGT-ACAGGGGGTA AAAGAAGAAG GAAATTAAGA AAAGCAGCCC ATTTGGAAGT      360
ACATAGGGAA GGAGATGGTT CTAGTACCAC AGATAACACA CAAGAGGAAT GCTCGAG      417

```

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

```

GAATTCGGCC TTCATGGCCT ACCCTCCTCC AATGAGTCCC GCCAATGCCC CAATGCCCCGT      60
TGCCAGTTCTG CTTTCTACGG TGGTGAGTCG GGCTACCACC GGGCCCTGCT GGGCCTGCAG      120
ATCTTCAATG CCTTCATGTT CTTCTGGTTG GCCAACTTCG TGCTGGCGCT GGGCCAGGTC      180
ACGCTGGCCG GGGCCTTTGC CTCCTACTAC TGGGCCCTGC GCAAGCCGGA CGACCTGCCG      240

```

GCCTTCCCGC TCTTCTCTGC CTTTGGCCGG GCGCTCAGGT ACCACACAGG CTCCTTGGCC 300
 TTTGGCGCGC TCATCCTGGC CATTGTGCAG ATCATCCGTG TGATACTCGA G 351

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAATTCGGCC TTCATGGCCT AATTTTTTTG AGACAGAGTC TTA CTCTGTT GCCCAGGCTG 60
 GAGTGTGGTG GTGCGATCTC GGCTCACTGC AACCTCTGCC GCCTGGGTTT AAGCTATTCC 120
 CTGCCTCGGC CTCCCAAAT ACTGGGATTA CAGGCGTGTG CCGCTGTGCC CAGCCGCTGT 180
 CTAGTCTTTT AAAACTTGGT GTTTGAGCAT GCACATTCTC CTTCTGGAAT ACCTGATCAC 240
 CCAGCACAAC TCACGTTNTC TTTCTGCTGG CTACCCTTGC CTGCTGTGA CTGTGTCATG 300
 GTTCTCAGCT AGACTCGGTG GCGTGTGTTGA TGGCCAGGC ATCGTCTGCC CAGTGGGTGT 360
 CCTGTTACCC ATGTATGACA GACTGTACCC AAGATATCAG TCTTACGAAT AAGGCCACGA 420
 TGAACACTTT GAGCTTTTTC TGTATCTAGC ATATCCCCAG GGTAGATGCT CAGGCAGGAA 480
 ACTGGTGGGA GATGAGGGAT ACACAGATGG CTCCCNACAG GTGCTGTGAG GTGCTCAGGA 540
 GTTTATCATC ACTTAACTGA GCTCGAG 567

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GAATTCGGCC TTCATGGCCT AGCTCCGCAN AGGTAGGGAG GGAAGGGCCC CTCAAATANA 60
 TGGAGGGAGC AACATCCCTC CAAGGGAAAG GGCTTCCAAN ACNAAATCCT GGACAGAAGC 120
 GGAGCANGGG ATGGGCCTCC TTACAGAGCA GGAGGAAGAC AGCGCTCTTC NAANANGAAA 180
 GGAGAGGGGC ATCAAGGTCC CTCACAATGG TGGAGGGGGC GGGGCTTCTC ACCGAAGGCA 240
 GAGGAGGGGG CCTTAACTGA GGGGCAGGGC GCCTCCAGG GATGAAAGGA GGAGGCCTGC 300
 CGCAGAGCAG GGA AAAAGTT CAGTCCTTTC CTGCATTCTT TGGCTGAAGG GGTCTTAAGA 360
 TGAAGGGTTC AGTGTCCAGA AGGAAAAAAC CCTGAGATGG GCCTAGACCA ACATGAACTC 420
 AGCTAGCAAG TTCATACATG ACATGGGACT GATAGACTTG TGTGGCATCT CGAG 474

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

| | |
|---|-----|
| GAATTCGGCC TTCATCCTTG AGAATATCAG AATTAGAAAG CCAGGTTGTT GAAATGCATA | 60 |
| CTAGTTTGAT TTTAGAAAAA GAACNAGTAG AAATTGCAGA AAAAAATGTT TTAGAAAAAG | 120 |
| AAAAGAAGCT GCTAGAACTA CAGAAGCTAT TGGAGGGCNA TGAGAAAAAA CAGAGAGAGA | 180 |
| AAGAAAAGAA AAGAAGCCCT CAAGATGTTG AAGTTCTCNA GACAACACT GAGCTATTTT | 240 |
| ATAGCAATGA AGAAAGTGA TTTTAAATG AACTCGAG | 278 |

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

| | |
|---|-----|
| AGGGAGAGGA GGCTGGGAAC AACGTGACCC ACTAAGGATT CTGCTCCAAG GACAGTGGGT | 60 |
| TTCCCGCTGG GCACCCACTC TTAAGTCAG ATCGGGAGAC TAAGACAGGA ACACCCGCCG | 120 |
| TGGGCAGGCC AGGCTGGAAG GATAGAGGAC TGTGGTCGAA CCAAGAGGAG GTTCAACTGT | 180 |
| GACTTATGCC AGTGTGGTCA CGAAGGCAGA TGGGTTGAAC TGAAAAGGGG GCACCGGTTT | 240 |
| CTGGCATGGA GGCACCCAAG GTCTTAGGAG GTGGATGGAC TGTCACTG GCAAAGAAAT | 300 |
| GTCCAGGGC AGGACTGCAA AGGCCACAGA AGAATAATT GGGAGAGAGA CAACCCATGA | 360 |
| GAAGTCACTC AGACCAGGT CAGAAACAGA ACAGGAACAA CAATGGACTC GAG | 413 |

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

| | |
|---|-----|
| TTTCNTCCCT TNGAATGTTT GTCCCTTTTT CCTGTTTTTT TTTCGCACAA AATTNCAAGT | 60 |
| TNTACCAAGC AAACATTAAA TCCAAGTTGG AATTTTAATT AAGGAATTCG GCCTTCATGG | 120 |
| CCTACTGGTG CCTTCCCGGA AGGGCTCAGA GCGGGGCTCG GGCAAGCACT TTAACCTTTT | 180 |
| AAGCCCAACC AGATGAGTTG CTGTCAGTTT TGGAGGCCTT CAGAGCATT CACTAGACCT | 240 |
| CTGTCTGTGT CGGTCCAATG TCTTTAGCCA AGCTTTGATT AAAGATGACT TCCTTGTTG | 300 |
| CTCAAGAAAT TCGCCTTCT AAAAGACATG AAGAAATAGT ATCACAAGA TTAATGTTAC | 360 |
| TTCAACAAAT GGAGAATAAA TTGGGTGATC AACACACAGA AAAGGCATCT CAACTCCAAA | 420 |
| CTGTTGAGAC TGCTTTTAAA AGGAACCTTA GTCTTTTAAA GGATATAGAA GCAGCAGAAA | 480 |
| AGTCACTACA GACCAGGATT CACCCACTTC CACGGCCTGA GGTGGTTTCT CTTGAGACTC | 540 |
| GTTACTGGGC ATCAGTAGAA GAATATATTC CCAAATGGGA ACAGTTTCTT TTAGGAAGAG | 600 |
| CACCATATCC TTTTGCTGTT GAAAATCAAA ATGAAGCAGA AAATACCATT CCTTCGAG | 658 |

(2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

| | |
|--|-----|
| GAATTCGGCC TCATGGCCTA CCAAAGAGTG TTATACATGC TCAGCAAACA ATATCTACAG | 60 |
| GAACTAGCCC TCAGGAAAGT AAAAAAAAAA AAAAAAAAAAG GCAGCAGAGG GCCAGCCCAT | 120 |
| TCTTCTCATA GCTCACTGAT ACACTTGGTC ACATTCTGCC ACTACCTGCA AGGGAGGCTG | 180 |
| CGGAAAGGTA TCCCTACAGA GGCAGACGTG CCCAGCAAAA ACTTTGGCCG GTGGGGGGAC | 240 |
| ACTCCATGAC AAAAAATACA AAGGAGAGAA TGGGAGCTCG AG | 282 |

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCTTTCTCT GACCTGTGCC CTCGGCCTCT TGGCCTCCAT | 60 |
| CGCCATGACC TTGCCCACCC AGGGCAAGGC ACTGCTGGCT GCCTGCACTT TTGGGAGCTC | 120 |
| TGAACTACTG GCCCTCGCAC CTGACTGTCC CTTGACCCC ACACCACTCG AG | 172 |

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCAGAAACC GGCCAGGCAA GGAAAGAGGC CGGTCACCAG | 60 |
| AAGCCAGCAG GCGTGGGGTG TGATACTCTC TATAGCCACT ACAGGGCGCG CGCAGGTCCG | 120 |
| GGATCTCCCC AGTTGCTAAT CCCGGCTCTG CCACTCAATC CTATCCCTAG TTCCCGAGCG | 180 |
| CGGGTCCCCC GCCTTGCACT CTCCAGCCGT GCGGGGCCGG GAGCAGGCCT CCGGCCTCCC | 240 |
| AGACTTCTAG AGCCCGCCGG GCCCATCTTT GTACTCATCC ACCCGGCTC GAG | 293 |

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

| | |
|---|-----|
| GAATTCGGCC TTCANGGCCT ACAGAAACAG AAATGCTAAC TGAAATGTAT TCTTCTAACA | 60 |
| AAGCATTTCT AACTTTCTAG AATGTAGTCT TTCATTTTTC TTTATCTTTT TTCAGTTTAT | 120 |
| TCCCAAATAT ATACTTTGGC CATTTAAATA AATGGCCAAA GAAATGGCCA AAAAATGCTT | 180 |
| TATTTAGTTT TTGTTTTATT ATGAAGGATG ATTACTCTTT AATGCTGCTA AATTCTTTTC | 240 |

TAGCTCTGTA TTTCACCTCA AGAAAACTCG AG

272

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

```

GCGAGCTGTT GGGATTACAA AGTTGCGCGT TTCATCGGTA CAAACTGGTC TTTGAACCTC      60
CTTTGTGAGA GCAATTGTAG TGTCCAAATT GTTAGGGAAA AAAAAAAAAA AAAATCCCAA      120
GGAGGAGGGT TTTTCCCCCT TCCCTGTTTG GTTTATCACA GCATTTTGCT TTTTITTTGG      180
CACAGCTTTT TACG TTCTT TCCATTCAGC CATCACAGAG CCTGTTCGG GTGGAAACCA      240
ATCCACACGC CTCGAG                                     256

```

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

```

GAATTCGGCC TTCATGGCCT ACCCACCTTG GCCTCCCAACA GTGCTGGGAT TCCAGGCGAG      60
AGTCCCTGCG CCCAGCCCCA CTGTCTATT CTGTGTTTTG CTGCCTGTTT TTGGTGTCTT      120
ATCTGCACAT GAATATTTAT AGCAGCTTTA TTCATAATTG CCAAACTTG GAAGAAACCA      180
CAATGACAAAT GTCCTTCTAT AGGTACACCC ATACAATGGA ACATTCAGTG ATAAAATGAG      240
CCATCAAGCC ACCCAAAAGG CTCGAG                                     266

```

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

```

GATTTCTCAG CTTTGAACA GAGTGGACTT GTCAATATCA GAGCAGAGCA CCAAACTGAA      60
GATGTCTCAC AGAGACAGTA ACCACCAGCT TCAGCTTTTG GACACTAAAT TTAAGGTAC      120
AGTTGAGGAA CTCAGTAACC AGATATTATC TGCACGGAGT TGGTTGCAAC AGGAACAAGA      180
ACGGATAGAA AAAGAGCTTT TACAGAAAAT TGATCAGCTT TCCTTGATTG TTAAGGAAAA      240
CAGTGGAGCC AGTGAAAGGG ATATGGAGAA GAAGCTCAGC CAGATGTCAG CCAGGCTTGA      300
CAAAATAGAA GAGGGTCAAA AGAAGACTTT TGATGGTCAG AGAACAAGGC AAGAAGAGGA      360
GAAGATGCAC GGGCGAATCA CCAAGCTGGA GTTACAGATG AACCAGAACA TCAAGGAAAT      420
GAAAGCAGAA GTTAATGCTG GGTTTACAGC CGTCTATGAA AGCATAGGAT CCCTCAGGCA      480
AGTTCTCGAG                                     490

```

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```

GAGATAGAGG GGACCCTGGC TATGGACATT TTGAATTATG TCGGGAGAGC TGATGGANAA      60
AGAGGCTCCN GGAGGACTGG TTAACTGAA GCCNGGAATG AGATGAAATG TATAAAATTC      120
TCTTGAATGA TTATGAATAT CGTCAGAAAC AAATCNTAAT GGAAAATGCA GAACTTAAGA      180
AGGTTCTTCA ACAAATGAAA AAGGAAATGA TTTNTCTTCT TTCTCCCAA AAGAAGAAAC      240
CTCGAGAAAG AGTAGATGAT AGTACAGGAA CTGTTATTTC CGATGTTGAA GAAGATGCCN      300
GGGAACTAAG CAGAGAGAGT ATGTGGGACC TTTCTGTGA AACTGTGAGA GAGCAGCTTA      360
CAACACGCAT CAGAAAACAG TGGAGAATTT TGAAGTCA TGTAGAAAAG CTTGATAACC      420
AAGTTTCAAA GGTACACCTG GAAGGTTTTA ATGATGAAGA TGTAATCTCA CGACAAGACC      480
ATGAACAAGA AACTGAAA                                     498

```

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

```

GAATTCTTCT TTCTCTATAA ATTTGCCTAC TATTGAAGAT TCTTCAGAGG AAGAAGAATT      60
GAGAGAGGAA GAAGAATTAT TAAAGGAGCA AGAAAAGCAG AGGGAAATAG AACAGCAACA      120
AAGAAAGAGT TCTAGTAAAA AATCAAAGAA AGACAAAGAT GAACTTCGAG CTCAGAGAAG      180
AAGGGAAAGG CCAAAGACTC GAG                                     203

```

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

```

GGAAAGAAAN GGACAAACCT ATAAATTAAC TCAACCTATA TCTCCCTTGA AAATACTTTC      60
AGGCTCCACC AAAACGTAGA ACTGAAAGCA TGTATTTTGG AAGAAAGAGA TACATTTTGT      120
ATGCTTTCTT TTCCTTTTGT AGATTCCCAG TTTATTTTCT AAGACTGCAA AGATCACTTT      180
GTCACCAGCC CTGGGACCTG AGACCAAGGG GGTGTCTTGT GGGCAGTGAT GGGGNCCTCG      240
AG                                     242

```

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

```
GATTCGGCCT TCATGGCCTA GGGAGGAGAA GAAGGGGGAG AAATCACAAA GAGATTGGGG      60
AGGAGATGAA GTAGCAGGGC TCAGCGATTC TTTCAATTCC AGTGCACACC CAATAGTGTG      120
TTGGAAGAAT GCACACTGTT CGGGATTGTG GGGAGAATTG TCCCATGACA AAGGAGGCAG      180
GGTTATGCTT GTTATAGTCC AATAAGCCGT GCCAGTCAAA CAAGAACCCA CACTCCTCGA      240
G                                          241
```

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

```
GAATTCGCCC TTCATGGCCT AGTGGTGAGA CTGAGCAGAT TTAATTAATG TCTGTTATGT      60
TCAGGGCACA AGGGTGAGCT CTTGCGAGGG GCTGATGCAC TGGGTGTGGA GCTGAGCAGA      120
GAGGCCTAAC CAGGATCAGG CAGGAGGGCA GGGATGGTGG CAGCCATAGG AGGGCAGGGT      180
AGGGTAGGGC CTCTGAGGAG GAGGGAAAAA GTGAAGGAGA GGCTTTGGAC CTGGTGACAG      240
AGTGATCAGA TGACAGAGGG GTTTTGGGA GACTCGAG                               278
```

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

```
GGAAGGAGAA GTGGAGAAGA AATCAGTCAG CCGCAGTGAA GAGCTCAGAA AAGAAGCAAG      60
ACAATTAAAA CGGGAACCTCT TAGCAGCAAA ACAAAAAAAA GTAGAAAATG CAGCAAAACA      120
AGCAGAAAAA AAGAAGTGAA GAGGAAGAAG CCCTCCAGA TGGTGCTGTT GCCGAATACA      180
GAAGAGAAAA GCAAAAGTAT GAAGCTTTGA GGAAGCAACT CGAG                               224
```

(2) INFORMATION FOR SEQ ID NO:657:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

```

ATACAGTAAT CAAAGTAAGT AATATTTCAA TCCAATATTT TTAAAAATCA GAATTAATGC      60
AAAAAAAACC ATGATGAACA AAATATTAAA ATTTAAAATA AAGACAGGAT TAGTATTACT      120
GAGTTTTCCT TTTGTCCCAG GCTCTAATAT GGCTTGGCAT GGGGCAGAAC ATTACAACAT      180
ACCACTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCCTGCCA      240
CAGCAATCTC GAG                                                         253

```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

```

GAATTCGGCC TTCATGCACT TTTGAGCATC AGTTTCTTTT CACTCCTTCT TCATGTGCTA      60
TTCCTTCCAA ATCTTTCCCA CCTTCTTCCT TCTCTCCTCT GTCTTTTCCT CTCCTCTTC      120
TGTTGTCTC TGTTTCCAT CTGTTCTCC TTCTCCTTCC CCATTCTCA CTATCCTCTC      180
TTCTGTCTCC TCACTTACTT CTCCATCCCT CCTCTCTCCA GCCCTCTCTC CCCCCTGTCT      240
CGAG                                                         244

```

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

```

GAATTCGGCC TTCAGCCTAG TCTCAAACCT CAAGCAAACC TCCTGCAATC CCAGCGCTTT      60
AGGAGGCCGC TCGAG                                                         75

```

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

```

GCNTTCATGG CCTTAAGTCA CCTTTAANTC TTTTCATGACC ATTCCAGAN GCCCTTACCG      60
TGGGCTATCT TAGCTTGATG TGCTAATCAA GTTCCCCCTA ATTTGACATA CTAGAATCTA      120
ATACTAGAGG CAGCATGACA TTATTAAGGG GGAGGAGGTT GAGAAGCACT AACCTCGAAG      180

```

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| TTAGAATTTT | TGGTTTGTC | TCCCAGTCTG | CTAATTAGCT | TTCTGATTTA | AGACAAAATA | 240 |
| CTTTTCTGT | GCCTTCTGGG | GGTCAAATTC | GATTTTAAAG | ATTCTCTCAG | TTGGAAGAAA | 300 |
| TCTAACTAAA | AATATACTTA | AAATAATTCT | TTGGTAGTAT | ATTATTTTGA | AATTTGGTCC | 360 |
| AGAATCCTAT | TTGTTTATTC | CTGTAGTATA | CATACATCTG | TAGTTACCCA | GCAAGCGCGC | 420 |
| TCCCTATAGT | GAGTCGTATT | AATTTTCAGAG | | | | 450 |

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGAGAAAAAA | AATTAGAGTG | ATTTCAGGAC | TCAAAGGAAG | 60 |
| AGCCTTGCAA | AGAGTTGGGA | GGATTAAACT | CTATGGATT | AAGCTCTGCC | TGCAAAATAA | 120 |
| CATCGCTGGG | AATTAGACA | CAAATTAGGA | ATATTCTGGA | ATTCATTTAG | CAGCAAATCT | 180 |
| CCTGACTAGT | TGTCAAATGG | AGCTGTTCTA | ATTGGCCTGT | TCTAAATGGG | CCTGTCCTAA | 240 |
| TTGCAGAAAT | ATTGCAGAAT | ATGTTTTTAG | TAAGCTCTCT | ATAGAAAGTC | ACCTCTGAGT | 300 |
| TGCTCAGCAT | TTAGATTCAA | ATATTCAAAT | GTTTTTTAAA | AATGCCAGCA | TATCAATTAT | 360 |
| ATTTGAAGAA | CAGTATAGAG | GCTTGAAACA | TGCCAAACAG | CAGGGAACAG | GAATAACCTT | 420 |
| TAATGAGTGC | CTACTCTGGT | GCAGGGTCCT | TTACACACAT | TACATTATGT | GATCTTCACA | 480 |
| ACAAACCGAC | TCGAG | | | | | 495 |

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ATAGGCCATG | AAGGCCGGCC | TTCATGGCCT | ACGAGGAAAG | 60 |
| GTCAGAGAGA | TGCGAAGTTT | CTGGCTTTGA | AGATGGGGAA | AGGTCTCCAG | CCAAGTGTGA | 120 |
| GCAGCCTCTA | AGAGTCAGAG | AAGCCAAGGA | ACAGCTTCTA | CTCTAGAGCC | TCCAGAAGGA | 180 |
| TGGCAGCTCT | GCTGATGTCT | GGCCTTATCT | CAGGGAGCCC | TGTTGGATT | TGAGCTGGTG | 240 |
| GAAGTGTGAG | ATAATGACTG | TGGTGTTTAA | GCCAGTAAGT | TGGTGTAAAT | TGTTAATGTG | 300 |
| ACTGCAGAAA | CCCAATAGAC | CGAGTGCGTG | TTGGGCTCTC | CCTGTACAAA | GGCAGAGGGA | 360 |
| CAGCAAGTGT | GAGCAGGCCC | TGCTGTGAGG | TAGAGGGCAT | CCTCTGAAGT | GTGTGGGGAA | 420 |
| GGGGGAGCCT | CACATGAGCC | CAGGGCTGCC | ACATGTTTCA | TCTGAGCGCT | CGAG | 474 |

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

```

GAATTCGGCC TTCATGGCCT ACTCTACTCG TCGGGTGCTT CTCTCCTTG GCATACAGCT      60
CACAGCTCTT TGGCCTATAG CAGCTGTGGA AATTATACC TCCCGGGTGC TGGAGGCTGT      120
TAATGGGACA GATGCTCGGT TAAATGCAC TTCTCCAGC TTTGCCCCTG TGGGTGATGC      180
TCTAACAGTG ACCTGGAATT TTCGTCTCT AGACGGGGGA CCTGAGCAGT TTGTATTCTA      240
CTACCACATA GATCCCTTCC AACCCATGAG TGGGCGGTTT AAGGACCGGG TGTCTGGGA      300
TGGGAATCCT GAGCGGTACG ATGCCTCCAT CCTTCTCTGG AAAGTGCAGT CAACCTCGAG      360

```

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```

GAATTCGGCC TTCATGGCCT ACCCTGTGAA AGTGGTGCCT GACTGTCTGA GGAGGGACGT      60
GGGCTAGAGA GTTCTCCCTG GGCTCAGGAA GGATAGCTTG GTGGTAAGG GAATGCAGTG      120
TGGATGACAC TGAGGCTGCC AGAGGTCTTG GGTGGCTGTC TCCTAGGTGG CTTGATGAAA      180
ATGGGAGGAC CAGAAAGAATT GGAAGTTGCA GCCAACTGAT GGCTGCTACT GAAGATTCTT      240
GACAGGAAAT AGAAAATAGG ATGTAAGACC CTCCTCTCCT CCTTCTGGCT CCCAATATTT      300
TCTGGTGATT CCCATTGGTG GATGCTAACA GGAATCACC TGGCAAGGGA GCTTGAGACA      360
TGTAGTTTGA GAGCTCGAG                                     379

```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

```

GAATTCGGCC TTCATGGCCT AATCACACAC CAACAAAACA CATTTATTTT GTAATTTATT      60
TTCTCCTGAT ATTTATGCTA GAAAAGTCCA TTGTATTTC TTTTACTATG GCATGTTTTT      120
ATAGGTTCTG TCTTATTTT ATTAAGTTCA TGTTTTTACT CTTTATTATC AGGAGTTCCT      180
ACCATATTTT ATNGCAAGC CTCGAG                                     206

```

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

```

GCCGATGAGG ACCAAGATNA AACAGTGCT CAAAAGTCGT GGCCGCCAC CTACAGANCC      60
GCTGCCCGAC GGGTGGATCA TGACATTCCA TAACTCTGGA GTCCCGGTGT ACCTACACAG      120

```

```

AGAGTCTCGG GTGGTCACCT GGTCCAGGCC ATACTTCTTG GGAACGGGAA GCATACGGAA 180
ACACGACCCT CCTCTGAGTA GCATCCCTTG TCTGCATTAT AAGAAAATGA AGGACAACGA 240
GGAACGGGAG CAAAGCAGTG ACCTCACCCC TAGTGGGGAT GTGTCCCCCG TCAAGCCCCT 300
GAGCCGATCT GCAGAGCTGG AGTTTCCCCT GGATGAGCCT GACTCTATGG GTGCTGACCC 360
GGGGCCCCCG GACGAGAAAG ACCCACTAGG GGCTGAGGCA GCCCCTGGGG CCCTGGGGCA 420
GGTGAAGGCC AAAGTCGAGG TGTGCAAAGA TGAATCCGTT GATCTCGAG 469

```

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

```

GAATTCGGCC TTCATGGCCT ACACATACAA CAAACCGAAG CTTTCCGAAC CCGAAGAGGA 60
ACTTCTCCAG CAATTTAAAC GGGAGGAGGT GTCCCAACA GGGAGTTTCA GTGCCCCACTA 120
CTTGTCGATG TTTCTCTTAA CTGCTGCCTG CTTATTTTTC CTAATACTGG GACTGACTTA 180
CCTAGGAATG AGAGGGACAG GAGTATCTGA GGATGGAGAA CTCAGCATAG AAAACCCCTT 240
TGGTGAAACA TTTGGAAAAA TACAAGAAAG TGAAAAAAT CTTATGATGA ACACATTATA 300
TAAGCTTCAT GATCGATTAA CACAGCTCGA G 331

```

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

```

GAATTCGGCC TTCATGGCCT AGGACCCAAA GTCCGCGTGG AACCGCGATA GGGATCTGTC 60
AGGGCCCGCG GCCGGGTCCA GCTTGGTGGT TGCGGTAGTG AGAGGCCTCC GCTGGTTGCC 120
AGGCTTGGTC TAGAGGTGGA GCACAGTGAA AGAATTCAAG ATGCCACCTA ATATAAACTG 180
GAAAGAAATA ATGAAAGTTG ACCCAGATGA CCTGCCCCGT CAAGAAGAAC TGGCAGATAA 240
TTTATTGATT TCCTTATCCA AGGTGGAAGT AAATGAGCTA AAAAGTGAAA AGCAAGAAAA 300
TGTGATACAC CTTTTCAGAA TTAATCAGTC ACTAATGAAG ATGAAAGCTC AAGAAGTGGA 360
GCTGGCTTTG GAAGAAGTAG AAAAAGCTGG AGAAGAACAA GCAAAATTTG AAAATCAATT 420
AAAAACTAAA GTAATGAAAC TGGAAATGA ACTGGAGATG GCGCACTCGA G 471

```

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```

GAATTCGGCC TTCATGGCCT AGAGAGGTTG CTCATTGCTC AGAGCGTGCT GCCCACCCTC   60
CACCCCTGCA TGGCAGAAAC TGTGCAGGGG ACGAGGCCAA GGAATCAGGA GACCCAGAGG   120
CAGGGGTGGC CCGGAGACGG TGAAGAAACC AAGACGCAGA GAGGCCAAGC CCCTTGCCTT   180
GGGTCACACA GCCAAAGGAG GCAGAGCCAG AACTCACAAC CAGATCCAGA GGCAACAGGG   240
ACATGGCCAC CTGGGACGAA AAGGCAGTCA CCCGCAGGGC CAAGGTGGCT CCCCTGAGA   300
GGATGAGCAA GTTCTTAAGG CACTTCACGG TCCTGGGAGA CGACTACCAT GCCTGGAACA   360
TCAACTACAA GAAACGGGAG TATCTCGAG                                     389

```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS: ..

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```

GAATTCGGCC TTCATGGCCT AGTGTACAA AATATAGAAA GAAAAGAACA AACAAAAAAA   60
GAGACAAAGG TGGAAATACCT TTTGAAATA AAAGAGAGCT AGCAATGCAG TACATGGTCC   120
TTGCCCTATT ACTATCCATC CTCATCTAG CAATAATCCC CATCTCCAT ATATCCATAC   180
AACAAAGCAT AATATTTGCG CCACTCGAG                                     209

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```

GAGTTCATTC AAGATATTTT TCACTTGCTG TTCAGGAGCT TTGATGTGCG TCACCATTC   60
TGGCATGTTT ACGCTGTTCC TGTGCAGGTA TTTAGGAAG ACGTCTGCAT TCCTCCGAGC   120
AAGGGTGCAA GCCTTCAGGA ATGCCTCCTT CTGCTCCAGG TGCTTGCTGA TCATGGGCGT   180
CACGTGGTCC GTCTCAGAGT TTGGGCCCAG CTTATCCGCC CCGCCACACC AGTCTTCTTC   240
TCTCTGTAC TCCCTGTTCC AGGCTCTCGA G                                     271

```

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

```

GAATTCGGCC TTCATGGCCT AAGATAAATT TGACAAAGTT AACTGAAATT TATCTGGTCC   60
ATTTTATTCA TGCTACTAAG ATGGGAATCT TTAACACAA GGGTCAGCAA GCTTTGGCCC   120
ATGGATTGGC CACCTGTTAC GTAAATAAAG TTTCTTTGAA ACAAGCCTAC ACTCATTAT   180
TTATGTTTTG TCTGTGTTG CTTCCACAA CTGCAGAGTT GTATGGCTTG CAAGTCTAAA   240

```

AACATTTACT ATTTGGCCCT CTAAGAAAAA GTTAAGACAC CTAGTCTAAT GGCCTTTTGG 300
 GAAAAAACAA ATCACTAACT CATAATCATT TATATCCATT ATTTTCTGCA TAAATGTAAT 360
 GCTATTGTAC AGGGTACTCG AG 382

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GAATTCGGCC TTCATGCCTA CCAAATTGT CTAAGCACTG GCCAGTCTGT TGTGGGCATT 60
 GTTTTCTACA ACCAATCTG GGTTCCTTTT TTCTTTCTTT AAACATAGAG GTACCACCAC 120
 AAGGGATGCC CTACTCTCTC GCAGCTCTTG AAAGCATCTG TTTGAGGGAA AGGTCTCTGG 180
 GCAAGCAAGT GGTATTTGG ATTGCTTGCT TCCCTTTTTC CACCTGGGAC ATTGCAATCA 240
 TAAAATAACA GTAAATTCCA AACCTCAAAA ACTATTATGG CCTGAGCACA GCTGAAATCT 300
 AGCAGAGTTT AACTCTTCTG CCTCCATGTC TGTCACCTAT AAATCAGGTT CTGCTGTTGG 360
 CTTTCAAGCA TGAGCAGAAG AATCGTTTTA TGCTAGTTAT TGCATTCATG GTTGAAATCT 420
 AACTTAGGGA AAGGGTTCCA ATGTATTAAG CAATGGGCTG CTTCTCCCCA ATCCTCCCTA 480
 ACAATTTGTT GTGTGGACTT CTCATCTAAA AGGTTAGTGA CTCGAG 526

(2) INFORMATION FOR SEQ ID NO:674:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GAATTGCTTC TCAATTTACC CGAGATTTCA TTCGAGATTC AGGTGTTGTC TCACTTATTG 60
 AACCTTGCT TAATTATCCA TCCTCTAGAG TTAGGACAAG TTTTGGGAA AATATGATTC 120
 ACTGGCTCGA G 131

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCGGCC TTCATGGCCT ACCTAATCTT CCTTTTCTTT TTAGCATTTT TGGGCTTTTC 60
 AAAGCAATCT CCCCAAAAAA AGAATCATTT GGTTCCTTGGAA AAGAAAACAG AATCAGCAAC 120
 TTTTCGGGTG TGTGGTGAAA ATGTCACGTG TGTGGAATAC GCTATCTCCT GGCTACAAGA 180
 CCTGATTGAA AAAGAACAGT GTCCTTACAC CAGTGAAGAT GAGTGCATCA AAGACTTTGA 240
 TGAAAGGAG TATCAGGAGT TGAATGAGCT GCAGAAGAAG TTAAATATTA ACATTTCCCT 300

GGACCATAAG AGACCTTTGA TTAAGGTTTT GGGAATTAAC AGAGGACTCG AG

352

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA --

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAACCCATAA AACAGGAATT CTTATAATC CTAGAGGACA | 60 |
| AGGCATTATA GAATGGGCAC ATCAAACATT ACAACGAATG TTGAAAAGAC AAAAAGGGGG | 120 |
| TATAGGAGGC CAACTACCAC CTCAATCAAA ACTACATTTA GCCTTATTTA CTTTAAAATT | 180 |
| TTTGACTCCT GGTACGGATG GTAAGACTCC AGCAGAAAGA CATTGGCAAG TGTTAGAGGA | 240 |
| AAAGACTCGA G | 251 |

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

| | |
|---|-----|
| GGGCATTGTC AGTTTTCTTC CCTGCTGCAT GTAATGTCTC AGAATCAACA TTCTTTTAAA | 60 |
| ATCTAGACTA TATTTTGAGG CAATGAATTA CTTATATTCA ACTTAGGCTT GTTTTGACAT | 120 |
| TCAGTAGAAC TTAAAGTTCA ATCTAAAGGC TTCAGTCCAC ATTTTTTTAT ACGTTGTATT | 180 |
| TTAAAAACGT TTGAAAGGAG TCTTACACCT GTATCATGAA AACTGAATCC TTTTGAAATA | 240 |
| CCACTATATG AAGAGAGAGA TGAAATTTAG TGAACAGAAT TGAAAAGGTG CTCATAATT | 300 |
| CACTATGCAA ACTTACCCCA GTCAACTCGA G | 331 |

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

| | |
|---|-----|
| GAATTGAACA ATGCTGACAG GCTGGTANTC CTGCCCTGAA GCAACTCACA GACTCATAGT | 60 |
| TATAGAACAT CTTTATCTTT AGTTAATCCA TNGCACAGCA TTGGCCAAGG GTCAATACCT | 120 |
| TGTAATAAGC ATGTGTGTAT TGGTCAGGGT TCTACAGAGA GACAGATCAA TAGGAGCTAT | 180 |
| CGATAGATAT AGACATATGA GAGGGGGTTT GTTAGGGGAA TTAGCTCACT TGATTACAGA | 240 |
| GGTTGAGAAG TCGCTCCTCG AG | 262 |

(2) INFORMATION FOR SEQ ID NO:679:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

```

GAATTCGGCC TTCATGGCCT AGCAGCCCGA GGCCTTGAGG CCACTGCCTC CCCAGGGCTC      60
CTGAAGCCAA AGAATGGAAG TGGTGAGCTG AGCTACGGAG AAGTGATGGG TCCCTTGAG      120
AAGCCTGGTG GAAGGCACAA ATGCCGCTTC TGTGCCAAAG TATTTGGCAG TGACAGTGCC      180
CTGCAGATCC ACCTTCGTTT CCACACGGGT GAGAGGCCCT ATAAGTGCAA TGTCTGTGGA      240
AACCGTTTTA CCACCCGTGG CAACCTCAA GTGCATTTC ACCGGCATCG TGAGAAGTAC      300
CCACATGTGC AGATGAACCC ACACCCAGTA CTCGAG      336
  
```

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

```

GAATTCGGCC TTCATGGCCT AAATTAAAGA TGATTTTTTT AATGTGAATA AAGTTATGTT      60
CTGATAGTTT GTACAGAAAA AATAAAATGG ATGCCCATGT TTTATTGCTA TTAATAAATG      120
TCAAGATTGT ATGCTATTAT GTCTTGTAAT TTTCTTTTGT TGGTGTAAT ATGGAAATGC      180
CACATTGGTT AAGTGCCATC ATTTGTAATG CAATGTGTCA CTTGAAAAGA GATTTGAAGA      240
AACTGACAAC TTCAAAAACA AATGAGAAGC CCAAGGAAGT GTGAGCAATT AAAAGCAAAC      300
CGCGACACCC TTTGTCTCCA CCACACATAG TGTACTTTGG AAGCACAACG TCCAGGCTGG      360
TACCGCAGCG CCATGCCCAT TCCTCGCCG      389
  
```

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

```

GATTTCTCTG TTGACTTCTG CAGTGAACCA CCTCAAAGCC AATGTTAAGT CAGCTGCAGA      60
CTTGATTAGC CTGCCTACCA CTGTAGAGGG ACTTCAGAAG AGTGTAGCTT CCATTGGCAA      120
TACTTTAAAC AGCGTCCATC TTGCTGTGGA AGCACTACAG AAACTGTGG ATGAACACAA      180
GAAAACGATG GAATTACTGC AGAGTGATAT GAATCAGCAC TTCTTGAAGG AGACTCCTGG      240
AAGCAACCAG ATCATTCGGT CACCTTCAGC CACATCAGAA CTTGACAATA AAACCCACAG      300
TGAGAATTTG AAACAGGATA TCCTGTACCT TCACAACCTT TTAGAGGAGG TAAACAGTGC      360
CCTAGTGGGG TACCAGAGAC AGAATGATCT TAAACTCGAG      400
  
```

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

```

GGAGATCGAA AATTGAACT CTCAAAGAGA CAACAAATAG CATGGTAGAA TCAATTAAAC      60
ACTGCATTGT GTTGCTGCAG ATTGCCAAAA GTACTATTAA TCCCGTAGAT GCAATATATC      120
AACCTAGTCC TTTGGAACCT GTGATCAGCA CAATGCCTTC CCAGACTGTG TTACCTCCAG      180
AACCTGTTCA GTTGTGTAAG TCAGAGCAGC GTCCATCTTC CCTACCAGTT GGACCTGTGT      240
TGGTACCTT GGGACATCAT CAGACTCCTA CACCAAATAG TACAGGCAGT GGCCATTACAC      300
CACAACTCGA G

```

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

```

GTGAGGGGTT CCGTGACTGA GGTTCAGAGC TGCTGTTGAT GTGCTATACC TCCTTCAATT      60
CTCAGCTCTC AAAGGGGAAA ACAACTGCAG AGGATGGGAA ATGCTATACT GCCATGCCTG      120
GAAACACCCA CAGGAAAATT ACCAGTTTGT AGCTTGCTCA ACTGCAAGAA AAAGTGAAGG      180
AGACAGAAGC AGCCATGGAA AAATTAATCA ACAGAGTGGG ACCTAATGGT GAGAGAGCAC      240
AGACTGTGAC TTCTGACCAA GAGAAACGGT TGCTACATCA GCTCCGAGAA ATCACCAGAG      300
GTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

```

GCTCCGGACA ATGAAACATA ACCAATACTA CCAATCAATA CTCATCATTATAAATCATAA      60
TGGCTATAGC AATAAACTA GGAATGGCCC CCTTTCATT CTGAGTCCCA GAGGTTACCC      120
AAGGCACCCC TCTGACATCC GGCCTGCTTC TTCTCACATG AAAAAACTA GCCCCATCT      180
CAATCATATA CCAATCTCT CCCTCACTAA ACGTAAGCCT TCTCCTCACT CTCTCAATCT      240
TATCCATCAT AGCAGGCAGT TGAGGTGGAT TAAACCAAAC CCAGCTACGC AAAATCTTAG      300
CATCTCCTC AATTACCCAC ATAGGATGAA TAATAGCAGT TCTACCGTAC AACCTGACA      360
TAACCATCT TAATTTAACT ATTTATATTA TCCTAACTAC TACCGCATTC CTACTACTCA      420
ACTTAACTC CAGCACCAGG GGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

```

GTTGACAAAC AAGCTCAAGC TCGGATAAA ATGAAGGAGC AGGAAGACCT GGCCAAGGTG      60
GTATCTAAAG AAGAATCAAT TGTTCATCA TTACGATTAG CCTATAAGGA TCTTGAAATT      120
CAAATGAAGA AAGACGAAAA GATGAACATT AGTGGCAAAA AAAATGTTGA CTCAGACAGA      180
CTCGGCATGG GATTGGAAA TTGCAGAAGT GTTATTTTAC ATTCAGTGAC TTCAGATATG      240
CAGACCATAG AGCAGGAATC ACCCATTATG GCAAAACCAA GAAAAAAGTA TAATGATGAC      300
AGTGAACCTG AG                                     312
  
```

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```

GTAATGGCAC AATGGATTCA AATGGGACAT TTGTTAATGT AACAATGAGC ACATTTAACT      60
GGAAGGATTA CATTGGAGAT GACAGTCACT TTTATGTTTT GGATGGGCAA AAAGACCCTT      120
TACTCTGTGG AAATGGCTCA GATGCAGGCC AGTGTCAGA AGGATACATC TGTGTGAAGG      180
CTGGTCGAAA CCCCAACTAT GGCTACACAA GCTTTGACAC CTTTAGCTGG GCTTTCCTGT      240
CTCTATTTTC ACTCATTCTT CGAG                                     264
  
```

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```

GGGAACAGCA GTTCCTATGG CTTTTTTTTT TTTTTTCTG TGTATGAGCA ATTCGACTCA      60
GTGGGATGAT ATTTTCTTTT ATAATCATT AATGTTTGCG ATACCGTGTA CTCAAATATT      120
CAATGTCAGC TGTCAGCTAC CATTGGGATC CATCCACAG ACCATCAAAA TGTACTTTTG      180
GGCTGAATTA GTCCTATGCC AAGACTTGTG GGTGGATCCA GCAGCAGTTG GGAACCACGT      240
GCCAGGCCTG GTGTATGTGC TCACGAACAC ACTCGAG                                     277
  
```

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAATAGTTTA | GTTCTCTGGT | GCAATTTGAA | GTATATCTTA | 60 |
| TAGTCACTTT | TAGTAATGTG | TGTTACTTCC | CTGTAAGGAA | TAGCAATGTT | ATACTTCTCC | 120 |
| TTTTCAGTG | AAGAAATTGA | GATGTAGAAA | GGAAGAGACC | TGCCCAAGGT | CAAAGAGCAA | 180 |
| GGCAGTGGAA | AGCCTGAGAT | TAGACTTGTG | GTCTTTTAGA | TTTTTCATCT | GTTGTTCCAC | 240 |
| ACTGAGGAGC | CAGCTTTCTG | TTTGCTGGAG | ACAGTTCAGC | CTAATGGAAT | TTTCTCTGCC | 300 |
| AGATGTCCAC | ATTGTGTTAG | GTGATGATTC | TAACCATCCT | CTAATACCCA | TTCTCCTCCA | 360 |
| AACTGGCCCT | TTAGTTCCCC | ACCAGAACTC | GAG | | | 393 |

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTGTTCTGC | TCCTCCCAGA | CAGAGCCTTT | CCCTCAGCCC | 60 |
| AGGGGGTCAG | GGGGTGAGGG | AAAGGCTCTG | TCTGGGAGGA | GCAGAACAGC | AGAAGAGAGG | 120 |
| AGGAGGCAGG | GAGTTACAGG | AACCTGGGGT | ACCAGGCTGC | TGGGAAGATG | CAGATTATGA | 180 |
| CAGAGCTTGC | ACGATGCTGG | CACCCCATGC | CAACCACTCT | ACGTGGCTTT | CCTCTTCGGA | 240 |
| GAGGTGGTGG | GCTCCCTTCT | TCACTGTGCC | CTCCCTCCTC | TGGCCACTAG | GGGTGGGAAA | 300 |
| TACGAGTGAG | AATCCTTCCA | GATTTACTTC | CGCCAATCCA | GAGGTACAGG | CTTTTAGGCA | 360 |
| AGGGGCAGAG | AACTGCCCAA | TTTGCTGCTT | CATGGCCTAG | GGGTGGGGTT | CCTTAGGAGC | 420 |
| TGAAAAGTTG | AACAAGGTGT | GTGAGCAGGT | GGCTTGTTC | TGGGTTTCAA | GCTCGAG | 477 |

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 598 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | ATCATGGGCT | AAGACGTGGT | ANTGACATGC | CTGTAGACCC | AAGTATTTGG | 60 |
| GAGGCTGAGG | TGAGAGGTTT | GCTTGAGCCC | TGGAAGTCGA | GGCTTCAGTG | AGGCAAGATC | 120 |
| ACACCACTGC | ACTCCAGCCT | GGGAGAGCAA | GACCCTGTCT | CCAAAACCAA | AAAAAAGGG | 180 |
| AAAAAAGTAA | ATGTTATAGA | TACTTGCTAA | GGGCTTTGTA | TATACTTATT | ATTGTTATTT | 240 |
| CTCAGCACGT | ATGTAGCAGA | TGAGGAAATG | AAGGCTAAAG | GTCATATATN | TACAAAGTGG | 300 |
| GGAGGTCAGA | CTTTGAACCC | ACAACCTGAC | TGTGGAGCCA | CTTCAGTATA | CTCTCTCCCC | 360 |
| ATAAGAAAGT | TCCAATAGAA | AAAAAATGCT | ACTTAAGTAG | GGAAATCACA | AAATAAGTGC | 420 |
| CAATGAACAA | TAAATGTTCA | ACCTCACTAC | AGTTAAATG | TATATTAAAG | CAAGAGTTGA | 480 |
| GATGACACTT | TTCTTATAA | AACAGACAGG | GATTCAGGGA | CATTGGGACT | CTAATGCTGC | 540 |
| TGGTAAGACA | TGAATAAATA | CATACCATCT | CTGGCAATCA | ATACCAGAAG | ATCTCGAG | 598 |

(2) INFORMATION FOR SEQ ID NO:691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTTCTCCCT TCCATTCTGC CCTGTATCT TTGCAGTCAT | 60 |
| TGTATACAGC AGATTCTAGA AAGTGTTAAT CATTGTCACC TAAATGGCAT AGTTCACAGG | 120 |
| GACCTGAAGG TCAGTATATG GAGTCCATAA ATCTGAATCA AAGCAGTTTT ATTTTTTTT | 180 |
| CTGGGGAAG GGCAGAGGT GGGTATTTAA AATGGTTCCC TTGCCTTTCC CAACTTGTTT | 240 |
| CTAAATGAG TAAATGATGA AATGATAATG CATGATGCCT CTTCCAGTTT GCTCATCTAC | 300 |
| AGGCTAAATA TACATCATAG CAAAAGGGA AGAATACTAA AGAATACAAC CTGCTAAGTT | 360 |
| TCCAAGCAGT AACTACCTA CAAAAGGGA TTGAGGATCC CTCGAG | 406 |

(2) INFORMATION FOR SEQ ID NO:692:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

| | |
|---|-----|
| GTCCTGGAAG AATGTGTCCA GCAACCCAAA AACTAATAGA AGAGTCACAG AGAAAAATGA | 60 |
| ACGCTTTATT TGAAGGTAGA CGCATCGAAT TTGCAGAACA AATAAATAAA ATGGAGGCTA | 120 |
| GGCCTAGAAG ACAATCAATG AAGGAAAAAG AGCATCAGGT GGTGCGTAAT GAAGAACAGA | 180 |
| AGGCGGAACA AGAAGAGGT AAGGTGGCTC AGCGAGAGGA AGAGTTGGAG GAGACAGGTA | 240 |
| ATCAGCACAA TGATAGACTC GAG | 263 |

(2) INFORMATION FOR SEQ ID NO:693:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

| | |
|---|-----|
| GCCGCCGAAG AAGCATCGTT AAAGTCTCTC TTCACCCTGC CGTCATGTCT AAGTCAGAGT | 60 |
| CTCCTAAAGA GCCCGAACAG CTGAGGAAGC TCTTCATTGG AGGGTTGAGC TTTGAAACAA | 120 |
| CTGATGAGAG CTTGAGGAGC CATTTTGAGC AATGGGGAAC GCTCACGGAC TGTGTGGTAA | 180 |
| TGAGAGATCC AAACACCAAG CGCTCCAGGG GCTTTGGGTT TGTCACATAT GCCACTGTGG | 240 |
| AGGAGGTGGA TGCAGCTATG AATGCAAGGC CACACAAGGT GGATGGAAGA GTTGTGGAAC | 300 |
| CAAAGAGAGC TGTCTCCAGA GAAGATTCTC AAAGACCAGG TGCCCACTTA ACTGTGAAAA | 360 |
| AGATATTTGT TGGTGGCATT AAAGAAGACA CTGAAGTCCT CGAG | 404 |

(2) INFORMATION FOR SEQ ID NO:694:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

| | |
|---|-----|
| GAATTCGGCC TTTCATGGCC TACTGGATGG CTTTTTATCT TTTGCTTTTC TTTTATGGCA | 60 |
| GATGCCTTTC CATCGGCATC CCAGCTGTGG CTGGGGACGT TTTGGGAAGT GTGTTTGGCT | 120 |
| CACTCCGAGA GAACGAGGTC TCAAGAGGAA GTGTGTCTGG CTTGCAAAGA TGTCCTGGG | 180 |
| CCTGGACAGG ACCCCGCTGT GTTCTGCAGC CCTCGACGCA GTGGGTGAGT GAGGCCTTCC | 240 |
| TCTCTGCTG GCTGCCCTGG AGGATTTCAT CATGTCCCAG GATTTGCTCC ACCCTCGAG | 299 |

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCTGTTGAA AACTCTCCAA TGAATTCCCA CTCCATCATC | 60 |
| CTGTGGGATG GGTCCACCAT GCTGGACCAC AAGGCTCTGC ACAATGCGGC TCCCACCAGC | 120 |
| CTCTCCCCTT GGCCAGATT GCTTCCTCCT ACCCCTTCT CTAGCTGCCA GGCCCCCCTA | 180 |
| CCCCCGCATG GAGCCCTTCA GCAGCTCTGT GAGCTCCCTG CCTGTTGGCA GCCATCACAG | 240 |
| CAACGGGCTC TGGTGTGCCC CTTGTTATCC CTGTATTCAG GCCATTATCT GTAATGACAG | 300 |
| CCTGGCATAA TTTTATTTTC ACAATTTGTA TAATTATATT CTATTGAGCT AAATGATCAT | 360 |
| TATAATCATT ATTAAATATT TATTAAGCAC TTCTAGCTGT GCÁAACATAA TAAGATGTGG | 420 |
| CCTCAGCTCT TAAAATCTTT CTTCTAATT CCAACCCAAA TACTCGAG | 468 |

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACAAGGGAAC ATGTAACTA ACATAACCAA TTGTCAGTTC | 60 |
| TCCATGTATT CCTCAAAGA ATGTCAGAGT AAATGTATTA GAAATACAGT ATCCAGACTG | 120 |
| CTAGTCCTTG CCAGAGACAT TCTTACCTCT GCCCTGTGAT AATATTTTAT GCTTGACAGT | 180 |
| GAAAACAAGT GTGGCCCTT GCACCGGTTA GCTAGAAGTA CAGCCAGATT TCAAGCTAGT | 240 |
| GCAGTCACCT CTTCCGTCAT TCTTCACAAA TCTTGTC AAC CTGGATCTTA GACTTCATCT | 300 |
| GAACTCGAG | 309 |

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```

GAATTCGGCC TTCATGGCCT ACACGGATCC GTGTGAAGAC CTACACAGAT GAGCTGACGC      60
CCATTGAGTC TGCTGTCTCT GTGTTCAAGG CAGCCAACTG GTATGAAAGG GAGATCTGGG      120
ACATGTTTGG AGTCTTCTTT GCTAACCACC CTGATCTAAG AAGGATCCTG ACAGATTATG      180
GCTTCGAGGG ACATCCTTTC CGGAAAGACT TTCCTCTATC TGGCTATGTT GAGTTACGTT      240
ATGATGATGA AGTGAAGCGG GTGGTGGCAG AGCCGGTGGA GTTGGCCCAA GAGTTCCGCA      300
AATTTGACCT GAACAGCCCC TGGGAGGCTT TCCCAGTCTA TCGCCAACCC CCGGAGAGTC      360
TCAAGCTTGA AGCCGGAGAC AAGAAGCCTG ATGCCAAGTA GCTCCAGGGA ACGCATGTGG      420
ATCTTAGACA GCGCCTTATC TATGATTGAG TGCCCATCTT CGAG                        464

```

(2) INFORMATION FOR SEQ ID NO:698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

```

GAATTCGGCC TTCATGGCCT ACGGTGGTGA ACGAGTCTCC AGCACCATGT CTGGTTTGTC      60
TGGCCCCACCA GCCCGGCGCG GCCCTTTTCC GTTAGCGTTG CTGCTTTTGT TCCTGCTCGG      120
CCCCAGATTG GTCCTTGCCA TCTCCTTCCA TCTGCCATT AACTCTCGCA AGTGCCTCCG      180
GTGAGGAGATT CACAAGGACC TGCTAGTGAC TGGCGCGTAC GAGATCTCCG ACCAGTCTGG      240
TGGGCGCTGGC GGCCTGCGCA GCCACCTCAA GATCACAGAT TCTGCTGGCC ATATTCTCTA      300
CTCCAAAGAG GATGCAACCA AGGGGAAATT TGCCTTTACC ACTGAAGATT ATGACATGTT      360
TGAAGTGTGT TTTGAGAGCA AGGGAACAGG GCGGATACCT GACCAACTCG AG              412

```

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

```

CAGCTCCTGT GACATTTGAA GTTCTTTTAA AAGGGGTTTT TCTTAATCAA AGTTTTACAT      60
TTGGTAGCAT AAGTAGTTCT TTATGCTTCA CAGGACATTG TCTTCAGAGT AATCTCTCTG      120
CTAAAATGGT ACATGTGGG                                           139

```

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | TTCATGGCCT | ATGAAATGAT | ACCTATGGAG | TGTGATTCAT | TTTGCAGTGA | 60 |
| CCAAAATGAA | TCTGAAGTTG | AACCATCTGT | AAATGCTGAT | CTTAAACAAA | TGAATGAAAA | 120 |
| TTCTGTGACA | CACTGTTCTG | AAAATAATAT | GCCGTCTTCT | GATCTTGCGG | ATGAAAAGGT | 180 |
| TGAAACTGTT | TCTCAACCAT | CTGAAAGCCC | AAAAGATACC | ATAGATAAAA | CCAAAAGGCC | 240 |
| TCGTACTCGA | AGATCTAGAT | TTCATTCTCC | ATCTACAAC | TGGTCACCCA | ACAAAAGACAC | 300 |
| TCCACAAGAA | AAGAAGCGGC | CCCAGTCTCC | ATCTCCCAGA | AGAGAAACTG | GGAAAGAAAG | 360 |
| CAGGAAGTCT | CAATCACCAT | CTCCTAAGAA | TGAGTCAAAC | CTCGAG | | 406 |

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGCAAGATGG | TGTTGCAGAC | CCAGGTCTTC | ATTCTCTGT | TGCTCTGGAT | CTCTGGTGCC | 60 |
| TACGGGGACA | TCGTGATGAC | CCAGTCTCCA | NACTCCCTGG | CTGTGTCTCT | GGGCGAGAGG | 120 |
| GCCACCATCA | ACTGCAAGTC | CAGCCAGAGT | GTTTTGTACA | GCTCCAACAA | TAAGAACTAC | 180 |
| TTAGCTTGGT | ACCAGCAGAA | ACCAGGACAG | CCTCCTAAAC | TGCTCATTTA | CTGGGCATCT | 240 |
| ACCCGGGAGT | CCGGGGTCCC | TGACCGATTG | AGTGGCAGCG | GGTCTGGGAC | AGATTTCACT | 300 |
| CTTCACCATC | AGCAGCCTGC | AGGCTGAAGA | TGTGGCAGTT | TATTACTGTC | AGCAGTATTA | 360 |
| TAGTAGTTGG | ACGTTCCGCC | AAGGGACCAA | GGTGGAAATC | AAACGAACTG | TGGCTGCACC | 420 |
| ATCTGTCTTC | ATCTTCCCGC | CATCTGATGA | GCAGTTGAAA | TCGGAAGTCT | CCTCTGTTGT | 480 |
| GTGCCTGCTG | AATAACTCCT | ATCCGCTCGA | G | | | 511 |

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGGGATGGTC | TTAACAGGGA | ANAGAGAGGG | TGGGGGAGAA | 60 |
| AATGTTTTTT | TCTAAGATTT | TCCACAGATG | CTATAGTACT | ATTGACAAAC | TGGGTTAGAG | 120 |
| AAGGAGTGTA | CCGCTGTGCT | GTTGGCACGA | ACACCTTCAG | GGACTGGAGC | TGCTTTTATC | 180 |
| CTTGGAAGAG | TATTCCCACT | TGAAGCTGAA | AAGTACAGCA | CAGTGCAGCT | TTGGTTCATA | 240 |
| TTCACTCATC | TCAGGAGAAC | TTCAGAAGAG | CTTGAGTAGG | CCAAATGTTG | AAGTTAAGTT | 300 |
| TTCCAATAAT | GTGACTTCTT | AAAAGTTTAA | TTAAAGGGGA | GGGGCAAATA | TTGGCAATTA | 360 |
| GTTGGCAGTG | GCCTGTTACG | GTTGGGATTG | GTGGGGTGGG | TTTAGGTAAT | TGTTTAGTTT | 420 |
| ATGATTGCAG | ATAAACTCAT | GCCAGATATT | CTCGAG | | | 456 |

(2) INFORMATION FOR SEQ ID NO:703:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

```

GAATTCGGCC TTCATGGCCT AGTCCTTTGC TCTACTGTTG AATGGAGGAG GATTTTTTTT      60
TTTTTCCCTC NACACAGGGG TTTTCTTGGA GCTCAAGTTT GGATGACCCC AGACAGTAAG      120
ATAATCTCAT CATGGTAAAG TTAATATGAA ATATGTGGTC TCCAAACAGC CTCTCCCAGA      180
GGCCAGGATC AGCAGGTTT AGTGGATAAT TGGCTTGTGG TCATTTTCTC ATAGGATTTT      240
TCTTTTAGTA GTGGAAGCTG TTTTTCAAAT CAAATTTGGA TGCCAATAT GTGGAACAGA      300
AGTGTGGCTG CTCTGGTGA AGTGGCAATG GTAGTCCTAG AGTCTCCCTG TCAGCCACAC      360
CCTTTGTCTC CCCCTACCCA AGGGACCCTG TGGCCTGGAA CCGCAGTGTG AAATGCTATA      420
TAGTGCAATG AAGCTCGAG
                                         439
  
```

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

```

GAATTCGGCC TTCATGGCCA ACAGCTGAGA TAACGAGGAA ATATTCTGAA ATGGATCCCA      60
AATATTTTCAT CTTAATTTTG TTTGTGGAC ACCTGAACAA TAATTTTTTT TCAAAGACAG      120
AGACAATTAC AACAGAGAAG CAGTCACAGC CTACCTTATT CACATCATCA ATGTCACAGG      180
TATTGGCTAA TTCTCAAAAC ACAACAGGGA ATCCTTTGGG TCAACCAACA CAATTCAGCG      240
ACACTTTTTT TGGACAATCA ATATCACCTG CCAAAGTCAC TGCTGGACAA CCAACACCAG      300
CTGTCTATAC CTCTTCTGAA AAACCAGAAG CACATACTTC TGCTGGACAA CCACTTGCCT      360
ACAACACCAA ACAACCAACA CCAATAGCCA ACACCTCCTC CCAGCAAGCC GTGTTACCT      420
CTGCCAGACT ACTCGAG
                                         437
  
```

(2) INFORMATION FOR SEQ ID NO:705:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

```

GAATTCGGCC TTCATGGCCT ACATTCACAT GTTCCCAATC ACTTCCCTCA CACACATATG      60
CTCACTGATT TACACAGCCA TCGCACTTA TACATACTCG NTCACATTCA CACAGGGTCA      120
CCCATTACCA CAACTCGAC ACATTTACCC TCACATTAC CCACTCACCA TTCCCACTCA      180
CCAGTTACCA TGCACTCACC CAAGCTCACA CTTGACCACG GACACACCCT CAAACATAGG      240
TGCTTACACA CAAGCCNACA CAACTCACC TAGGCATTCA TACTCAGGTG CACCTATACC      300
TTCACACACA TCCTCACATA CCCACACAGC TCTACACATA CCCACTTTCT TACACATTCA      360
CACACATACC TATAGACACA TTCAAACACA CCCNACGCTC GAG
                                         403
  
```


(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

```

GAATTCGGCC TTCATGGCCT ACTCAGAATC ATAATGAAGT CCAGTCTACC ACACCACCCT      60
TCACTACTGT TGATTACAG AAAGACTGTA GAAAATTTCC AGTTCCACAG AAGGATGGTA      120
GTGCTTTTGA GGATTCTAGC ACTTCAGGGG CATCCTGTTC CAAGTCAAGA CCACATTTAG      180
CTGGGACACA TACTTCTCTT AGACTTCCGC AGGAAGGAAA AGGAACCTGT ATTCTTGTAG      240
GTGGTCATGA AATCACTTCT GGATTAGAAG TAATTTCTTC CCTAAGAGCA ATTCATGGGT      300
TGCAAGTAGA AGTTTGTCTT CTTAATGGCT GTGATTACAT CGTGAGTAAT CGCATGGTGG      360
TGGAAAGGAG GTCTCAATCT GAGATGTAA ATAGTGTCAA TAAGAACAAG TTCATTGAGC      420
AGATCCAGCA CCTGCAGAGT ATGTTTGAAA GAATATGTGT GATTGTGGAA AAGGACAGAG      480
AAAAACAGG CGAAACTCGA G                                     501

```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

```

GAATTCGGCC TTCATGGCCT AGGACAACCTG TGATATTTCA GTTCCTGATT GTAAATACCT      60
CCTAAGCCTG AAGCTTCTGT TACTAGCCAT TGTGAGCTTC AGTTTCTTCA TCTGCAAAAT      120
GGGCATAATA CAATCTATTC TTGCCACATC AAGGGATTGT TATTCCTTTA AAAAAAAACC      180
AATACCAAAG AAGCCTACAA TGTGGCCTT AGCCAAAATT CTGTTGATTT CAACGTTGTT      240
TTATTCACCT CTATCGGGGA GCCATGGAAA AGAAAATCAA GACATACACA CAACACAGAA      300
CATTGCAGAA GTTTTAAANA CAATGGAAAA TAAACCTATT TCTTTGAAA GTGAAGCAAA      360
CTTAAACTCA GATAAAGNAA ATATAACCAC CTCAAATCTC GAG                                     403

```

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

```

GAATTCGGCC TTCATGGCCT AGGTGGGGGG CTTTCTGCAC AAAAAGGGAG TAAGTCCACG      60
CTATACCTGT GCTCAAATAA CAGCGCCATT GATGCTTGG CANACTTGGG ANGACATTCC      120
TTCTGCAAGA CTTGNTGAGC ATATTTCTGA GCTCTCTTTA CATGGTCAGG GTCCACATAA      180
TGCATTTTTT TCATGTCACA TTCTTCAGTA GTATAATTTA ACTTGAGGAT ATAAAGGATC      240
CACACTCCAA ACACAAGCAA TGTACATTG AGGATGTCTT TTAATNACAA GCTGGGCCTT      300

```

CTCATCTTGC TTTGAGCTCG GGTGTACCAT TGCAGGGAGG GCCTCGAG

348

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | TTTCATGGCCT | ACAGAATTGG | CAGCACAAAG | AAAACGCCCT | CTCCTGACTT | 60 |
| GTATTGTGGC | AGTCTGAACG | CCCCCAGAAA | ATTGTGCCAA | AGAGTTTGA | AAAATAAATA | 120 |
| TACAATAAAA | GTAAACACAT | ACACACAAAA | CAGCAAACCT | CAGGTAACCTA | TTTTGGATTG | 180 |
| CAAACAGGAT | AATTAAATGT | TCAAACAATC | TGATAAAATA | ACCATTGGA | AACCTGCTTG | 240 |
| CCTTCTGTTT | TTTTATTGTA | TTGACTACAA | TGCGGTATTG | GTCTCTTGCT | GCACTTCAAA | 300 |
| AGCAACCAAC | AAAACCCTCG | AG | | | | 322 |

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | TTTCATGGCCT | AGCCATAGAA | ACTGCCTCTT | TTTCATGTGGG | ATGAAGACAT | 60 |
| CTGTGCCAAG | AGTGGCATGA | AGACATTTCG | AAGTTCTTGT | ATCCTGAAGA | GAGTAAAGTT | 120 |
| CAGTTTGGAT | GGCAGCAAGA | TGAAATCAGC | TATTACACCT | GCTGTACACA | CACTTCCTCA | 180 |
| TCACTGCAGC | CATTGTGAAA | TTGACAACAT | GGCGGTAATT | TAAGTGTGA | AGTCCCTAAC | 240 |
| CCCNAAACC | TCTAAAAGGT | GGATTCTCT | AGTTGGTTTG | TAATTGTTCT | TTGAAGGCTG | 300 |
| TTTATGACTA | GAATTTTATA | TTTGTTATCT | TTGTTAAGGA | AAATAGAGGA | ANNCAAAGGG | 360 |
| ACTCGAG | | | | | | 367 |

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTTCATGGCCT | AGACTTCCAC | AGAGACCTAT | CTGGAACCTC | TGGTTCCTTA | 60 |
| CCTCTGCTTC | TGTCAGAGCA | GCTCTGGGTT | TTGGTTTGT | ACTATTGTAC | ATATTAGGCT | 120 |
| TCTATACAAG | AAGAAGTGGT | CCCATTGGTT | TAAAAATAAG | TTTGAAAATC | CTAGAAACAG | 180 |
| TGAGAGTCAG | AAAAAAAAC | TGTTTTTATA | TACATATTCT | CTCCCCCACC | CCCTTTCTCT | 240 |
| CCAGTTGAAA | TATGTTGCAG | AGCTCTAAAT | TAGGGATGC | TTTGGCGTA | TTTCTTATAC | 300 |
| ACTCCAGAGG | CACTCGAG | | | | | 318 |

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

| | |
|---|-----|
| GAATTCGGCC AAAGANGCCT AGGTTTGAAA ACTCTGCTTC CTTTGTGAAT TTGGTGTAG | 60 |
| GAGTTCTTAT TGTATTCTG CAGCCTTTAC TATTGTCCTT TATTTACTGA ACACAGTGAA | 120 |
| TACCAAGCAC TGTTTATTAG AGGTTAGGAG TAGGGGCAGG TGATTAAAA AACAAAAAG | 180 |
| CTAATAATCT CCTCAAGCAA TTTCTGGCCT AATAGAATTA TAGTAGACAG TGAAGTATCT | 240 |
| AAACCCAGGG AATCAGATTG AGGCACCATG TCCATCGCCT TGAGAATTAA TAGGCTGCAT | 300 |
| TTCTGGGTTT TCCNTTTTTT TTTTTTTTTT GCCCAACTGA GTCTTTCTGT GGACTTACAT | 360 |
| GGAATTCTT ATTCTCTTAA ATCATTAACT TACTTGACAA TATCTTGGA TTTGGAGAAA | 420 |
| CTGGATGTAG GGCCGTATGA AAAAATCATT CGAAATCAGA ATCTCGAG | 468 |

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTATTGC CAAACTTCTG AATAAACTGA AACAGCAGCA | 60 |
| ACAGCAGCAA CAACAGCATT CTGAAAATAA GAGAGAAAAC TCTGAAGATC CCGAGGAATC | 120 |
| TTGGGAAAAT TTAGTTTCGG ATGAGGATTT TTCTGCACTG TCCTTGGAAT CAGCAAATGT | 180 |
| GGAAGATTG GAACCTGTGA GAAACCTCTT TAGAAAGTTG CAAAGCACAC CTAAGTATCA | 240 |
| GAAACTTCTA AAGGAAAGAC AACAGCTACC TGTATTAAA CATCGGGTCC TCTCGAG | 297 |

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAAATACTG GGAAAAGGA CACTTACTGT GTGACTTAAA | 60 |
| TTGATTAAAG GGTATTTCAG TTCAACTCTC TTGAATCTAA TTAGTATTTT TGTGTCATTT | 120 |
| ATTATTATAG GGCACACATT TTTTACATT GATTAACTT GACCAAAATT AAATGAGCAA | 180 |
| ATGTTTATTG CTATGTCCAT TGTTTTCTT TCTCTGTCAC TGTTAAAAAG AGGAGCCATG | 240 |
| GCTTCTGCTT CTCTGTGTA TTCTCCATTA GACCTTCTTC ATCCACCCTC TTCCCCATCC | 300 |
| CTTTCAGCTC TGAAGGGTCC TCTCGAG | 327 |

(2) INFORMATION FOR SEQ ID NO:715:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

```
GAATTCGGCC AAAGAGGCCT ACTTCTCCAA GCATTCATGT ACATCCTTGG GATCTGCCTC      60
ATCATGGAGC TCATTGGTGG CGTGGTGGCC TTGACCTTCC GGAACCAGAC CATTGACTTC      120
CTGAACGACA ACATTCGAAG AGGAATTGAG AACTACTATG ATGATCTGGA CTTCAAAAAC      180
ATCATGGACT TTGTTCAAG AAAGTTCAAG TGCTGTGGCG GGGAGGACTA CCGAGATTGG      240
AGCAAGAATC AGTACCACGA CTGCAGTGCC CCTGGACCCC TGGCCTGTGG GGTGCCCTAC      300
ACCTGCTGCA TCAGGAATCT CGAG                                     324
```

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

```
GAATTCGGCC AAAGAGGCCT AAAGGGATTT AAAACCTCTG TAGAGGCTGG GCGCGGTGGC      60
TCACACCTGT AATCCCAGCA CTTTGGGAGG CCAGGGCGGG CAGATCACCT GAGGTCGGGA      120
GTTTCGAGACC AGCCTGACCA ACGTGGAGAA ACCATGTNTC TCTACTAAAA ATACAAAATT      180
AGCCAGGCGT GGTGGCACAT GCCTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA      240
TCACTTGAAC CTGGGANGTG GAGGTTTTGG TGAGCTGAGA TCGTGCCATT GCACTCCAGC      300
CTGGGCAACA AGAGTGANAC TCCATCTCNA AAAAAAAAAA AGAAGAGTTT ACACGAAGTC      360
ACCTCTATTT CAGAAGATAA TCTAGACTCT ATTCCCTCAG AGTCTTTTTT CTCCCCAAAG      420
ATAACACTGT CCTAGGTATT TCCTCATACC CCCAGGCCCA CAGTTCATGG CCCACATGTC      480
CCCTGTAAGC TCGAG                                     495
```

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```
GAATTCGGCC AAAGAGGCCT ATTTTTTAGA TCATCAGCTA TTGTTAGTGT TTGTGTATGT      60
TATGTGTGGC TCAAGACAAC TTTGCTTCTT TTAATATAGG CAGGGAAGTC AAAAGATTGG      120
ATATCCCTGC TTTATACCAA GAAAGACAAC ACCCCACATT TGCAGTGCCT GAAAAACTA      180
CCAGCCATCT GAAAAACATG TGACTTCTAA CTTCTGTTCT TTTTGTAGC AGTGAATCC      240
CACGGTGATA TCTGAGGGAT GTGGTTACCT TTTGGAGGAG GTTGACGGTT TCTAAGGATG      300
ATTCTTTCTG AGTGAAATAT TGTCAGTGTC ATTGACCTTT TCATTATTTT AACTATTATT      360
ATTCCAGGTT ATCAATACTC TGGCTGACCA TCATCATCGG GGGACTGACT CGAG                                     414
```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

```

GAATTCGGCC AAAGAGGCCT AGGATGAGAA TGA CTGTGCC TCATTGCATC TTCCTGGCTG      60
CCTGATGGGC AGAAAACCTG GGTCTCCTCC CCATTTTAGG AATGGAAGG CTGAGTCTCT      120
GCGATGAGCC TTCCTCAGGG ATGGTGAGGG GCCGGCCCGG CACTAAGCCC CATTCTCTGA      180
GTTAGGACCT GTAGGAGGGT GGCAGGGGCA AGCGGGGCAG GTGGGTGGCC CAGGCAACTT      240
TGCAACATC TTCCTTTTTT CCGGGAGAAG CAAACGCGCT GTGTGGAAAG GCACATTCGG      300
AAGATGGAGT TTCACATCAG CAAGGTCAGC TGGCTCGTGG ATGTTGCAGG GTGGGGTGGG      360
GCAGTGCCAG CTGCTGGGC CTCAGCTAGG TTAGCAGGAG CTGGGGAGGT GCCCTCGAAG      420
CAGGGATCAG GGCCTCTGGG TATGTTGCAG GCTCGAG                                457

```

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

```

GAATTCGGCC AAAGAGGCCT AACTGTCAGA AGCTGTTTTA TGCAGAGATA AATTGGAAGA      60
ATGGTCAGCC TCTTAAGCTA GCTTATTCGA AGAGGTACTG GAAAAAATAT GGCAAAGACT      120
TCAACGACAT ATGCCAAAAC TTTTCCCTT GGAAATCATT GACTAGCATC ACTGAATGTT      180
ATTTCTTGTG GAGAACTACT GACAGATATG TGCAACAGAA ATGGTTAAAA GCAGCAGAAA      240
CTGAGAGTAA GCTGAAACAA GTATATATCC CAATTTACAG GAAACCAAAT CCCAACCAAA      300
TATCTACCAG CAATGGCAAG CCTGGTGCTA TGAGTGAAAC CATGAGGTTG ACATTCCTGC      360
CTCAGAAATCC CCTGTAGTG CAAGCCTGGG AGGGCTGCTG TGCTACACAG TCTAACCAGT      420
AGTATTCTTG GGGCCACCT AATATGCAGT GCAATTTGTT GGCTTTATTG AGAAAAATAT      480
GGAGACCTGA AAATGCCAC CCGCTCGAG                                509

```

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```

GAATTCGGCC AAAGAGGCCT AATGTGTAGT CATCTGGGAT ATGCTAGCAT CACAGTTACC      60
TGGAGTCATC TTGAATATGG AGATGACAGG GACTGATTTT GCAGATTCGT TGAGTTGGTG      120
GGATATGTAA ATATGTTTTT CACCAACAAA TCAGATATTT CTGTTGGGCA GCCAAGTGTA      180
ATAACCATG CTGTAAATGA TCTCTGTCCT CTCCAAATCA CATGATTAAT TAAATTATGT      240

```

GAATGCCTAG TTGACTGCTA GGAATGCTT GTACTTTGGA AATATTTTAA CCAAGGACAC 300
TCTAGAAATT CTCTTGCTCT CCCACCTCAA CAGTGCAACT CGAG 344

(2) INFORMATION FOR SEQ ID NO:721:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

CGGTAGAGAG GCAGAAGCAA GAGAGCTACG GTTCAGGTTG GGCACCACTG ATGCCACTGG 60
 TTCTCTGCAA GGCGATTCCA TGACAGAAAC CGTAGCAGAA AACATCGTTA CCAGTATCCT 120
 GAAGCAGTTC ACTCAGTCTC CAGAGACAGA AGGCATCTGC TGATTCTTTT CCAGACACAA 180
 AAGTCACTTA CGTGGACAGG AAAGAGCTTC CTGGGAAAAG GAAAACAAAG ACTGAAATAG 240
 TTGTGGAGTC TAACTGACT GAGGATGTTG ATGTTCCGA TGAAGCTGGC CTGGACTACC 300
 TTTTAAGCAA GGATAATAAG GAAGTTGGAC TCGAG 335

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GGAACACACC TGTGGTGCTA GTGTTGGGAT CGGGGGCCTT TAACGCTGGT GGGCAGCAAT 60
 AAGGGGCAGA TGTGCCCAGA TGCCTGCATC CCCAGGGTGC CGAGGGCAGC AGGAAAAAGT 120
 GGGGACCTCG GTGCATTTCG CCCACCCCTC CCCTCCCTGG GCTAAAGCAC AATGTTCTCC 180
 CCGCAGATTA ATGACCCTGC ACCCTCCAGG CCCCTACTCA CATCCTCCCC CAACCGGCTT 240
 CGGGTCTTCC CACCACACTC TGGTTTTCTA TGCTGTTTTG GTGCAAGTAC AACTGTCGTA 300
 GTCATGGCTT TGGGATGGGT TCTGTTTATT AAAATCCTAT TACTCGAG 348

(2) INFORMATION FOR SEQ ID NO:723:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GAATTCGGCC TTGATGGCCT AGTAGTTGTT CCATGCTGTT GTTTTTTGTT TTATCTTTCA 60
 TTGCCTTTCC CTCTGCAGTC AACATTATGA CCTGGGGACT CCAGCATCCT TCAAGCAAGC 120
 CATTTCCGAA GAAGGTGAAA AGAAGCCAGG ATGATTGGCA CCTCCTCCTC CTCCTCCTCT 180
 TCTTCCTCTT CCCTTGCCCA GCCCCCTCCT GTGCGTGTGT TTCAGACAAC ACAGGAGCCA 240
 GCACAGGAGT GGAAAATCCT GTAGCGCAAC TCGAG 275

(2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

```

GAATTGGCAT CTTTTCATTG CTTTGGCCCT TTGAGAGTTG TTTAGTTTTT TAAAAGTCAG      60
ATAATTTTGG ATTATATTCT AGACCTTTTG AATATTATGT TATAGGACTC TGGAGTCTGT      120
TAAAATCTTT AGGAAGACAT TAATTTTTTG AATTTTAACA GACAGAAGTC CTTGTTATAT      180
TGATCCATTG GTTTGTTCTA CACTTGTGCA CCTTGGAGAT GAGTCTGACT TCATATGCAG      240
AATTTAGTAT CCCTTCTTGG AGCTCCCTCC CCTCTGTGAT CCTCCCCATT CTTCTTTTCT      300
CCCAAGAACT TCTCGAG                                     317

```

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

```

GAATTCGGCC TTCATGGCCT AGGGTCAGTG AATCTGCATT ATTACATAAA AAATAAGGCA      60
GAGGAAGCAA TCAAATATGC GTTTGTCTCT GGTGAGCCTC AGCAGGGATG ACTTTGAGTT      120
CTGTCTGTCC TTTGTCCACA AGGAATTTCC TTGTGGAAAA TTGTGAAGGA GGTATGTGCG      180
TTCTTAACTC TGTACCTATC TTATTTAGGA ATAAAATGGG AGGCAGGTCT GTCTGACATA      240
GTTCCCAATT TGAATTTTCC CCTGACTTAG TGATTTTGAG GTCTCGAG                                     288

```

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

GAATTCGGCC TTCATGGCCT ACACACTAAT AGGATTGGAT TTATGTATGT CCAGCTTGGG      60
AATTATTACA GGAATTAAAA ACAACTTTTT AGAGTGCTTT CCTGAGCTCT CTTTCTATTT      120
GTTCCCCCTT CTAATTTTTG CTTCCCTGTG GCTGCTGTTT CTATCCTCCA GCCAGAGAGC      180
TAGTGTATTAT TTTCTCCATT GTGTTACACA CTTGTGCAGC TGCAACCACC ATATCCAGGG      240
GCTCGAG                                     247

```

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAATTCTAG ACCTGCCCCG GTCTTCCTCC TCGTCCTGCC | 60 |
| GCAGGGCCAG AACCCCTGAC GGTATTCAGC TCGCGTAAG TCTGGCCGGT GCCATCTGTC | 120 |
| TCCGCAATGC CCCCCAAGAA ACAGGCTCAG GCCGGGGGCA GCAAAAAGGC GGAGCAAAAA | 180 |
| AAGAAGGAGA AGATTATCGA AGACAAAAC TTCGGTTTGA AGAATAAGAA AGGAGCAAAG | 240 |
| CAACAGTTAT CTCGAG | 256 |

(2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGTGCTTGC GCTCTAATAA CCATGTTTAT CTCATGCCTT | 60 |
| TGGGCCTTTG CATATGTGTT TCCTCTGCTG ACACCAACCT CCTCCTCCTC CTCCTCCTCC | 120 |
| TCTGCTTGGC TGGCTTCTCT CAGTCTCAGT TCGGATACCT TCTCTTCTAG GAAAGCTCCC | 180 |
| CTGACCACTC TTTCTTTGGG CTTCTATAAC CCCCCTGTCT GCCCCCATCA GGGCACCTCC | 240 |
| CAAATTCAG TGTTCCTTT CCTCCTCCCC AATCTCGAG | 279 |

(2) INFORMATION FOR SEQ ID NO:729:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGAGAAACCT ATTTTTCAT TTAACCTGTT CTTTAAATCC | 60 |
| AGTATGTTCC AGAACATACA AAAATGTTTA AATGTCCAT TTGTAAGAGG ATATCATGTA | 120 |
| TTTTATATCA ATTTAAATGC AGTTATCCTA ATCATTTTTC TTTCATTTT ACCCTTTATT | 180 |
| AATCTTTCAT TTGTTTACAA AACAAATCCA CTCTATAAAC GCAATCTCGA G | 231 |

(2) INFORMATION FOR SEQ ID NO:730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACACACATAA TTAGTTATTT TACCATTCTT TCATAGTTTT | 60 |
| AAGAGCAAGT TTTCACAAGG GCGATTTGAA TTAGAGGGTA GAATAATATT TTAATAATCG | 120 |
| TTTTCTATTA TTCAAATATA GAATGTTATT AAATTTTTTG GTATCGCTGG TTAAGTGCCT | 180 |
| AGAACTTGAT CATCTTCTAT TTCTTTTCC TTTTGGCTAT GAGAAAAATA ATGCTCAGAG | 240 |
| AAGTATACTC GAG | 253 |

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGAGACTTA ATTATTAACA AAGTATTAGA AGCTAGAAGT | 60 |
| AGGTAAATA AGTGATTATT TTAATAAAAA TTATCCTTAC TTTACAAAAT CCATATTAAC | 120 |
| CTCACTTGAA ATTTTATGAG CTTTTCCTAT AAGTTTAAAG AGATAGAAAT CAGTGAAAGA | 180 |
| CCTCAGTAAT TCCTGCAATG ATCTTAATAG AAAATATTTT ATACCTTCTC TCCCTCGAG | 239 |

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AAATAAATAT CTCATTTTAA TTGTTACTTT GTTGACTTG | 60 |
| ATTACTGCAA ACCTATCACT AATCTTTCT GAGTTCACCG AAAGAAGTGC AAAACCCCTC | 120 |
| AATATATTAC CATCATGTGC TTCTTCTGTC CCACTCTTTT CCTAGAGAC ATTTTGTTTT | 180 |
| TGTTGTTTTT AATTGGTATT GTATTGTTTT TCAAATCTTT GTCCCCCAG GCTCGACCTA | 240 |
| TAGTGAGTCG TATTAATTC AG | 262 |

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACACACATAA TTAGTTATTT TACCATTCTT TCATAGTTTT | 60 |
| AAGAGCAAGT TTTCACAAGG GCGATTTGAA TTAGAGGGTA GAATAATATT TTAATAATCG | 120 |
| TTTTCTATTA TTCAAATATA GAATGTTATT AAATTTTTTG GTATCGCTGG TTAAGTGCCT | 180 |

AGAACTTGAT CATCTTCTAT TTCTTTTCC TTTTGCTAT GAGAAAAATA ATGCTCAGAG 240
AAGTATACTC GAG 253

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

GAATTCGGCC TTCATGGCCT AGTATCACAG GCTTTCTTCA AATAACCAGT TCCTCTAAGA 60
CATTGAAAAT ATAATTCGGT GTTTAAAATA AATTCATACC CGTTTTGTGT GCTGTGCATA 120
AATAGCAAGT ATATGTGTAC CTTACCAAAC TTATGGTCCC CAGTCCCCAA ATTCCAAAAT 180
TATGCAGGAG GGAAGGTTAG CCATTGCAGT AAACAATTTC TCCCTATTGA CCCATGCTCT 240
CCAGCTGATT ATGATGTGGG CAGTACTCAT CCAAGGCTAT ACAGACCAGC CGGGTCTCGA 300
G 301

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTTGAAA TCCCTCATCT 60
GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG 120
TAACCTAGGG TTTTCAAATT ACAGAAGAGG AAGAACAATG GAGGCTGATC TCCAGTTTGT 180
GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA 240
G 241

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GAATTCGGCC TTCATGGCCT AGTGTCTTCTA TCTTCCAATT TTCTTCTAAG TTTGTACATT 60
TTGCCCTTAG CTTTTTGTCT CTTAGCTTGT CTTTTTCTT CTGCTTCCTA CTTTTCAGGT 120
TTAAATTTAT CTTTTTCTT CTAAAAGTAT GTTTTTATCT TCTAATTTCC CTATCTTCTC 180
TATTCTTTTC TTGCGCTTCC CGTACTTCTG TCTTCCAGTT TTACACTTCA AACTTCTATC 240
TTCTCCAAT T 251

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

```
GAATTCGGCC TTCATGGCCT ACAGGGTTGC TGGGATGATC AGTGATTTTG CTAATATCAA      60
AAGTGCCCGAG CACAGTGCTT GGGTTGTTGG AGGCATTGAA CACACGGCAT TGTTATTATT      120
TATATGCCTT GTAACGGAA GAGCCTGTGG GCAAACAGTG GATGCTAAAA TTCAGTTTGT      180
GGAAGAACCA GGTGCACAAA CTCCTGTTCT ACCTGTGGTT GAGTCTACAC TCCCCACCA      240
CACCCAGCT GCTCTGATCT ACCTCCTGTT CCTTGAGCAG GCCATTTTCT TTCTTGCTTC      300
AGGGCAACTC GAG                                         313
```

(2) INFORMATION FOR SEQ ID NO:738:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

```
GAATTCGGCC TTCATGGCCT AGTGTGTTG TTCCATCTGG TTTTCTTCTT TCAAATTCGC      60
ACTGACTGTT CACAAGCCGC CTGGTCAGCT TTCTCCAGA TTCCTTCAGC ATGCGGTCAA      120
GCTGCTCCTG CTCTCTCTCT AAATTATTGC TTTTAACTT ATCTTCAAGC ATATCTTTGT      180
CTTTCTTTT ATTTTCTTTG CTGGGACTCT TGAAGGCGTG TGCTTCGGCA TCTCCAGAGT      240
CCTCTCTCTC TCTCTGCCAG CAGCCTCCGT CCTCCCCACT CTGTGAGGTG TCTGTTCTCG      300
AG                                         302
```

(2) INFORMATION FOR SEQ ID NO:739:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

```
GAATTCGGCC TTCATGGCCT AGGACTGTAC CAGCGCTATA CTGTAGTTAT TTTTAAAT      60
GAACTTCACA TATTTTGTA TTCTTTCAA TTGTTTGCTA TATATAAAG AAGCTCACTG      120
CAAAATGCTT GAAGGAAAAA AGGAAACAAA AGAAATTCAG AACTTCCAG AAATGTACAG      180
CTTTTCGGCC TTCATG                                         196
```

(2) INFORMATION FOR SEQ ID NO:740:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

```

ATGGCCTATG CCTCCCCACT CCACCCACCT CTGCCTTCCT TACTGCTGTA TCTGCTGCTT    60
GAACTGGCAG GAGTCACACA TGTGTTCCAT GTGCAACAAA CGGAGATGTC ACAGACTGTA    120
TCAACTGGGG AGTCAATCAT CTTGAGTTGC AGCGTACCCG ATACCTTACC AAATGGACCT    180
GTCTGTGGT TCAAGGGAAC AGGGCCAAAC CGGAAATTAA TCTACAATT CAAACAAGGT    240
AACTTTCCCA GAGTAAAAGA GATTGGAGAC ACCACCAAGC CTGGCAACAC AGACTTTTCC    300
ACACTCGAG                                     309

```

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

```

GAATTCGGCC TTCATGGCCT ACTGAAGGTA GGTGAGTTCA TCCTCTTCAT AGTAATGCTG    60
TTTTACCAAG ACTTTATAGC AGATGGACCC AGAAAGAATT TTCTGCTATT GTGTCTACTA    120
CAACAGGATA GGGACATCAG ACAGCCCCAG AAACCCCTTC CAGATCTGAT ATGGGACTAT    180
TAATTTTAT GCTGTTAATT GGTATTCATT CACAATGCAG TTGAAGGGGG AAGGCTCCAC    240
TGCATTCTTT GGCTAAGGCC TGAATGCTTG CTCATCTGTA AGATCTATAC TCGAG        295

```

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```

GAATTCGGCC TTCATGGCCT ATAAAAAGTG GGCCAGTTTA AAGAAAAATT TTATCTAAGC    60
AGTAGTACAG CTGGCTTCC AATATGGCAA AATAAGTCTT TCTGTAGGAG ATATCACCAT    120
TTTGGCAGGA TTGAAAAGCC TCTGTTTTG TGCCATATAA TCAAACTATA TCTGTGATTT    180
GAAAAATGAC AAAGGGTATA ATAATTCCTA GAATTGGTTT TAAATGAAG GAAAATAGTA    240
TCCTAGTTCA AAAGTTATGG CTCATTGTAA GTGCTGGTCT GGTATAACCA TACAGATTGT    300
TTAAATCTT TAAATAAATA CTGGCCCAA TCCCTTTTGT TCCCCCTTC TCGCTGCCCT    360
GTAAACTCGA G                                     371

```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

| | |
|---|-----|
| GAAATGACTC TAGCCTGTGG AAAGAGAATC ATAATTCTAC GGACCTTTTA AATCCGCCAG | 60 |
| GAACCCTGAA TATCTATCTT TTTTGCTTGA CATGTCTCAT GACTTTTGCA GCCTTGGTGG | 120 |
| GCAGCATTTA TTCACTAATT TCCCTGCTGA AAATGCAGAA CAGAACTGTT GTGTCCATGC | 180 |
| TGTGGCTTC CTGGTCTGTG GATGATCTCA TGAGCCTCTT GTCGGTGACC ATCTTCATGT | 240 |
| TTTTCAGTG GCCAAACGAG GTCCCCGTT ACTTCCAATT TCTGTGCAAC ACCTCTCGAG | 300 |

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACCCTAAGAG AACTTCCTG GTGATAATCA CAGGGTCCAA | 60 |
| AAGTAAAGGA AACCTGGCAG TCTCTGGTGT CCATCATGTG CTTATTCCAC TTGGTAAAAT | 120 |
| AATTGAGAT GCCTTCTAGT AAGGAATGGA CCTTAGTGGT GATGGTTAGT TGCGTTATGA | 180 |
| TGACAGCCAC TGGGTTGGAG TACTTAGAAA GCTTCCGAGT ACTAGACAGC TCCACAACCTT | 240 |
| CTTCAAAAGT ATCCATGGGA TACAAAGGCT TAGGATCATT GAGACACTGA ATCAAGGGCT | 300 |
| CAATCTGGTA AAAATCTGCT TCTTCCGAA GCAGATCAAA TTCCTTAAAA TCCNACGGTA | 360 |
| AGGTCAATTC TGAAGTTCTT AAGAAGTTGA GGACATATCG GAAAAGAGGT CCATCTCGAT | 420 |
| CAATAAAGTA ATTGCCTTGA GGGTCTCGAG | 450 |

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTTATTAAC CCCAATCAAT AGAGTTGAGA GACTATGGCT | 60 |
| TTAAAAAATT AATGCAAACC TGGCTTTAGC TGTAATAACA CCCACCGTAA GCACTTGGAC | 120 |
| TTAGTTATTA TAGACAAATG TAAAGAAAAT TTAATGAAAA ATAACACCTT CTCTCTTAA | 180 |
| AAAAAGAAGT CTCAGGCAAT AGATGCCTGG TACTATGAGG AAGAATGTGA GAAATAGAAG | 240 |
| TGAAATCCCA GAGAAGCCCN AAACCCCA ATCTCGAG | 278 |

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

```

GCAATATCAA ATAGCTAACT TCACCCCAAA CCACAGTCCT TGCTGTGGC ATTTACTCAA      60
CTAGTCTTTA ATTCCTGTTT GACAACTTT ATAAGGTGCT ACAAGACAGA TGATTTTTC      120
CCATCTACCA TAATGTGGAA CAGATATTTT GTCTTCTATC TCCTGCTTTT GTCAGCGTT      180
ACGAGTCAAA CAGTATCCGG ACAAAGAAAG AAAGGACCAA AATCAAATTT GCTTGCAAGG      240
AAAAGTGATG TCCAGGGGCA CCTCGAG                                         267

```

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

```

GTTCTACCTG GAATATGGTC CTTCTACCTG GAATATTTTT TCCTCAGGCC TTCTCTGGCT      60
TCTTCTTCTT TTATTCCTTG GATCTCAGCT TAATCATCTC TTTGGCAAGT ATCCATGATC      120
CAAACTGGGT TAGTGCCGCT CCAAGACCC CCTTTATTAA CCCTGTACTG GCACTTAAAA      180
CATACTCTAT TGATTTGCC AGCTCCTTGG CCTGTCTGCA AGTTCCTTCA GGCATGCTGC      240
CATCATCTC ATTTATCACT GTATCTCTCTG TGCCAGCAG TCTCGAG                     287

```

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```

GAATTCGGCC TTCATGGCCT ACTTTATCTG CCTCTACACT CTCTTCTGGT TATTCAGGAT      60
ACCTTTGAAG GAATATTCTT TCGAAAAAGT CAGAGAAGAG AGCAGTTTTA GTGACATTCC      120
AGATGTCAAA AACGATTTTG CGTTCCTTCT TCACATGGTA GACCAGTATG ACCAGCTATA      180
TTCCAAGCGT TTTGGTGTGT TCTTGTGAGA ACTTAGTGAA AATAAACTTA GGGAAATTAG      240
TTTGAACCAT GAGTGGACAC AAGAAAAACT CGAG                                         274

```

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

```

GAATTCGGCC TTCATGCCTA GGCAGTTTTT GTTGCTGCC ATTTTTTTT TTTTTTTT      60
CATATCTCAT TATATATTTT TTGTGATCTT TGGAAGTGA ACATTTTACA GAATACATTA      120

```

| | |
|---|-----|
| TAGCAACTCT GAGTAACCTT CTCCCAGGTT TATTTGTATT TGCTCATTGC TTATTTATTT | 180 |
| ATTACTAGCT GGGTTTTTTT AGTGGCACCT ACTCCTCTCC CCACTTAACC CTCTGATGTT | 240 |
| ATGCTTGTTA TGCCTGATCA GGGCAGTTAC GGATTGAATT GTGTCCACTC AAAATGTATA | 300 |
| TGCTCATGCA CTGACCTCCA GTGCCTCAGA ATGTGACACC TCGAG | 345 |

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ATAGAGTAGT GATTTTGGTC ACGGTGTGTG CTATTTCCGGT | 60 |
| GTTTCAGTTT TTCAGCTGGT GGAATAGCTA CAATAAGGCA ATCAGCTACC TAGCCACAGT | 120 |
| GCCCAAGTAC CGTATCCAAG CTACAGAGAT TGCCAAGCAG CAGGGACTGC TCAAAAAAGC | 180 |
| CAAAGAAAAA GGCAAAAACA AAAAGTCCAA AGAAGAAATT CGTGACGAGG AGGAGAACAT | 240 |
| CATAAAGAAC ATTATAAAAA GTAAAATAGA TATAAAGGGT GAACTCGAG | 289 |

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACGTAGGCAG ATGGAGCTTG TTATAATTAT GCCCCATAGG | 60 |
| GATAGTACAA GGAAGGGGTA GGCTATGTGT TTTGTCAGGG GGTGAGAAT GAGTGTGAGG | 120 |
| CGTATTATAA CAAGCTCCAT CTGCCTACGA CAAACAGACC TAAAATCGCT CATTGCATAC | 180 |
| TCTTCAATCA GCCACATAGC CCTCGTAGTA ACAGCCATTC TCATCCAAAC CCCCTGAAGC | 240 |
| TTACCCGGCG CAGTCATTCT CATAATCGCC CACGGGCTTA CATCCTCATT ACTATTCTGC | 300 |
| CTAGCAAAC TAACTACGA ACGCACCTT CTCGAG | 336 |

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGGAAAGAA GAGCAACTTT GTCAGCTTGA GAAGGAACAG | 60 |
| AAAGCCGCCC TTCCAGCTA TTTCCAAAAT AGAGTCTGCC TTAACTGTG GATGTCCGAG | 120 |
| GTTGCGCTGA TTTTCAGGGC TATTCTCAA GAGAAAGGCA GAGTCAGTCT TCCTGCCTTT | 180 |
| CTACTCTCAG GCCTCTTTCC TGAGTGCTAG AAGGAGCTCT TTTAGTTGGT TTATACCTCG | 240 |
| GGACCCTTAT TTCCCTCTCA CCCTCGGCCC CAATCTCGAG | 280 |

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

```

GAATTCGGCC TTCATGGCCT AAGAAGAAGT AACTGCCTT GCCTGGACTA TTTCCAATGA      60
TGCCAAACAA TAATTGTTGC CCCTTGCTT TCTTAAAAGG AGACTGCATC CATTAAACCA      120
AACTAAGAAA TTTCAATTA GTCCTCTGCT GAAGTCATAC TATACACATC TACTTAATTA      180
AAGATACATT TATTGAAGAG AACAGGTCTC CTCCGGGTTT ATCTGCTATA GCCTTGCTTA      240
GGAAAGGAAT AATAGTCTGT CTTTAAATTA GGTGTGGCTA TTGATTGGAG CAAATGTTGT      300
CAGGTGGCCC AAGCATGAAT CAATGAGTGA CCATGAGGTC ACCCATCAGT GAGGGCACCC      360
CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

```

GAATTCGGCC TTCATGGCCT AACCTATTTG CCTCAGTCCT ATCTGATTCA TGAGCACATG      60
GTTATTACTG ATCGCATTGA AAACATTGAT CACCTGGGTT TCTTTATTTA TCGACTGTGT      120
CATGACAAGG AAACCTACAA ACTGCAACGC AGAGAAACTA TTAAAGGTAT TCAGAAACGT      180
GAAGCCAGCA ATTGTTTCGC AATTCGGCAT TTTGAAAACA AATTTGCCGT GGAAACTTTA      240
ATTTGTCTT GAACAGTCAA GAAAAACATT ATTGAGGAAA ATTAATATCA CAGCATAACC      300
CCACCCTTTA CATTGTTGTC AGTGATTATT TTTTAAAGTC TTCTTTCATG TAAGTAGCAA      360
CGGGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```

GAATTCGGCC TTCATGGCCT ATGGAAACT ACTCATTTCAT TCTTCAGAAC TGTTTTCAGG      60
ACTTCAAGGA GGCCTTCCCT AACCACCCTA TTAAACATTC CAGTTCTTGC ACCATCCCCA      120
CCCCTACTCT GCCCTCACTT TTTCTCCAT GGCCTGGGC ACCAGCTGGC TAACTCTGTC      180
TTCAAAAGT ACTTTTCTTT GGGGGAGGTT TTTCTTTTGT TTTGTTTTTC TTTCTTTCAG      240
TCCTGTATCT TCAGCACTTA GAAGAGTTCA TGGCACACAT CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:756:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

```
GCGCCGAGTG GGACAGCGCT GGTGCGGAGA CTGCTTCCGG ACTCCAGGTA CCGCGCTTGG      60
CGGCAGCTGG CCCAGACTT CTGTCTTTTC AGCTGCAGTG AAGGCTCGGG GCTGCAGAAT      120
TGCAACCTTG CCAATGGACC TGATCGGTTT TGGTTATGCA GCCCTCGTGA CATTTGGAAG      180
CATTTTGGGA TATAAGCGGA GAGGTGGTGT TCCGTCTTTG ATTGCTGGTC TTTTGTGTTG      240
ATGTTTGGCC GGCTATGGAG CTTACCGTGT CTCCAATGAC AAACGAGATG TAAAAGTGTC      300
ACTGTTTACA GCTTCTTCC TGGCTACCAT AATGGGTGTG TTCTCGAG      348
```

(2) INFORMATION FOR SEQ ID NO:757:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

```
GCGAGGTCAG GAGCTATGGG ATGGTATTAA TACATTGGCA GAGCAACCCA AGGGGGCAGC      60
ACATGCAGTG AACTGCCATG CAGAACTCCC GACGGGCCTC TTCCCCATCC CAGAGTGGGG      120
AACAAACAGC CGTCACAGAC AAGGAAGTGG GTGCCCCCGT CCCCTCCCGG ACCCCGAGAC      180
CCAGGAGTGC TGGGCTCCGA GCAAGTCTAT TGCATGCTTT CCTGGCCAAA GCTATATGGA      240
AAGCGGGAAC AGCAGGCTGG GGAGATGATG CTGGGGGGTG GGGAAGGAAA GCGTCTCGAG      300
```

(2) INFORMATION FOR SEQ ID NO:758:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

```
GAATTCGGCC TTCATGGCCT AGAATATTTT ATTATAAATA TAATATATGA TTTTAAACC      60
TGTTTTGTG CCTCATATGC TGTCAAGTTA ATTTGTTTTT CTCGTGCCA GAGGTGGGGA      120
GGAAGGCACT CTGTCTGCTG GGTAAATGCC TAAATTCAC CACCTTCATG GTTTGGGGGC      180
AGCATGGTCA TTGTGGATAT TGGTTTTGTG GAGTTGAGG AACCTAGGAT ATAAGTTCAC      240
TCCCTCTATT TTTCTTTGTG ATTCAGTTT TCAAAAATCT TTTTCTTCT CCTTCTCCC      300
CATTGTGAA ATTACAAATC AAAGGCCTTT TTCTTTAATG TAAAGTGTAT TTATTTAAAA      360
AAAATACAAA ATAACTACA AGTCTATCTC GAG      393
```

(2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCACATTC AAGATGCCCA CNAGAACCAT CGTGTTGGGC | 60 |
| TCATGTTTAT TACTTAAGCA AGAGAGCTCT TACCCAAATT CCTTTGTTTC CCCACTGTCA | 120 |
| GAAACAACAT AGTCTGGAAC TGGAGGCCTA GAACTCTGGT TGTATTTCCT GTAGTGGGTA | 180 |
| AAAGTCNACA AAGATAATGA ATGAGGCAGT GTCTCCTCAT GCCTTCATAT TTTCTTTTGT | 240 |
| TATTTTAATT TTTTATTATT TTTTATTTT GTGGGTGATA GTAGGTATAC GTATTGTGG | 300 |
| GGTACGACTC GAG | 313 |

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

| | |
|---|-----|
| GGAAAAAAA GGTAAGATGG ATGAAAAGGA GGAGAAGGAA TTAAATACTA AGGAAACCAG | 60 |
| AATGGATCTT CAAATAGGAA CAGAGAAGGC TGAAAAGAAT GAAGGTAGGA TGGATGCAGA | 120 |
| AAAGGTGGAA AAGATGGCAG CAATGAAAGA AAAGCCTGCA GAAAACACTT TATTCAAGG | 180 |
| CATACCCAAA TAAAGGAGTG GGTCAAGCTA ATAAGCCTGA TGAACTAGT AAAACTAGTA | 240 |
| TTTCTGGCTG TATCAGATGT ATCTAGCAGT AAACCAAGGT CACTCGAG | 288 |

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

| | |
|--|-----|
| GCTCGAGGCA GGGGGAATG GCGGCTTCAG GAGAGAGCGG GACTTCAGGC GGCGGAGGCA | 60 |
| GCACCGAGGA AGCATTTATG ACCTTCTACA GTGAGGTGAA ACAAATAGAG AAGAGAGACT | 120 |
| CGGTTCTAAC TTCGAAAAAT CAGATTGAAA GACTGACCCG TCCTGGTTCC TCTTACTTCA | 180 |
| ATTTGAACCC ATTGAGGTT CTTAGATAG ATCCTGAAGT TACAGATGAA GAAATAAAAA | 240 |
| AGAGGTTTCG GCAGTTATCC ATCTTGGTGC ATCCAGACAA AAATCAAGAT GATGCTGACA | 300 |
| GAGCACAAAA GGCTTTTGAA GCTGTGGACA AAGCTTACAA GTTGCTACTG GATCAGGAGC | 360 |
| AAAAGAAGAG GNCCCTGGAT GTAATTCANG CAGGAAAAGA ATACGTGGAA CACACTGTGA | 420 |
| AAGAGCGGAA AAAACAATTA AAGAAGGAAG GNNAACCTAC NATTG TAGAG GNGGNACTCG | 480 |
| AG | 482 |

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

```
GGGGGATGCC AACATTTAAA GCAAGAGGCA GAAGGGCTCC TGCAGGAGAC AGGGAATCGG    60
GAAGGCAGCA GGTAAACTC GAG                                         83
```

(2) INFORMATION FOR SEQ ID NO:763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

```
GAATTCGGCC TTCATGGCCT AGGAATTGAA AAGAAAGGCA GAGGAGGAAA GGATTGCGCT    60
AGAAAGAGGA AGCCCGAAAG CAGGAAGAAG AAAGGAAGCG GCAGGAAGAG GAAAAGAAAA    120
AACAGGAAGG GGAAGAGAAA AGAAAGGCAG GCGAGGAGGC CAAGCGGAAG GCTGAGGAGG    180
AGCTGTTGTT GAAAGAAAAG CAAGAACAAG AAAACAAGA GAAAGCCATG ATTGAAAAGC    240
AGAAAGAAGC AGCAGAAACA AAGGCCCGGG AGGTAGCTGA ACAGATGCGT CTCGAG      296
```

(2) INFORMATION FOR SEQ ID NO:764:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

```
GAAAAGAAAC TAACCAGGAT TCCCTCAGTG TTATTTACTG GGATTGGCAT ACGTGTTCAC    60
AGGCAGAGTA GTTGATCTCA CGCAACGGGT GATCTCACAA AACTGGTAAG TTTCTTATGC    120
TCATGAGCCC TCCCTTTTTT TTTTAAATT GGTGCCTGCA ACTTTCTTAA CAATGATTCT    180
ACTTCCTGGG CTATCACATT ATAATGCTCT TGGCCTCTTT TTTGCTGCTG TTTTGCTATT    240
CTTAAACTTA GGCCAAGTAC CAATGTTGGC TGTTAGAAGG GATCTCGAG                289
```

(2) INFORMATION FOR SEQ ID NO:765:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

| | |
|---|-----|
| GCACCAAGAG ATGTTTATTA GGGCAATCAA AAGATGATTT ATTATTTTTT AAAAAATCAA | 60 |
| TGTGGCCTTC CCTTCCTCTT TCTTTTGATT CCCCTCTTTG AGTTTTTATG TGTCTCTTTT | 120 |
| GCCTTCCCTT CCCAGAGTGG AGGAGTTAGA CCTGCATTGT GGGATGAGAG GAGTTGTGGC | 180 |
| TATGTGTCGT CTGGCACCAA GAGGGCTGAG GGTGAGGTGT GGAAGGGACA GGGGGAGGAG | 240 |
| ATGGGCAGCA TTGTTAAGAG ATTGGTACCA CTGAGCAAAT ATGTTGAGAA TGATGATTGG | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

| | |
|---|-----|
| GAACTTTGAC ACCTACACTT AAATTCTGAG TCATTAAACA GGCCTACATT TATCAACTGT | 60 |
| GGAAATATCA GCCAGTTTTT GCAAACCTCT TCTTAGGACA CTAAGTTGTT TGCAGAAATC | 120 |
| ACTAGCATTG ACTGACTCAG CAACAATGTG GTTATATTCT TTGATTAACT TAGTCCTTTT | 180 |
| TCTTGGTCAA GAGTCAGTAG ACAGGACTGA AGCTTATGCC CCTTGCCCCC CCACCACCAC | 240 |
| TCCATTACTA CCACCTTGGT TTAGCCATCC TTTTCTTGAT CTGTTCTCCC CACTTCTACT | 300 |
| GTGCTACTCT ACAGACTTGC CTTGAATGTA AGAGCAACAA TTACCTTGTA AAGTCCAAGT | 360 |
| TGGGGCAGGT CACTCCCAA CTCCACAACC TCGAG | 395 |

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT GCCTCGCTGC TTTCTTTTCT CCAAGACGGG CTGAGGATTG | 60 |
| TACAGCTCTA GGCGGAGTTG GGGCTCTTCG GATCGCTTAG ATTCTCCTCT TTGCTGCATT | 120 |
| TCCCCCAGC TCCTCGTTCT CCCGCGTCTG CCTGCGGACC CGGAGAAGGG AGAATGGAGA | 180 |
| GGGGGCTGCC GCTCCTCTGC GCCGTGCTCG CCCTCGTCTC CGCCCCGGCC GGCGCTTTTC | 240 |
| GCAACGATAA ATGTGGCGAA TCTCGAG | 267 |

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCATGTCTT CTGCCTCGGC CTCCCGGGTA GCTGGGATGG | 60 |
| CAGGTGTGCA CCACCACGCC TGATTTTGT ATTTTATAGTA GAGATGGGGT TCCATCCATC | 120 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CATTCCTAGG | CCATGAAGGC | CGATCTTGT | TTCTGAAAG | TATGGCATCA | AAAATACTTG | 180 |
| TAGAAAAACC | TTGTCACAAC | TGATTTGAAT | GTTCTATTT | TCTTTTCCTT | TGACTTTGAT | 240 |
| ATTGGCTTGT | AATGTCTCTT | TTCATCATAT | GTAATATCAG | TGGAACAGGC | AGCGCTACTC | 300 |
| AAGTCCTAAG | GATTCCTCAG | TGATCAGTGA | TCCAGGGCCG | TTCATGAACC | ACTGGGCTGG | 360 |
| ATTTGACTGT | TGAGTGTGGC | AGTTAATGCC | CCTCAAGAAA | TCAAAGGATG | TCTTATAAGT | 420 |
| GTCTTCCAAA | AAAAAAGCAA | ATGCTGAAAT | CCTATTGGCA | AAGTAAACTG | AAATTGGCTG | 480 |
| CTACCACTCG | AG | | | | | 492 |

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS: --

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | TTCATGGCCT | AACGTGAGCT | GCAGGAGCTG | GCCCGCAAGC | TGCAGGAGCT | 60 |
| GGCCGATGCC | TCAGAAAACC | TCCTTACCGA | GAACACGTGG | CTCAAGATCC | TGGTGGCGAC | 120 |
| CATGGAGAGG | AACTGGAGG | GCAGGGATGG | AGCTGAAAGC | CTGGCGGCCC | AGAGAGAGGT | 180 |
| CCACCCCAAG | CAGCCTGAGC | CCTCAGCCAC | CCCCCAGCTC | CCTGGCAGCT | CCCCCTCCACC | 240 |
| TGCCAATGTC | AGCGCCACAC | TGGTGTCTGA | AAGGAATAAG | GAGAACAGGA | CAGACTAACT | 300 |
| TTTAAATGA | TATGAAGTAA | ACTCGAG | | | | 327 |

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTGGANTCT | TGGAGATAAG | CTGAGCTTGA | TGCATTGCTA | 60 |
| CCACACACTC | CAAACCATGA | AGAAGGTACC | GTTGGGCTTT | TTGTTGTTGT | GACAAAATCG | 120 |
| TAGGAAATGG | CGCCTGTATT | TCTTAATCTG | TTCTCTAATC | TTCTCATTAA | AAAGAACTTC | 180 |
| AGTTAGAACA | AGAGGGCCCA | TGGCTTTTAC | ATCCAGTCTT | TCTGCTTCAG | CAACGATTTC | 240 |
| TTTGTGAGAT | GAATCAATAA | CACCCTCTTC | TTTCTTTTTC | TTAACAAAAT | CAAAGAGGAT | 300 |
| ATTGACCCTC | TCCTCAATTG | TTCTTTCCAA | ATCATCACTG | AGTGTGAGAA | CTTTTGATG | 360 |
| GTCACTGATT | TCATCCATTC | GACGCCTTTG | AGCTTCCTCA | GTTGTATCTT | CTCCCCAGTC | 420 |
| ATCATCCTCC | TCTTCTTCCA | TTGTATGTGG | AGGAGGATTA | ATTCATTG | GTGGTGGTGG | 480 |
| TGGTGGTGGT | GTCTCACTGC | TGGATACGGA | ATTGAATTCT | AGACCTGCCT | CGAG | 534 |

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTAGAATGT GTGACTCTGT GGGGACTGCA TAGGTTTGTT | 60 |
| AATTGACCTA TAGCTAAACC TTAATGTGTT TGTGTGTCTA TACATTGCTT TCCGCATTTT | 120 |
| AAGACATCCA GACGCTATTA CCAACATTTT CCTGTGCATT AACCTCTGCA TGTGAAAACT | 180 |
| TTTAACAGTT ACTGAACTAT GTAAATATGT GAAATTTTTT ATTTAGGTGG ATGCATTTTT | 240 |
| TGTCTGTTTA CTGCTCTTCT CAGCTTTATT CAATAAACTT GCATTTTAAG GGTTGTATTG | 300 |
| GCAATTTTAA CTTAAATGT GCATCATGAT GGAAGGTGCA GACTTTTTTG GAAGTTTCCG | 360 |
| AGAGGAGGGT CTATAGACCA TTTGTCAGAA ATCAGATCAA CCCTCGAG | 408 |

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

| | |
|---|-----|
| GAATTCGGCC TTCATGGTGT CGTCTCCATT CTGATGCATC AGCTCAAACA GCTCTGAGTC | 60 |
| CAGGATCTGG ATGAGGGAGC GCATGTTGGC AAAGTGGGTG TCCATGGCAC CCCCCTGGG | 120 |
| GAAGTTCTGG CTCATCTCTT TCATGAGGTG GCTGAAGCAG CTGTAGGCCA GCTGATCATT | 180 |
| GTCGAGGGTG ACCAGGAGAG GCGCCAGCAG ATCGCACATG CCCTGCACAT AGCCACGTC | 240 |
| CAGGTGCTCC CACACGTAGC TGCACATGAC GTCTCTGAGC CTCTCGAG | 288 |

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATCCAGTGA CTGACAAAGC AAAATGTCAT GAAATTTACA | 60 |
| TTTTTTTTCT TCTTGTAATT TAAAACTTGG TTCTGTATA CCTTCCTGGA TCTTTATACT | 120 |
| TTTGTATCTT TTCTACCATT TCTGTAAAAC CTCAACTGCA GGGTGCAATA ATGGGCCTTA | 180 |
| TTTCTATAT TTCAGCAGGA CAGTTGCTGA AAATGGGTTT AACTCCACT GGCATTATAT | 240 |
| CCCACACAAC TCGAG | 255 |

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

| | |
|--|-----|
| GCNTTCAGGC CNAAGGTACT TTAATCAGTC TAAATACTTG AACATTTTAA TTTTCAGTGGT | 60 |
| AAAAAATAGA CTGAGGCAGA GTGAAGTTAT AAATTAGAAT CTAAAAATTT ACCCTTCAAC | 120 |

ATTAATATTT TTTAGTGCCT CTAATATAAA ACACAGAAAA CCTATCTCAA ATATAAAAGA 180
TGAATATAAA ATTATTAATT AAACAACNGG CGCTCGAG 218

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GCCTTCATGG CCTAGAAAGG AGCATCCCTG TTTTGGAGT CAGGACCATT CAGGGGGTGA 60
ACGAGGCCCA GGCCAGGTGC CTTTTGGAG CCTGGAATAT TAAAACCAGG ATGCCAAAAT 120
TGTAAGTGA TCTCAGTCTT TACATTTAAC AATTATATAC ATTTTAAACA TGGAAGATTA 180
CAGTATAATT TATTTAGGCT AATCAGAAGC TAATTATAGG CTATTTAAAA ATGTTAATTT 240
GTAACACANT ACTCGAG 257

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GAATTCGGCC TTCATGGCCT AAAGAAACAA AGAAACAAAC COTATATATA TATCTTCAGA 60
GTAAAAAAT GGTGAGAACA AGAGCATTGT TTTATATATT TTTCAACTC TCTTTAACTT 120
CTGGCTTAAT AGAAGACAGC TGCATTCTCA TTATTATTTA TTATTTTTT TTTAGATGGT 180
GTCTCGCTCT GTCACCCATG CTGGAGTGCA GTGGCGTGAC CTTAGCTCAC TGCAACCACC 240
ACCTCCCCAG GCTCGAG 257

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

AGCTTCATGG CCTAGTCTCA GGTTAAGTTT TTTGCAGTAA TCTTTCTTTC CCCTAGAAGT 60
GAGTAAACT TTCTGTATCC CTTTTCTCC CCACCTATGT TCCCTAAATT AGTGATTCTC 120
TTACAAGGAA TTATTATCGC CCCTGCAGTT TTGGAAGGAT ACCTCCAAAA TATATCTTGG 180
GGACTTCGAT TTATAGAATT TGGTTTAAGC TTAGATTCTG AGTCCCAGGG TACCTGCCTC 240
GAG 243

(2) INFORMATION FOR SEQ ID NO:778:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

| | |
|--|-----|
| GCTGACAGGA GCATTATGAA GCAAATGGTC ATTGATACAG TTTCAGTGAG GGAGTATAAC | 60 |
| ACTGGGATTT TGCAGCCTGT GGTGTTTCAGT CTCCTGACCT CTATGCCAGC ACACAGACAG | 120 |
| CAAGAAGCAG TGGGGAACCTT TGAGCTTCAA GCTCTACATT GGTTTGACAA AATCAATTCA | 180 |
| TCACTGTCTC ATTCATTAAT GTGCTGTCTG ATACTGACAT TTGTCAATGG CTTGTTTCTG | 240 |
| GAAGCCCCCTG GTCCTCAAGG CTGGTCAGCT CTACAGTCAC AGCCCCAGGG TGAACCCAG | 300 |
| CAACTCGAG | 309 |

(2) INFORMATION FOR SEQ ID NO:779:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

| | |
|---|-----|
| GAATTCTAGA CCTGCCTCGA GCCTGGGTGA CAGAGTGAGA CAATGTCTCA AAATAATAAT | 60 |
| AATAATTTCA ACATGATTTT TGGTGCGGAC AAACAAACCA TATCCAAACC ATTTACTCAT | 120 |
| CCTAGTTCAG GACAGTGTCC TGGGACTGAC ACAAGGGCTC ACAGCCAGCT AGCACTGTGG | 180 |
| GCTCTCACGG GTCCCTTCTG CTGTTTATT TTAGTAGTTA TTTATTCCA TTCCTCACTT | 240 |
| CCACTACCAC TCGAG | 255 |

(2) INFORMATION FOR SEQ ID NO:780:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

| | |
|---|-----|
| GAATTCTAGA CCTGCCTCGA GCTAATGGGT GCATGCTACC ACGCCCGGGT AACTTTTTTT | 60 |
| TTTNCGTGTT TGTGTTGTTT TGTGTTTGAG ATGGAGTCTC ACTCTGTTGC TGAGGCTGGA | 120 |
| GTGCAATGGC ACGATCTCGG TTTCACTGCAA CTCGAG | 156 |

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

```

GAATTCGGCC TTCATGGCCT ACTCCACACA TTCATCTCCC AAAGGACTCC TTGAATATTT      60
GCCCCAAAAC ATCAGCTCCC AGAAAACACC CTTCCAGTC ACACACACAC CCAAATTCTC      120
CGATGTATTT TCATTTTTTT TCTCCTCTTC TCTTCTCTT TTCCTTCCTT CTTTCTCTCT      180
TTTCTCTCTT NCCATCCCTC CTTTCTCTTC TCCCTCCCTT CCTTCTCTCC TCCCTTCCTT      240
CCTCCCTCCC TCCTTTCCTT CCTCCCCCA CCCACTCGAG                               280

```

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

```

GAATTCGGCC TTCATGGCCT AGCCGTGTTG TTA CTGTTG AATGATAAGG CCTAGATCTG      60
GTAGTGCTTT TGTTGCTCT AAGGTCTATT AATTAAATGT AGCAATCTTT CTTTCCCTT      120
TTTCTTTTCT AACTTCACAT CAACCTAACT GGCTACCTAA ATGTTTCATTG AATGACTGTT      180
TTTGCTTTGG GATAGAATCC TCCTTTTTTA TTTTtagggT GTTAAATTGA TATAGTATTG      240
TTTAATAGCT AATAAGATAC ATTTTGGGCT AAGTTTCTTA GGCCATGAAG                               290

```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

```

GAATTCTAGA CCTGCCTCGA GAATGGCTTT GCAGATCTGG GATCTGTGT TCCTTCTTTC      60
TGGGTGGTT TTATACGTTA ACTGTCAGAG GCATATGCCA CTTTATTCAG GTTCCTCGAG      120

```

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

```

GAATTCGGCC TTCATGGCCT AGTTTAGGTC AGTAGCAAAT GGGCCAGTG GGAGAGAGTA      60
TGCCAGAGT TTGGAGAGGG TCAGGGTGTC GGGTGCTGGG ATGAGGGCTT CATGTTTGA      120
AGACGCAAGG TAGAGAGCAA GAGAGGAGGA AAGGTAGAAC AGGATGGAGG GCAAGACCTG      180

```

TGTAAGAAGA AGTCTTAAAC TGTAACATG GGTGTAGTGA GGGTAGTGTG GCTAAGAGGA 240
 AATGGATCCA GATGGGCTTG ATGGGTAGCA CTCGAG 276

(2) INFORMATION FOR SEQ ID NO:785:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAATTCTAGA CTTGCTCTCA GGCAGTGAAG GACTGGCACA TTGTGTAATA AACAGAATCA 60
 AAGGCAGAAA TTAGATTACA AGCCACCTGA TGATGATAAA ATCAATCACC CTCATCAAAG 120
 GGATTTGCTT TGTGTGTGTT TTTCTCTTC ATTCTTGTGG ATGCAGACAG GATATTGAAC 180
 AGCAGCTGGG CTCCTTGATC TTGGCAACAG ACATCAACAG GCAGCGTCTC GAG 233

(2) INFORMATION FOR SEQ ID NO:786:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTAC TGAAACCAGA 60
 TCGTGAGACA CGCTTTTCAT TCATACTGA AACTTGATAA AATGTTTGGC TTTATATTAA 120
 TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCCTTGATAA CCCTTTTCAA GTAAATGAAC 180
 TGATTAGAAC CAGTAAGCTC GAG 203

(2) INFORMATION FOR SEQ ID NO:787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGGCC TTCATGGCCT ACGAGATTGT CCTGGGTCAC ATAATGCCAG CTGAGCGTAA 60
 AAAGCCAGCA AGTATGGAAG AAAAAGACTC TTTACCAAAC AACAAGGAAA AAGACTGCAG 120
 TGAAAGGCGG ACAGTGAGCA GCAAGGAGAG GCCAAAAGAC GATATCAAGC TCACTGCCAA 180
 GAAGGAGGTC AGCAAGGCCC CTGAAGACAA GAAGAAGAGA CTGGAAGATG ATAAGAGAAA 240
 AAAGGAAGAC AAGAACCTCG AG 262

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAAACAGCT GGAATGTCT CCAAGCCAGA GTGGACTACT | 60 |
| AGTAGGTATT CGTTACTTCA TTGAATTCTG CAGTGECCCC TTTTGGGGTG TAGTTGCAGA | 120 |
| CCGCTTTAAA AAAGGCAAAA TTGTCCTCCT CTTTCTCTT TTGTGTTGGG TTTTATTCAA | 180 |
| CCTGGGCATT GGATTGTCA AACCTGCTAC CTTGAGATGT GTACCAAAGA TTCGCCAAC | 240 |
| AACTACCCC CAACTCGAG | 259 |

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

| | |
|---|-----|
| ATACTTTAAG TTCTGGGATA CGTGTGCAGA GCATGCAGNT TTNTTACATA GGTATACACG | 60 |
| TGCCATGGTG GTTTGCTGCA CCCATCAACT CCTCATCTAC ATTAGGTATT TCTCCTAATG | 120 |
| CTATTCTCCTC CTTAGTCCCC CGTCCCCTCG AG | 152 |

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGCAAATTT GGCAGTGAAT ATGTACTGGA CTGTGATTAT | 60 |
| TTTTATTGTT TTAAAGTCA GCTTCCCTCC CTCCTTCCTC CTCCCTCCTT CCCAAGCTGA | 120 |
| ATCTGAACCA AGGAAGTCTT CCTACAGAGC CACTGACTGG TCCCCACTAA GGCAGGGGTG | 180 |
| GAGGGAGGGG CAGGATGTTT TCCTCTCCAG CTTTGTCTT GCAGCAGATC CCCAACTCGA | 240 |
| G | 241 |

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

| | |
|---|-----|
| GTATTTGACT CAAAGTATTT TTTGACTGAT AGCAGTATAG CTCCCTCATT CCCTGCTCTC | 60 |
| TTTTGGTTAT CATTTCATG AAATATAATT TTCTATCCCT TTACTTTTAC TGTGTCCATA | 120 |
| AAAGTGAAAT GAGTCTCTTA TGGGCAGGAT ATAGTTGGGC AATTTTATA CTAATTCTGC | 180 |
| CG | 182 |

(2) INFORMATION FOR SEQ ID NO:792:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAATCTTCT TGGCCTGGCA CTAAGGACCT ACTACAGACT | 60 |
| GGCACTGAAA TATCTTCCCT ACCTTATCAT TCCTTGTGCT TCTCCACAAG CCCACTCTTC | 120 |
| CCCTTCATCA TACATGTGCC GACCTTTCCT GTCTCTTTTA CTTGCAGCA CCAAATGCTT | 180 |
| TCTACTTTGT GGTCTAGGAG GAACACATGT CACTTTTGTA AGCTGCTCGA AAGCAGGGGC | 240 |
| CACACCTTCA TCCTTGTTTT CCACACAACA CCAA | 274 |

(2) INFORMATION FOR SEQ ID NO:793:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

| | |
|---|-----|
| AATTCGCCTT TCANGCCTAG TGAGTAGTTA TCAACACCGG AGATGCATTA GATCAATCTC | 60 |
| TGGGGGCTTC TTCCTGGACC TGCTTCCATA TACACTTATT CATTTGTCT TCACCGGACA | 120 |
| TGTTAACTT CCAGAGTGAC TCTAATGTGC AGACATGGTG AACATCATTC GCTTAGCTGC | 180 |
| ATGTCAGCGC TCACTCAATG TCTGTGAACA GTGAAAGCTA CTTATTCTAC TTATAAGTTC | 240 |
| ATTAAGTCTG TGTATACTA TTGCAAAGCA GAATAGTTGT CCCAGCCACC TGTGTTGGG | 300 |
| GAGATGAAGC TGGGAGGCCA TCAACCTTCT TTGCAATAAA TTCCTCAG TTTTGTCAAG | 360 |
| CAACCTGTTT TTTGTATTCT CAGCTAGAGG CTTTCATTCT CTATCCCCCA CTCGAG | 416 |

(2) INFORMATION FOR SEQ ID NO:794:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

| | |
|---|-----|
| GAGATGGATG TCTCTCTTTG CCCAGCCAAG TGTAAGTTCT GGCGGATTTT CTGCTGGGA | 60 |
| AGCGTCTGGC TGGACTATGT GGGCTCCGTG CTGGCTTGCC CTGCAAATTG TGTCTGCAGC | 120 |
| AAGACTGAGA TCAATTGCCG GCGGCCGGAC GATGGGAACC TCTTCCCCCT CCTGGAAGGG | 180 |

| | |
|---|-----|
| CAGGATTTCAG GGAACAGCAA TGGGAACGCC AGTATCAACA TCACGGACAT CTCAGGAAT | 240 |
| ATCACTTCCA TACACATAGA GAACTGGCGC AGTCTTCACA CGCTCAACGC CGTGGACATG | 300 |
| GAGCTCTACA CCGAACTTCT CGAG | 324 |

(2) INFORMATION FOR SEQ ID NO:795:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

| | |
|---|-----|
| GATTGGCCT TCATGGCCTA GCAAAGGGA CAAGGGAGAG AACAGGAGTA GCAAAAATAA | 60 |
| AATAAGAAAT TATGATGCTG CTTTACCAG AGACAAGCTG CTGCCACCAC TAGGCTGGAA | 120 |
| CCTACAGGCT GCACCTGTCC CTAATTAGGG TATTGGATAC TATTCACACT GCTCCTGCAA | 180 |
| CAACTGCTAG CCTGTTCTAA TCAGTAACTT CTCTCTTCTT CCTGTCTTCT CACCCTCCAG | 240 |
| TTCTCTCTAA CAGGAACCCA GCTGGCAAAG ATGTCTGGGA AATGTCATTT GCATTCTCAG | 300 |
| CCCCAGCAGT GCAGAAAGGT AGGAGTGGGG CTGCGAAACA ACAGAAAAAT AAGGACCATA | 360 |
| GGTGACAAAG GAAATGCATA TACACTTCAC AGATGGCCCA TAAACATATA ATACAAAGAG | 420 |
| GTGCCTCGAG | 430 |

(2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTCATGAAA TGTCCCAAAG TCTTCTCATT CTGTTCTTCC | 60 |
| CTCTCCTTTT CTTGGTCTT ACTTCTGTAG ACTCTAGCAG AGATGGCATC CTGGGATGGA | 120 |
| ATGGCAGAGA TCTGATGCAG TGGCATGCTC ATCCCAACCT CTTATCTGGT CCGTCTTCTC | 180 |
| ACAGAAGAGA GTCTCCACTG GTAGAGTCAT TTTGGGCCAT GGATTCAAG CTATGCTTTC | 240 |
| CTTCTGGCAC CCCGAATGTA CGCAGGTCTC TCGAG | 275 |

(2) INFORMATION FOR SEQ ID NO:797:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

| | |
|---|-----|
| GCACAATATT TCAAGCTATA CCAAGCATAC AATCAACTCC AAGCTCGGAA TTTTAATTAC | 60 |
| GAGGAGGTTA GTTGTGGCAA TAAAAATGAT TAAGGATACT AGTATAAGAG ATCAGGTTCC | 120 |
| TCCTTTAGTG TTGTGTATGG TTATCATTTG TTTCGAG | 157 |

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

```

GAATTCGGCC TTCATGCCAA ATGACCAGCC CCTACTGAAG TCCCCAGCAC CTCCTCTTCT      60
GCATGTAGCA GCCCTGGGCC AGAAGCAAGG GATCCTGGGA GCTCAGCCTC AGTTGATCTT      120
CCAGCCTCAC CGGATTCCCC CACTCTTTCC TCAGAAGCCT CTGAGTCTCT TCCAAACATC      180
CCACACACTT CACCTGAGCC ACCTGAACAG ATTTCTGCCC CGGGGCCCTC ATGGACGGTT      240
GGGCTCGAG                                     249

```

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

```

GAATTCTAGA CCTGCCTCCC CCCCCCCTT TCAGAATAAT TTACATAAAT ACTCCTGAGT      60
TCAATTTTTT TNAATTTTTT TTCTGCTTTT ACTTATTACC CTTTAAGTGC TTGCTTACTT      120
TCTCTGATAA TTTACTTTCT TCTACTCTGT GATTCTTTT ACAAAATCAAT GAAATGGTGT      180
TGTCTTGTTT TCTCAAGTTT TTTCCTGTTA CCTTTCCTGT GGTACACCTGG ACATTCCAGT      240
CCGTTTTCCA CACTCTCCCT CTACCTTCTC CCCCAGTTCT TTAAAGAGAC ACATAATCTC      300
GAG                                     303

```

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

```

GAATTTTCGGC CTTATGGGCC TAGCCATGCA ATATCTTTTG CATTACAGTG CAGTCTTTGA      60
GAAGAGCCAA GTGGGTGAGA GGTATATTTT CGGTGGTAGT TGAAGAGAAG GACAAATTAG      120
CACAGGAACA AGAACTTCAT GTAGTTGTGT TTGAAGGCAG TAGAATTGCC TTTTAAAGT      180
CATATCTGGA TGTTAAGCTC TCTCTGGGAT CCAGTTATTA GGATGAAGAA ATTCTGCCGT      240
TTAAGTGCCT GCCATTTATA GAGGTTGCTT GTAACCTGTG TGGCTAGGTA ATTGTGCTGT      300
GTGAATTTTC TACTCAAGGT TGGTTTGGCA GAAAGTAGAA TTCTGAGTCT GGGTATAAAG      360
GGGTTTACTA ACATGGGAGA GATTTGTGTG GAACCCAAAC TCGAG                                     405

```

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

```
GAATTGGCCT AATTAGCATC CTCAAGGACA CCAAAATCAC GTGTGAGGAG AAGATGGTGT    60
CAATGGCCCC AAACACGTAC GGGGAGTCCA AGGGCCGGTG AGGGAGGGTA TTGCCCTCCG    120
TGAGCACAGA GACTCTCCAT GGGAGGGGGA GCAGTATTCT CCTGGATCCT GGGGCCTGGG    180
TGGGCTGGGG GACAGCTGAG GATGGGCCTA GCAGATGAAG CTTGCCAGCA AGGCCAAAGC    240
AAACGGTTTC TCCTGTGGAT AGTGGACAGA GACCTTTGTA ACCAATGGAA TTATTCATTT    300
TTCTCTATCT TTTATTTTTT CAAAGATATT ATTTGACTCT ATCAAAAGTC TCTCCTTTT    360
AAACCTTTTC TTATGGCGGG CTATCTCGAG                                390
```

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```
GAATTCGGCC TTCNTGGCCT ACTTTTGGAC CTTCTGAGTT TTAGTTTGTC CACTGAGTTT    60
TAGGTNAAAA AGAAAAA AAAAGGAAAAA TTATCTGTAA CCTCAAGACT TTTTATGAGG    120
ATTATGATTT TACTGTGTTT GATAATAAAT GCCTTTTGCA TGCACTGGTT TTCAGCATAC    180
AGTTATGAAC ATTTCTAGT GGATGAGCTT AAAAAAGGGG AAAAGCTCGA G                231
```

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

```
GGGACAAGGA CCTGTGCAGT GGCCTGACAT GACAGACGGA CCTGNTCAGC GTCCTATTTG    60
CAGTGATGTT CGAGTTTAGC CACCGTACTG TGGACATGCA CCCAGACAGC GGATTAAACG    120
TTAGTGTGTA CCCTATTCCC AGAAGAAAGG GTCCAAGAAA CACCCACACA GATCCCAAAT    180
GCAGCACACC TGTGTGTGGG CTTTCATCTT TTGGAGCCCA CCAATGCCTG CCATCCCTAA    240
CAACTGCCTT CGCACCACCC AGGGATCAAG GCATTCTGTT TTTCGGAACG TGCTCCGACA    300
GTGGAGAAGT GCAGCATGGG AAGTTGTAT CTAGGAACTT GAAGCAAATA AATTCTTTT    360
AATTCATGCT TGTGATCCCT GTTATTCTGT CTCTGAACTG TGCCTTTATG CTCCAGATTA    420
GCTTTGAATC TTATTGCTAG ATTCTCCAAT CTGTTTACAA AATAAATGCA CCTAATCTTC    480
GCCTGCCTCG AG                                492
```

(2) INFORMATION FOR SEQ ID NO:804:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 444 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

```

GATACATAGT TCAATTCAGT TCAATCAAAA CCATTCAATA CATATTTACT GAGTCCCTTC      60
TGCGTGTGAG GCACTGTTTC AGGCACTTGT GATATATCAG TGAACAAAAAC AAAGGCCCTCT      120
GCCCACATGG AGCTTACATT ATAGCCAGGG GAAACAACAG TATACAATAA ACACAAATAT      180
GTGAAGTATC TAGGGTGATA GGTGATATGA AAAACATAGA GCAGGTGAAA GGGGTATGGG      240
ATTTCTCGAT CTGGAAGGTA GACAGCTGCA GTATTAAATA GTATGGACAG GATAGGCTTC      300
AGTAAGAAGG CAACAATTGA GCAAAGATGA GTAGGTAAGG GTATAGGGCA TCTGCAACAG      360
CTAGTGAAAC GGCACAAAGG TTAGAACAAG GCTGGAGTTC GGGAGAGGTC TGGGCTGGAG      420
ATGTAGNCCA TGAAGGCCGA ATTC                                     444
  
```

(2) INFORMATION FOR SEQ ID NO:805:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

```

GAATTCGGCT TTCATGGCCT ACAAGAAGCT GGAGGAAAAA AATACGCTGG CTCAGGGCTT      60
TCAGAGAAGA GAGGAAAATG GTACAGGAAG ATGAAAAAAT TGGCTTTGAA ATTTCTGAAA      120
ACCAGAAGAG GCAGGCTGCA ATGACTGTGA GAAAGTCCC TACGCAAAAA GGTGTCAACT      180
CTGCCCCGTT CAGNTCCTCC TTCTTACCCA CCACCGCAGG ACCCGTTAAA CCACGGCCAG      240
TACCTGGTCC CCGACGGCAT CGCTCAGTCG CAGGTTTTTG AGTTCACCGA ACCCAAGCGC      300
AGCCAGTCAC CATTTTGGCA AAACCTCAGC ATGTTAACCC CCATCACTCG AG              352
  
```

(2) INFORMATION FOR SEQ ID NO:806:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

```

GCACCCCGGG AGCTGAGTGA TTGCAGAAAC TGGCCTTCCA TCTCTCTCAG ACACCAAGCT      60
GCAGATCCAG GCTTTTCTGG GAAAGTGAGG CCACCATGGC TCTGGAGAAG TCTCTTGTCC      120
GGCTCCTTCT GCTTGTCTCG ATACTGCTGG TGCTGGGCTG GGTCCAGCCT TCCCTGGGCA      180
AGGAATCCCG GGCCAAGAAA TTCCAGCGGC AGCATATGGA CTCAGACAGT TCCCCAGCA      240
GCAGCTCCAC CTACTGTAAC CAAGGTCTCG AG                                     272
  
```

(2) INFORMATION FOR SEQ ID NO:807:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```
GCCTTCATGG CCTAGGAGAA GAGCGGAGCG TGTGAGCAGT ACTGCGGCCT CCTCTCCTCT      60
CCTAACCTCG CTCTCGCGGC CTACCTTTAC CCGCCCCACC CTCAGGAACT TTTGTTAGGA      120
AAAAATTGAA AGAACTTAAG TCTCGAATGT AATTGGAATC TTCACCTCAG AGTGGAGTTG      180
AAACTGCTAT AGCCTAAGCG GCTGTTTACT GCTTTTCATT AGCAGTTGCT CACATGTCTT      240
TGGGTGGGGG GGAGAAGAAG AATTGGCCAA GCTCGAG                                277
```

(2) INFORMATION FOR SEQ ID NO:808:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

```
GAATTCGGCC TTCATGGCCT AAACACAGAA AAACCAACTT TCTGATACCT TTCTCCCTGT      60
ATGTTTATCT TCTTGTCTA GTTTTTCAGC AGAAATATGC CCGTTTCCCC CTGATAATTC      120
CCTTCCTTAG AGACAGCATA ATTGTAGACC TGGCCAGAGA AATGCTGAAA ACAAGGGGAA      180
CCCCCTTGAG CCCAGCCCTT CACCTGCTCT TAGCACTTCT TCAGAGGTTT ACTCTGGAGT      240
GAATGAAGTA GTGTGACCAG AACTCCTGG CACCTCGAG                                279
```

(2) INFORMATION FOR SEQ ID NO:809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

```
GAATTCGGCC TTCATGGCCT ACCTTCGCCT TCTGTCTTTC TGCCTCCTAC TAGCAGGTGT      60
TACTCCAAT TCCTATGGGC CAGAGTTTGC TCACTGCAGA GAAATACAGT GGAATTCGTT      120
GGGCAATGGT TTGGCTTATG AAGACTTTAG TTCCCCATC TTTCTCTTG AAGATGAAAA      180
TGAAACCAAA GTCATCAAGC AGTGCTATCA AGATCACAAC CTGAGTCAGA ATGGCTCAGC      240
ACTCGAG                                247
```

(2) INFORMATION FOR SEQ ID NO:810:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

```

GAATTCGGCC AAAGAGGCCT ACCCGGGCTC AGTGTGCCGA CTCTGACTG CAAATGATCT      60
CATTTTCTAA AATCTTTCTC CCATTCTCCT TTAAGAAAAA ATCTTAGTTA TTAATAATCT      120
GCCTCACAAA CTTAGAAATG CTTAGAGTA AGTATCTGAG AAGCAAGCCC ACCCCACATC      180
CACCATATAT CATCGTTTCT GTTAAGGGCC ANCCCATTTT TTCAGACAAA TTCTATCTTC      240
TTCCTCCCAT CCCACTTACT TTGACTTTG AAGGTGGATT ATCTCATCTC AAATTTCTTT      300
NCCAGAATAG NACCACATTT CAGCAAATA TTGGGTGGCT GGTTCCTTTT TTCAAGACCC      360
ACCTGCATCT GTGTTGGTCC TCTATGTGAG GAAGGTCCTC TATGTGAGAA GATCTGAGGG      420
GTAGGCAGGT TTTAATGGAC TAAGATTTT TTTATATGTA TAAGGGGGGT GGGAGGAGGA      480
TTTTAGAAAA CTAGATCCAT TGGCCTGCAG TTAGAAGTCG AACACTGAAC TTGGGAAGGC      540
TTTCTGTGGC CGAACCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

```

GAATTCGGCC AAAGAGGCCT ATCAATTNGT TTTNTTACTT GGTA CTGTGA TTTATTATNT      60
NTAATTATNG TNAANTNNTA AAGCTCAATT TTACCAGCTT CAGCAGTTTT AAGTGATAG      120
TTGCACAACA CNACATAACT CATCTAAGGT GAATTATACT GTAATTTTCT TTNGTGCCCT      180
AGCTTTTTGC NATTACCATA GTATCCTGAA GTTTTGTGAT TGNGTACCA TGAGACAGGA      240
TGTTATAAGA TTAATATTTC AATGTATATA TATGCCTAGC ATATTTTCNT TATGCATGCA      300
GCCACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

```

GAATTCGGCC AAAGAGGCCT AGGCGGCAGG AGGCAGTGGC GTTGGTGGGA AGCGCAGCTC      60
GAAAAGCGAT GCCGATTCTG GTTTCCTGGG GCTCGGGCCC ACTTCGGTGG ACCCAGCGCT      120
GAGGCGGCGG CGGCGAGGCC CAAGAAATAA GAAGCGGGGC TGGCGGCGGC TTGCTCAGGA      180
GCCGCTGGGG CTGGAGGTTG ACCAGTTCCT GGAAGACGTG CGGCTACAGG AGCGCACGAG      240
CGGTGGCTTG TTGTAGAGG CCCCAAATGA AAAACTCTTC TTCGTGGACA CTGGCTCCAA      300
GGAAAAAGGG CTGACAAAGA AGAGAACCAA AGTCCAGAAG AAGTCACTGC TTCTCAAGAA      360
ACCCCTTCGG GTTGACCTCA TCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGCAAGCTC TGCTTTAGTT TCCAAGAAGA TTACAAAGAA | 60 |
| TTTAGAGATG TATTTGTCAA GATTCCTGTC GATTCATGCC CTTTGGGTTA CGGTGTCCTC | 120 |
| AGTGATGCAG CCCTACCCTT TGGTTTGGGG ACATTATGAT TTGTGTAAGA CTCAGATTTA | 180 |
| CACGGAAGAA GGGAAAGTTT GGGATTACAT GGCCTGCCAG CCGGAATCCA CGGACATGAC | 240 |
| AAAATATCTG AAAGTGAAAC TCGATCCTCC GGATATTACC TGTGGAGACC CTCCTGAGAC | 300 |
| GTTCTGTGCA ATGGGCAATC CCTACATGTG CAATAATGAG TGTGATGCGA GTACCCCTGA | 360 |
| GCTGGCACAC CCCCTGAGC TGATGTTTGA TTTTGAAGGA AGACATCCCT CCACATTTTG | 420 |
| GCAGTCTGCC ACTTGAAGG AGTATCCCAA GCTTCTCGAG | 460 |

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAAGTGCTTT AAAACAATTT TTCCTGTGG ACAACCGAAG | 60 |
| ACCACAAAAC ATTTGAGAAC TACCATGACA GACAGAGAAC AAAATTACAA AACAGAAAAA | 120 |
| GTTAAAAAAC AGGAGAACTG CACCACTGCA CTCCAGTCTG GATACCAGAG AGAGACTCCA | 180 |
| TCTCAACAA AACAAAACAA AACAAAAAAA CCCCAAAAAC TCGAG | 225 |

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTATCGTT TAAAAAAGTC AGTAGAACTA AACATGAAAG | 60 |
| TGATTCTTCT GATTTTGTGG GGGGTGGTTA TTTGCACATG GAAACAACAA CAAAAATGCT | 120 |
| TCAGATACAA TTTGCTCGAG | 140 |

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:816:

| | |
|---|-----|
| GAATTCGGCC AAAGAGTCCT AAAACCAACA AGCCAGGCTG ATTTTCTAGA GGGATCAGTG | 60 |
| ATGTGGGGTA CAATGACACC TTCCCTGTGG CTTGTTATGC CTCCGGTTTT GTTTTGAAT | 120 |
| CTTGGTTGCT GGTGGGGTAT TCCCCCTCG GCTCCTCTAT GCTTTCGCGT GTGTGAAAAT | 180 |
| GCAGGAGTGG ACCACTGTGC ACAGCAGGAC CATGGCTGTG AGCAGCTGTG TCTGAACACG | 240 |
| GAGGATTCCT TCGTCTGCCA GTGCTCAGAA GGCTTCTCA TCAACGAGGA CCTCAAGACC | 300 |
| TGCTCCCGGG TGGATTACTG CCTGCTGAGT GACCATGGTT GTGAATACTC CTGTGTCAAC | 360 |
| ATGGACAGAT CCTTGCCTG TCAGTGTCTT GAGGGACACG TGCTCCGCAG CGATGGGAAG | 420 |
| ACGTGTGCAA AATTGGACTC TTGTGCTCTG GGGGACCACG GTTGTGAACA TTCGTGTGTA | 480 |
| AGCAGTGAAG ATTCGTTTGT GTGCCAGTGC TTTGAAGGTT ATATACTCCG TGATCTCGAG | 540 |

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

| | |
|--|-----|
| GAATTCGGCC ANANAGGCCT ACTNNNAGGC CTGTCCGANAN GCGTTGGGTN CTGANGTGAC | 60 |
| AGCTTTCCCC NTCCATGGGA CNCNTTCCA GACNNTCGNC ACNTCTNCTG AGGTGAATTN | 120 |
| NCTGTGGGTN TTANGTCTGG GGTGGANNTT CTCTCTCCCC NNNTCTNACT TCNGTAGATG | 180 |
| TGGACCTNGN CCNNCNNTCC ATTGGTCCNC TGCCCTGTGT CTCCAGGGTG CTGCCTCTGC | 240 |
| CTCCTCATAT CACCAGCGTC CCCACTGCCA CTAGTCTGTA GGGGGATTCC GGGCTAGGTG | 300 |
| CTCTTCCCAT TCGACTTCAA CCAACTTATA TAGCTCCATG GTGGCCTGGG CATCTTCCAC | 360 |
| AGAGGATGTC CGCTCTTCCC NACCTGGATA TCCCGGTTTA GCAGCTTCTT GGTGAGATGC | 420 |
| TTCAGAGACA TGGTGGCATT CTCCGGGCAG TCAGCCTTCC GGTGAGGGG GGGGATATGG | 480 |
| GAGGTGTCAC GGGTGAGGGA CTTGGGGTGA AAGTACTGAA GGGCTTTGAA GTCGTTGTGG | 540 |
| ATGGCATGCC CCACCACTAT CTNCCCTGT GAGTATCTTC AAGATCTGCC CCTCGAG | 597 |

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGAAATGAA ACGAATGCAT AAAGCTCTCC AGAAAGATCT | 60 |
| GCCAAGACCA TCAGAAGTAA ATGAAACTAT TCTAAGACCC TTAAATGTAG AACCGCCTTT | 120 |
| AACAGATTTA CAGAAAAGTG AAGAACTAAT CAAAAAGAA ATGATCACAA TGCTTCATTA | 180 |
| TGACCTTCTA CATCACCTT ATGAACCATC TGGAAATAAA AAAGGCAAAA CTGTAGGGTT | 240 |
| TGGTACCAAT AATTCAGAGC ACATTACCTA TCTGGAACAT AATCCTTATG AAAAGTTCTC | 300 |
| CAAAGAAGAG CTGAAAAAGG CCCAGGATGT TTTGGTGCAG GAGATGGAAG TGGTTAAACA | 360 |
| AGGAATGAGC CATGGAGAGC TCTCAAGTGA AGCTTATAAC CAGGTGTGGG AAGAATGCTA | 420 |
| CAGTCAAGTT TTATATCTTC CTGGGCAGAG CCGCTACACA CGGGCCAATC TGGCTAGTAA | 480 |
| AAAGGACAGA ATTGAATCAC TTGAAAAGAG GCTCGAG | 517 |

(2) INFORMATION FOR SEQ ID NO:819:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTAAATTCT | CATATACTCG | TGTTTCTAGA | ATACTTTGCC | 60 |
| TTTTTGGGCT | TAGTTAATGG | TAAGATTCTC | ATGTCTGTCT | ACATAGGAAT | ACTCCACCGT | 120 |
| ACAGGACACT | GCTTCTGGG | TTTAGTTCAT | TGATAATTTG | TCCGAATGCT | CATAAACATG | 180 |
| TCTATAGGAA | TACTCCAATA | TATCTAGGAC | ACAGTTTTCT | CCGCTCCTGA | ATACAGGCAG | 240 |
| ATTTTGTTC | TTTCTGCCTC | CCTGTGTAA | TGAGAAGGTA | GTCCAGCAGG | TTCTCTCTAC | 300 |
| CTCCTTGCTT | TTTTTCCCC | TTAATGCTCG | AG | | | 332 |

(2) INFORMATION FOR SEQ ID NO:820:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AACCTGCTCC | GTGGAGCGCC | TGAAACACCA | GTCTTTGGGG | 60 |
| CCAGTGCCTC | AGTTTCAATC | CAGGTAACCT | TTAAATGAAA | CTTGCCTAAA | ATCTTAGGTC | 120 |
| ATACACAGAA | GAGACTCCAA | TCGACAAGAA | GCTGGAAAAG | AATGATGTTG | TCCTTAAACA | 180 |
| ACCTACAGAA | TATCATCTAT | AACCCGGTAA | TCCCGTATGT | TGGCACCATT | CCCGATCAGC | 240 |
| TGGATCCTGG | AACTTTGATT | GTGATATGTG | GGCATGTTCC | TAGTGACGCA | GACAGATTCC | 300 |
| AGGTGGATCT | GCAGAATGGC | AGCAGTATGA | ATACCTCGAG | | | 340 |

(2) INFORMATION FOR SEQ ID NO:821:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGGAGCTATA | ATCTTGTAAC | AGAGTCTACG | TGATTGTAGG | 60 |
| ACAATAGGCA | CCACACAAAT | ATGAGGAAGC | AGGTCAGAGA | GCGGGCTGAC | TTAATGATTA | 120 |
| ATGCTGAATG | TGCTACAAGC | TTGTTTCATT | TTCATTTCTC | CTCCTCCCTT | TTTTCCTGAT | 180 |
| TAATTTAATA | AAGTTCATAG | GGGAGGCTTC | AAACACATGA | GAAATTAAAA | CCTTTATTAC | 240 |
| CAGAGTCAGA | GCCTGACTAT | ATTGATTGAG | TGAAGCTTTC | CTTTATAAAA | TGCAAAGCAT | 300 |
| GTAACAATT | CCAACACAGT | AACATATTCA | TGAGTTTTTA | AATTCATGAG | TTTAGAGAA | 360 |
| AATATTTTAC | TTAAAACCAG | CACTTGATGA | TCTCTGACAA | TGTTATGTAG | CCTGAACCTG | 420 |
| GAGTTTTGGC | TGATGGGTTG | TCTCAGCCTG | TGACAGGTTT | TAGCTGGCTT | TGGTTCATCT | 480 |
| TGTATCACAC | CCCCACACTC | ACATGCTCAC | CACTCGAG | | | 518 |

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

| | |
|--|-----|
| GAATTCGGCC AAAGAATTCT AGACCTGCCT CGTGCCTAAG GCAATTGAAT CGAGGGTTAA | 60 |
| GGGTTTCATCT TGCTAATGTC AAAAGTGACA CTAACAAGAT TCTTAGCCTC ATCCGCCAGA | 120 |
| TGACGGGCCT CCGCTCGAG | 139 |

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGATGAGAA AATCAAGGTT CTTAGATGTT CTGGAATTG | 60 |
| TTCATTTCA CATGATTGGA ACATTGTGGT CTGTCTTTC AAGTCCATGT CTACCATACT | 120 |
| CCACAGACCC TTTCTGTCC ACTTTGTCAC CTATAATTCT GAACTCCAAT ATAAAGACTT | 180 |
| CACCGTATTT GAAAGAGAAT AGTGGGAAGT CTGATGCTCA ATTTTGTGTA CAGAACAGTT | 240 |
| GCCTCTGTGA CATTGTAAT GCTGAAATAA GAAAATCCCC TTTTGATTCA GGAGCTCTCG | 300 |
| AG | 302 |

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AAATCAGCAG TGAATCAGA ATCAATTGAG TGACATNGAG | 60 |
| TCAGTAAATC TCTGACTGCC TCAGTTACCC CATATGATAG TTTTGAGGAT GGGAAACATTG | 120 |
| AGAGAGTTGA TTTGGAAGCA TATCAAGAGT AAAAATTCCA ACATTTTTCG TTCCTTTAAG | 180 |
| TTAAATCCAG GCACTGTCTT TTCCTGCAAG TCTCCTGTTT CTTTCAGATT GCACAGGTGA | 240 |
| GAGTGCTCAG ATTAGGGCTG GAGGTTGTAA ACCATTGCTC CCGTCCTCGA G | 291 |

(2) INFORMATION FOR SEQ ID NO:825:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

```

GAATTCGGCC AAAGAGGCCT AAGCTTTTTT TTTTTTACA GACTTCACAG AGAATGCAGT    60
TGTNTTGACT TCAGGTCTGT CTGTTCTGTN GGCAAGTAAA TGCAGTACTG TTCTGATCCC    120
GCTGCTATTA GAATGCATTG TGAAACGACT GGAGTATGAT TAAAAGTTGT GTTCCCCAAT    180
GCTTGGAGTA GTGATTGTTG AAGGAAAAAA TCCAGCTGAG TGATAAAGGC TGAGTGTGTA    240
GGAAATTCTC GCAGTTTAA GCAGTCGTAT TTGTGATTGA AGCTGAGTAC ATTTTGCTGG    300
TGTATTTTAA GGTAAAATGC TTTTGTGTTCA TTTCTGTTGG TGGGAGGGGA CTGAAGCCTT    360
TAGTCTTTTC CAGATGCAAC CTTAAATCA GTGACAAGAA ACATTCCAAA CAAGCAACAG    420
TCTTCAAGAA ATTAACTGG CAAGTGGAAA TGTTTAAACA GTTCAGTGAT CTTTAGTGCA    480
TTGTTTATGT GTGGGTTTCT CTCTCCCTC CCTTGGTCTT AATTCTTACA TGCAGGGAAC    540
TCGAG                                                                    545

```

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

```

GAATTCGGCC AAAGAGGCCT AGGTGGTGGA ATCAAGGCCA TGAAGGACCT GTTTATGCGG    60
TGCATGCTGT TTACCAGAGG AGGGCCTCGA G                                                                    91

```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```

GAATTCGGCC AAAGAGGCCT ACTAAGAAAT GCTATTGGAT CTTTAGTTTG TTCAGCTTTA    60
TTTTTCTTAT AAGGATGAAA GTGTTGACTT ACAAGCTCTT TATATATCAG ACCAGAACT    120
ACTTTTAAAT AAATATAAAA TGTAATCACC ATCTAAAGCA CTTNGCACAA TGCATGGCAT    180
GTAGTGAGCA CATATTTTAA GCTCTTACTG TTATTTATTA TTATTCCATT GAGAAAAACA    240
TTTCCTAATA ATAATGAAAT GACAACATGA TATGGTAGCA TCACAAAAAT CAATACATCT    300
TTCTAAACAT ATTAGAAAT ATTTCTGTAT GAAATAACAG GTTTAAGGAA AAAATTTAAT    360
TGGGTCAGAA GTGTGCAATC AAAATAATGA GATGACATTG GCATGAAGAA CAACTCGAG    420

```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAATTCTAG ACCTGCCTCG AGCTTAGGGT GACAGAGTGA | 60 |
| GACTCCGTCT CAAGAAGCTAG AAGAGTCCCTG AAGTTCTTTC TGGAGTATTG GTGTGATAGA | 120 |
| AGCATTAGTA GTTCTTTTA TGTCTGGAG AACTTCTGTG CACATAAATG TTTATAGATA | 180 |
| TATACCCCGT TTGTATACCA AAGGAATCTT CATTATTTT CACTGAACAA AACACCTTAG | 240 |
| AGAACATTTT GTTTGTTTG CCAATCAATC TAATCTTTT AAATGACCAC ATAGTATCCC | 300 |
| ACGGTAAGTT TTTTGTTTG TTTTTTTAA AATCATGATT TGTTTAAACA TGTCCTATTG | 360 |
| CTCTCGAG | 368 |

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATGTTTTTC AATACCTCAG TATATTGTAG GGAATTGTTG | 60 |
| AGAACTTGTT GAATGAATAT ATTGTTTACA GTTTACCATT ACTCAGTATT TTAGTTGTCA | 120 |
| CATCTTAAAA TAGATAATCA TTTTACCAT CACACTCCCT TCATAAGATA TAGAAATAAA | 180 |
| GCCCTTCTTG TTTGGAAATG GTGGTATTTT GGTTTTACTT TTTTAAAGT TACTGTTGTA | 240 |
| AGGTACTACT TTAATATTTT TATTTAACTT TATTTGTTG TCTTTAGTAG GACTAAGCTA | 300 |
| ATGAGAGCTT TGACTTGCTT AAACGTTGGG CAGGAAAACG CGAG | 344 |

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGTCT AGAAGACTTT TGTATTTTTC ACTTTGCTAG TTTGTGGCAG | 60 |
| AGTGGAGAGG ACGGGTGGAT ATTTCAAATT TTTTAGTAT AGCGTATCGC AAGGGTTTGA | 120 |
| CACGGCTGCC AGCGACTCTA GGCTTCCAGT CTGTGTTTGG TTTTATTCT TATCATTATT | 180 |
| ATGATTGTTA TTATATTATT ATTTTATTTT AGTTGTTGTG CTAAACTCAA TAATGCTGTT | 240 |
| CTAACTACAG TGCTCAATAA AATGATTAAT GACAGGATGG GGTCCCCCTG TGCTTTTACC | 300 |
| AGTAGCATGA CCCTTCTGA AGCCATCCGT AGAAAGTACC TTGTCCTCGA G | 351 |

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAAACAAGAT CCACTGGAGG GTCATGCTG AGTTGTTCTC | 50 |
| TTGATGATTT TGGCTGATTA TCTTAATGCC CTTTCCATT TCTGATGCTC TTGTTCTACA | 120 |
| TTTTGGGTGA AAATACCAAT ATTTCTAATT CTGTATCACA TCATCTCACT GTGTAGCAAG | 180 |
| GCAGGTCTCC ACAAATTACC CCGTTCCACC TGGAGAGCTC CTTATTGACT TAACGTGATA | 240 |
| TTCAGCCAGG TTTTCTTCC TGTAATAGTT GCTTGCCTT TAGCAAATTG CCTGGATCAT | 300 |
| TGACCTTTCT TAGCCCATGC ATAAATGCC AACTCGAG | 338 |

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS: ..

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATATTATAG AACCACCATA TGTACATTTT TCATAGAGTT | 60 |
| TGGGAATGAA ATAGTAAAAG GTATATAGAA AACTAAGAAA AGGGAAAATT CTGGGGGGCT | 120 |
| GGGATGAGGA AGTGATTAGC ACCAGGAAA ACCAAAGTTT ATACCAGAAA GGAAGCTAA | 180 |
| TATTAGGCTG CCATATTAAG CCATGTGGCT GGGCTACATT GTGTTAAGTC ACTGATGAAT | 240 |
| GATCTAAACA AGAGTCTGGA TATAACCAA TCAGGAAGGC TTGAAGAATG TGTGTGTAT | 300 |
| TGGGGGGAAC GGTGTCTACA GTAGGAGGTA GATGGTTATG TAAAGTAGA GAAAAGGAAC | 360 |
| TAATATAAAG TGTTAGTTGG AATATATTAA TAATTGTCAG TGAAAGCTCG AG | 412 |

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACTGTGGGTT TATATTGATG TGTAACAAGT TGATTGGAA | 60 |
| CACTGGACTC TCATTCTGTT ATTCTGGTTT TGTTTTTTTT GTTTGTTT TTTCTTTT | 120 |
| TAAAGGCAAT GAGCTAGTCC CAGATCTCGA G | 151 |

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

| | |
|--|-----|
| GAATTCAGCC TTCATGGCCT ACTCTCGTTG AAGATGTGAA TATCTGTCTG CAGGCATGCA | 60 |
| GCAGTCTACA CGCTCTGTCC TCTCCTTGC CAGATGATCT TTTACAGAGA TGTGTTGATG | 120 |
| TTTGCCGTGT TCAACTAGTG CACCGTGGAA CTCGTATTCTG ACAAGCATTT GGAAAGCTGT | 180 |

TGAAATCAAT TCCTTTAGAT GTTGTGCGGA TTGAATTCTA GACCCGCTC GAG

233

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAACTGGGA GGTAGAAACA AAAATGACTG AACATCTTTT | 60 |
| TATCCCCCAA TCGTTACAAA GCCTAAATAA CTCTAAACGG GATGGGAGGG CAAATTTTAG | 120 |
| GTCAGTTGAC ATCCTGGAGA AGATATCCTA GGTCTGTCT CATTCCTAG ACCGCATAAC | 180 |
| ACTCCAACCG TGTAGGCCAT GAAGATTGAA TTCTAGACCT GCCTCGAG | 228 |

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

| | |
|---|-----|
| GAATTCGGCT TCATGGCCTA GGCTGGTGAT CCATGATGCA AATAATAATA ATAATGATGA | 60 |
| TTTTTTTAA TGTACAGCTC TCACACAAAT TTCATTTTGT GAACACACTG GTAAGTACAC | 120 |
| GATGCTGGGG CTTCCAAAT GTGGCGTATC CCACTGATGG CTCAACTTG CGAGTGGGCT | 180 |
| CAGTTATGAA AAACCTCGGA GAGGACGGGT TGTCGCTGCT CGAG | 224 |

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGAGCTGTT GCACTTTGGG CCTTGGCAGG ACAAACACTA | 60 |
| AAACAACAAA AATATATGGC AGAACAAATT GGATACAGCT TTATAATAAA TATGCTTTT | 120 |
| TCACCATCAG CTAAAATGCA GTATGTTGGT AAGTTATTTT CCTTATTTTA TTTTATTTT | 180 |
| TTAGAGACAG GATCTTGCTC TGTGCCCAG CCTGGTGTGC AGTGGCACAA TTATAGCTCA | 240 |
| CTGCAGCCTC AAACCCCTGG GCTCGAG | 267 |

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATCAAACCTC | AAACTACGCC | CTGATCGGCG | CACTGCGAGC | 60 |
| AGTAGCCCAA | ACAATCTCAT | ATGAAGTCAC | CCTAGCCATC | ATTCTACTAT | CAACATTACT | 120 |
| AATAAGTGGC | TCCTTTAACC | TCTCCACCCT | TATCAACAACA | CAAGAACACC | TCTGATTACT | 180 |
| CCTGCCATCA | TGACCCTTGG | CCATAATATG | ATTTATCTCC | ACACTAGCAG | AGACCAACCG | 240 |
| AACCCCTTC | GACCTTGCCG | AAGGGGAGTC | AGAAGTAGTC | TCAGGCTTCA | ACATCGAATA | 300 |
| CGCCGAGGC | CCCTTCGCCC | TATTCTTCAT | AGCCGAATAC | ACAAACATTA | TTATAATAAA | 360 |
| CACCCTCACC | ACTACAATCT | TCCTAGGAAC | AACATATGAC | GCACTCTCCC | CTGAAGTCTA | 420 |
| CACAACATAT | TTTGTACCA | AGACCCTACT | TCTAACCTCC | CTGTTCTTAT | GAATTCGAAC | 480 |
| AGCATACCCC | CGATTCCGCT | ACGACCATCT | CGAG | | | 514 |

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTACATAGA | CGTGGATT | AGGGGGACAA | AATTCAACCA | 60 |
| CTACCGTCTC | TTTGCTTGAA | ATCACACACA | ATTTCCAGAG | GCCTAGAGAT | GCCACTTTGT | 120 |
| CCGCAGATCT | CTTCCTGGCC | CCGCCTCTGT | CTGGGCAGCC | TGGGTCTGAT | TGTCCTTCTG | 180 |
| TCTGCCACCC | TCACAGTCCT | CAGCCGTGGC | CTGGTTCCTG | TCCTGGGGGC | TGACCAAGCCT | 240 |
| TCTGGGGCCT | GGGACCTGGG | GCATCGCTGC | TGCCTGCCGG | GTGACCTCGA | G | 291 |

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATAGCCT | ACCTAAATTA | ATAATAATGT | ATAGTTCAGA | ATTGCTAAGA | 60 |
| GTACTTTTTT | TTTTTTTTTT | TTGAGACAGG | TTCTCGCTCT | GCCCTCCAGC | CTGGTGACAG | 120 |
| AGCAAGATTC | CATCTCAAAA | AAGAAAAAAA | ACACACAGCT | AATAGAATTG | CCATTGTTTT | 180 |
| TCATAATAGA | ATCTAGCTGC | TTACTCCAAC | CTCACCTCGA | G | | 221 |

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

```

GAATTCGGCC TTCATGGCCT AGTAAAGTTT CTCTCACCCC ACTTTAATT CATGTGCCAC      60
ATTTTTTCTT TTCTGAAACT ATATTGCTTC CCACATTCGG ATTTTAGAAT TTTTCTTTT      120
AAAGAGATTG TATTTTAAAT TATATTGGC CTACTTCCCC ATTGTCAATG CTTGTACCGT      180
GTGAGAAGTC CCTAGGATGA TAGTCATGGT TTTTCCCAT CTTATTAGCT TATTATTCTC      240
CTGCCCCACC CCCCACCCCT GGCAGCTTCC CACCTCTCT AATGCTTCTG GAAGCTACTA      300
AGAAGTTTAA GTGGCCTATG TGAAATATG TCAGTGTCCC ATTTTAGCAT ATATATGTAA      360
CATTTACAAT TTATACCCCT GCCTACATCC GAGAGGGTTG TGAGGTGGCT TATGATGATA      420
AAGAAAAAAA CCCACATATC TCGAG                                           445

```

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

```

GAATTCGGCC TTCATGGCCT AAATTTATAA GGTACTCTTT AACAATTTAT ATCAGAGTTA      60
GTTGCTATCT TTAGCACCAT TGTCCTGATG GCCTCCACTT CTAGCTATAC ATTGCCTCTT      120
TGAAATGAGC CATTGGGAG GCAAATATAT CAATTAGAAT GCCTTTAAGA ATAAAAAACT      180
TAAAAAGCAA AGAAAAACAG AATGCCTTTA GGAAAAAATT TAATAAAACC AACTCAAAAT      240
TGTGCAACA AGGAAATTTT AGTGTTCCTT ATAATAAAC CTCGAG                       286

```

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

```

GGTTCCTCAAG TAATTATATT CCAAGGAACA TAGGAGGGGC AAAAATAATT CTAAGACAT      60
AAAGAAAGAA ACAGGATATT TTCTAAATAT TTTTATCTTG AGACAGAACT TGGTTTTTTT      120
TTTGGCTTTA GCTTGGAATA TCTCGTGCA TAGATAAATC TTTCTCCTAT CTTGAAATTG      180
GTCTTATCAA GGAATACCC GCATTGAGAT ATGAAGCTCT GGGCCTCTCT GGTAGCCTTG      240
CACCCCTTC ATTCATCACC TGGTCCCCCA GATAAGACAG CCCTGACCTC AGAATACACC      300
TTGGATTTAA CATTCTATGG GACATTTATT TCTAGTCTAC CCCCATCCCT CGAG           354

```

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTGGAAAAA | ATAAGATATT | TCTTAAAGTA | ACAAGGCCTG | 60 |
| AATAAATGTG | TGGCAGTCTC | AAATTCTATT | CTATATCTCA | GGTGTAAATCC | TTACATACTA | 120 |
| AAGATAGTGG | GATCATCCTT | GATGATTTCT | AGCAGACTGG | TACATTAAAA | AGTGACAATG | 180 |
| TTTGGGGTAT | GACAGTATAA | AAAAAGGTTT | AATTTGAGAA | AAAGGATTAA | GTTAAATAGT | 240 |
| AAACTTAGTG | TGAGATTTTA | ATCACAAGTA | CAAAAGAGTG | AAGAGCAGCC | TTCATGACAA | 300 |
| GGAATCATGT | GACCAGCCCC | CACCCCAAAC | TCGAG | | | 335 |

(2) INFORMATION FOR SEQ ID NO:845:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGAAAGGGT | GGGAACTAAC | ATTGATCACA | TTTATGGAAA | 60 |
| CCTGCCTTCT | CGTGCTGGGC | ACTTTATATA | TGTTATCTCC | CTTTGTGGTG | CAATCTCATG | 120 |
| ACATGCAGTC | ATTGTCCATG | TTTGTGGGTG | AGGAAACAGG | CTTAGGGGTG | GGAGGCTCGC | 180 |
| CTGAGGCCCC | ACACTGTTGG | CTGGAGACAG | CGTGGGGCCT | GAGTCTTGCT | CACAGCCTGA | 240 |
| ACGCTGCACT | CTGCTGCTCC | GCGTCCCAGG | AAGGAAAAGC | TGCTGCAGTG | GGTTTGTTTT | 300 |
| GCCAAATACA | TGGAGGCTTT | TTTCTGGGTG | AGTGCCGAGC | AGTTGATTGT | TCTGTATGCC | 360 |
| TCGAG | | | | | | 365 |

(2) INFORMATION FOR SEQ ID NO:846:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATCCATGTT | GTACAACTGA | AATATAAATA | ATTTTGTCAA | 60 |
| TTATACCTAA | ATAAACTGG | AAAAAATTT | CTGGAAGTTT | ATATCTAAAA | ATGTTAATAG | 120 |
| TGCGTACCTC | TAGGAAGTGG | GCCTGGAAGC | CATTCTTACT | TTTCAGTCTC | TCCCATTCTG | 180 |
| TACTGTTTTT | TGTTTTACTT | TCGTGCGCTG | CAGGTCTAGA | ATTCAATCG | | 229 |

(2) INFORMATION FOR SEQ ID NO:847:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 575 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGGGGAGAGT | ATCATCTCAC | CAAAGGTGAA | AATGGCATT | 60 |
| CGGACATCAG | GACATCTCTT | ACTGGGAGTA | GTTCGAATCT | ATCACAGGAA | AGCCAAATAC | 120 |
| CTTCTTGCG | ACTGTAATGA | AGCATTGATT | AAGATAAAGA | TGGCTTTTCG | GCCAGGTGTG | 180 |
| GTTGACCTGC | CTGAGGAAAA | TCGGGAAGCA | GCTTATAATG | CCATTACTTT | ACCTGAAGAA | 240 |
| TTTCATGACT | TTGATCAGCC | ACTGCCTGAC | TTAGATGACA | TCGATGTGGC | CCAGCAGTTC | 300 |
| AGCTTGAATC | AGAGTAGAGT | GGAAGAGATA | ACCATGAGAG | AAGAAGTTGG | GAACATCAGT | 360 |
| ATTTTACAAG | AAAATGATTT | TGGTGATTTT | GGAATGGATG | ATCGTGAGAT | AATGAGAGAA | 420 |
| GGCAGTGCTT | TTGAGGATGA | CGACATGTTA | GTAAGCACTA | CTACTTCTAA | CCTCCTATTA | 480 |
| GAGTCTGAAC | AGAGCACCAG | CAATCTGAAT | GAGAAAATTA | ACCATTTAGA | ATATGAAGAT | 540 |
| CAATATAAGG | ATGATAATTT | TGGAGAAGGC | TCGAG | | | 575 |

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATCCTGGAGT | GCAAAAATAA | AATCCACTCA | AGAGTCACAA | GGCCCCGTGT | GCATAATCGG | 60 |
| TTTCACITTT | ACCTTTTTTT | TTTTTTTTTT | TTTTNGAGAC | AGGTCTCACT | CTGTCACCCA | 120 |
| GGCTGGAGTG | CAGTGGCACA | TTCTCGGCTC | ACTGCAATTC | CGCTTCCTGG | GTTCAAGTGA | 180 |
| TTCTCCACC | TCAGCCTCCC | AAGTAGGTGG | GATTACAGGT | ACTCACCACC | AGGTCCAGCT | 240 |
| AACTTTTGTA | TTTTTAGTAG | AGACAGGGTT | TCACCATGTT | GGCCAGGCTG | GTCTCGAACT | 300 |
| CCTGACCTCA | GATGGTCTGC | CCACCTCCGC | CTCCCAAAGT | GCTGGGATTA | CAGGCGTGAG | 360 |
| CCACTGCGCC | CGGCCACTTT | CACACTTTTT | ACAGTGAGTG | GTGAATTAGC | AACAGTAACA | 420 |
| CTGATTATCC | AACATATATT | TTGGAATATC | TACTATGTGC | AAGGAATTTT | TCTTAAACTC | 480 |
| TAAGGTTATG | AATCACTGGG | CAAATCCATA | TAATTAGAGA | ATTTTAAGTG | CGTCTCGAG | 539 |

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGGGGGAAGA | CGGGAAGCAT | ATAAATAAAC | AAATAATTTT | 60 |
| TAAAGCAAC | TTTTTTAAAG | CAAGTGGGAG | GGGCATGCTA | GTTTTAAGAA | CTGTAATAAA | 120 |
| AAACACCACC | CATTGTTTTT | TTTTTGTTTT | TTCTTTTGG | AGACAGAGTC | TTGCTCTGTC | 180 |
| ACCCAGTCTC | GAG | | | | | 193 |

(2) INFORMATION FOR SEQ ID NO:850:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

| | |
|---|-----|
| GAATTCTAGA CCTGCCATGG CTGTGGGCGC GCTCCCCTCT GACTGCGTCC CTTTCTCTCC | 60 |
| CTGCATCCCC TTCTCTCCCT GCATCCTTCT GTCTTCCTGT GTGCCCTTAT CTGCCTGGGC | 120 |
| CTTCCTGTCT TCCTGTATCT TCTCACCTGC CTGTGTTGTT TCTAGCTGTG TCTCTGCCCT | 180 |
| TCCTGTGTGC ATCATGCCCT TCTGTGCACT CCTGTCTGAC TGTGGCCTCT TGCTTTCTTG | 240 |
| TGTCCAGCA TCCACCTGCG TCTTCCTATC TGCACGTCCC CTCGAG | 286 |

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATCTCGTTC TCCATGTCTT CCGTGTGCTG GATACACTGG | 60 |
| CAGAGCTCAC AGATGAGAAA CGCCCCCAGG GTGGCCTCCT CGTGGTTGTC CTGGATGTCC | 120 |
| ACATTGACCA CGTGACAGG CTGGCAGGTC TCCTGTTCTC TGAATTCAG ATCTTCACC | 180 |
| ACCTGGTCAT AACTCTCTC TTCGCAAGTG AGGATCAGAT CAAACAGGTC TTTGCAGTTC | 240 |
| TGGAATCTTT CTGGCCGGGG CTTGATTCTC TTATTTCTGT CCAGCATATG TAAAATCCCA | 300 |
| TTCTGTGTAT AGAGTTCTTT GTCTTTCCTA AGAAGATCAT TGTACATCTG GTCATATGTG | 360 |
| GTTTGAAT CATAACATT GGGCTTGTG GAGAGCTGTC CTGGAAGCTT CACGTGAGTC | 420 |
| CCTGTTCAA AGGATCGGAC GCTGAATCCC CGTTTGCTGA GGATGTTGTG CGCCTCCATG | 480 |
| CTCCGGTTCT GGTGCTCGA G | 501 |

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGTTGTGCT GACACCAAAC ACATCCAGTT TATAATCAGT | 60 |
| ATATTGAAA GCTGGTATTG ATGTAGAACC AGTGCATAAC TTTTATGGG GTTTTGTAT | 120 |
| TGGTTTTTTT TTGTAAAGTG TGAATAAAG GTATGTTTAC TCATTTTCC TGAACACTGT | 180 |
| GTTGGTAATG TGCAATGA CAATTTCCAG TGAAGGTGAG CTGGAGCTGG TTGGACTAAT | 240 |
| GAGACTGAGG AAGCAGCTTT TCCTACGATC TGCATTATGT AATCACAGGT CCAGAGAGCT | 300 |
| TTATGGAAGC GGGAGAGGAG GAGCACTTAC TCATGTTGTA TTTGTTAATG GAGGATGTCA | 360 |
| TCTTTTCATA GATGCTGGA CTAGAGTGCA CTTGTTAGAT GCTAAAGGTT TGAGCTTTAC | 420 |
| ACAAAATGTC TTCATCTGTA TTTGTTATTG TCTACAATAT ATTTGAATTT GGGGCAAGTC | 480 |
| TCGAG | 485 |

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTTCATGGCCT | AGGTGGCTGC | ACCATCGGGA | TGTCCTGATC | CAACATCGAG | 60 |
| GTCGTAAACC | CTATTGTTGA | TATGGACTCT | AGAATAGGAT | TGCGCTGTTA | TCCCTAGGGT | 120 |
| AACTTGTTCC | GTTGGTCAAG | TTATTGGATC | AATTGAGTAT | AGTAGTTCGC | TTTACTGGT | 180 |
| GAAGTCTTAG | CATGTACTGC | TCGGAGGTTG | GGTTCTGCTC | CGAGGTCGCC | CCAACCGAAA | 240 |
| TTTTTAATGC | AGGTTTGTA | GTTTAGGACC | TGTGGGTTTG | TTAGGTACTG | TTTGCAATTA | 300 |
| TAAATTAAG | CTCCATAGGG | TCTTCTCGTC | TGCTGTGTT | ATGCCCCGCC | TCTTCACGGG | 360 |
| CAGGTCTAGA | ATTCAAAGC | AAGCATCTCC | GCATCGCATC | CTCTCCATT | AACCAGTGGC | 420 |
| CGGTTGCCAC | TCTCCTCCCC | TCCCTCAGAG | ACACCAAAC | GCCAAAAACA | AGACGCGTAG | 480 |
| CAGCACACAC | TTCACAAAGC | CAAGCCTAGG | CCGCCCTGAG | CATCCTGGTT | CAAACGGGTG | 540 |
| CCTGGTCAGA | AGGCCAGCCG | CCCACTTCCC | GTTTCCTCTT | TAAGTGAGGA | GAAGCTGATC | 600 |
| CAGTTTCCGG | AAACAAAATC | CTTTCTCAT | TTGGGGAGGG | GGGTAATAGT | GACATGCAGG | 660 |
| CACCTCTTTT | AAACAGGCAA | AACAGGAAGG | GGGAAAAGGT | GGGATTCATG | TCGAGGCTAG | 720 |
| AGGCATTGG | AACAACAAAT | CTCGAG | | | | 746 |

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCAATTCTAG | TGGTAAGGTG | TTAATAATTT | CACTCTTTTT | ATGTAGACGA | GAGGTTGAGC | 60 |
| CTTGAAGGAT | GAGAGGTGTT | TACCGTCTTA | GGATGGGGTA | TAGTAGATAG | AACCATATGA | 120 |
| ACCGAAGAGC | TGAGGAATGT | GAGCATGTAA | CACCTGACGT | GTACAGTAGT | AGGTATGAAG | 180 |
| TCATATGGGA | GCAGTATTTT | TTTTTCTATT | TTGTTCACTG | ATTTTCTCC | ACTGGTACTT | 240 |
| AATAGGCACT | CAATAAATAT | TTTGCTAAAT | AAATGAACTG | GTGATGTTGA | AATCCAGTTA | 300 |
| GTTTACATTT | TGGTTGGTTT | TGGTATTGTC | TTTTAAAGGT | AGCAAAGACC | AAGTAATTAA | 360 |
| ATTTGTTAGA | TGAATATGAG | ATAAAATGGG | CTCTCGAG | | | 398 |

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCCCTTTGCT | CCATTTCCAA | GGAAAGAAAT | TAAACCAAGA | TGGTGGCTGG | GATTACAGGC | 60 |
| ATGAGCCACT | GTGACCAGCT | CGCAAGATAG | AATTTTGAAA | AATGTATCTT | GAGCCTCTCT | 120 |
| TTCTCTTTCT | AGTTCTTTAA | GATTCAAGAA | ATCAAATAAG | GTGATAGCCC | TGAAGCCCTT | 180 |
| ACAGGCAGAG | GTGCCCTCGA | CTGTGGGTGA | GGAGGTATTC | ATCCCCAACC | AGTGAGATAT | 240 |
| TCTGAGTGGG | GAGAAGTGTT | TTCTATCGAT | GACACAGGGT | GGGCCCTATG | GGAGCAGCAG | 300 |
| CATGGCCCCA | CCTTCGACCC | AATGCTGAGA | GGAAAGGGGC | CTCAGGAAGG | GGAGACTGAA | 360 |
| GCCAGCACAC | TCGAG | | | | | 375 |

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

| | |
|---|-----|
| GAATTCGGCC TCATGGCCTA TGAATTTATT TTATTTTACT TATTTATTTA TTTGGTAGAG | 60 |
| ACAGGGTCTC ACTATATTAC CCAGGCTGGT CTCTTACCCC TGGCCTCAAG TGATCCTCCT | 120 |
| GTCTCTGCAT CCCAGGCCTC CCAAAGTGGT GGGATTACAG GCATGAGCCA CGATGCCTGT | 180 |
| CAGCCTTATT GCACTTCACA CACACACACA CACACACACA CACACACACA CACACACACA | 240 |
| CACACACTGA TTCAGGCCTT GAGAGTCAAG CCCAAGAGCT CCCTTGGCCC TGTCCCCAC | 300 |
| TCTCTCGAG | 309 |

(2) INFORMATION FOR SEQ ID NO:857:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

| | |
|---|-----|
| GGAGAAATAT GGCTTCAGTT TTTCATTACT TCCTGTTAGT TCTGGTCTTT CTGGATACAC | 60 |
| ACGCAGCTCA GCCTTCTGT CTGCCAGGAT GCACCTTGCTC AGAGGGAGTT TTNGCAGGAC | 120 |
| TCTGCAGTGC ACATCTGTCT CCTTGGGAAA GATCCCTGGG AACCTTTCTG AAGAGTTCAA | 180 |
| GCAAGTGAGA ATTNAAAAAT TCNACNNTA TTTGAGATGC CCCAAGGNTC TTTCATCAAC | 240 |
| ATGAGCACCT TGAATACCT CTGGCTCAAT TTAAACAATA TQAGTGTGAT CCACCTAGGA | 300 |
| GCCCTGGAAC ACCTGCCAGA ACTGAGGGAG CTGAGACTGG AGGGGAACAA GCTCTGCTCA | 360 |
| GTACCATGGA CAGCGTTCCG TGCCACCCCT CTCCTGAGGG TCTTGGATCT CAAACGCAAC | 420 |
| AAGATTGATG CACTCCCTGA GCTGGCTCTT CAATTCTTGG TCAGCCTGAC CTACCTTGAC | 480 |
| CTATCCTCCA ATAGGCTTAC AGTTGTATCC AAGAGTGTCT TCCTGAACTG GCCAGCCTAC | 540 |
| CAGAAATGCC GGCAGCCACT CGAG | 564 |

(2) INFORMATION FOR SEQ ID NO:858:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTGGTTTG GAGTCATAAC ACAGAAGTGG TGAGAAGTGA | 60 |
| TCAGAGGCGG ATTTCTGGT GCATTGAATA TGGGATGTGA GATAAGCAGA GGAGTCAGGA | 120 |
| TGGCTTCCC GACTATGGTC CAAACAGTGG AAAGGATGCA GTGGCTGTAA CCTGAAGCAG | 180 |
| GAAGTCTGCA GGTGGGACAG AAATGTTTGT TAAGGGAAGT GTTTTCAGAG TTTGGTTTGT | 240 |
| GATATGTTAA GTTTGCCAGT GTAAATGGAC ATACTGTGTA GACATTTGGA AATATGAATC | 300 |
| TTGGAAATAT GAGGTTCTGG GTATGAGCAG AGTCCAAGGA TGAGCCTAGG GATTGGAGAG | 360 |
| CTGAAACCAG AAAAAGAAGC TAGAAGGAGA GGCCAGTTAA GACAGTGAAA AGAAGCGAGG | 420 |

CATGAGGATC ACTTGAGGCC AGTAGCTCAA CAGCCTGGGC ATCATAGCGA GACCCTGTCT 480
 CAGCAACAAC AACAAAACGG ACAGTGAAGA GAGTATTGA AGGAGAGGGG AACAGGCAGC 540
 GTATTGCTTA TTGCTGAGGG GCAAAGTGAA GACCAAGGAT AGACTGCTGG GCTTGACAGC 600
 ATGGAGGGTG CTGGGGGCCT AGGCAAGTGC AATATTCATG TGGTGTCAAT GGGCCAAAGG 660
 TGTCAATTGGA GGTACTCGAG 680

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GCAAAAGCAA GTCACGTGGT CATGCAGGGC CTCAGTAAGC AAGAAATATT TACCCGCCCCG 60
 GGGATGGACA GGTAGGAAAG GGTCTGTAA GGAAGGGCAG CAAATATTTG GATAACAGTA 120
 CTATGTGTTT GTATGGAGCG ATATTTAAGA AGGTTTCCTA GGTTTTTTGA GGGGTATTGA 180
 AGCTGAGAGG TTGGGGGCAG GCAGGAAGCT CTGCAGCCTG TAGCCTATGG TATCAAGCTT 240
 CATGAGAACG AGAATTAAC AGTTACATCT TTATTACCAT TTTTGGCATC TCTGCAGACA 300
 GTGGATCTAA TGCATGATAG CTGATTAATA AATGTTGTT GAATTAATGA ACAAATAGC 360
 AAGAAACACG TGTTCGAG 380

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GATTTTGAAT ACACNACNAA GTTAGAAGAA TCTTATTACT TAGATTCCAT TAATATCTTA 60
 CTATGTTTTA TTACAAATCT ATGTATCTCT CTAGCCATCC TTTAATCCAT GTTATGTTTT 120
 TGATGCTTTG CAAAGTAAGT TGCGAATATT GGTTCATTT CCCTGAAATA CTTAAGCATG 180
 CAAATCATGA ACCAAGTTCC AATATTTGTG TGAAATGCAC AAATAAGTGT AAATTTGCAG 240
 AGTTTGGGCA TATGCGTATA CCTATCAAGA CACGGAGCAT TAATATCACC CTGGAAGTCC 300
 TCGAG 305

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GAATTCGGCC TTCATGGCCT AGTGAACAAG TAAAGACTGA ATGGGGCTGA GATGAAGGCA 60
 ATGTTTCCAA GGAAAGGAAA TGTTATGAGC AAGAGTGTGA GGCAAGAGAA GCTGAACCA 120

| | |
|---|-----|
| CATTCAGAGA GTATCCTGTA GATTGCTCCA CCTAGAATCT CAGGTGGGTG GAGCAGTGGT | 180 |
| GGGAGAAGAC TGGAAAGGTA AGTTGAAGGT AAGGAATGTG TGGTGGGCCT CAGATCCCAG | 240 |
| GCTCATTCTT CAAATCACTT CTTACTTCCC TCACTTATCT TTGTTTAAAT AAGGTTAGCA | 300 |
| CACTCACTCG AG | 312 |

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTGGCGGGC ATCTTGTGTT TATCTTCTGG AGTGAAATAT | 60 |
| GCTTTTCCAG TTGTCTTCGA AGTTTCACCT CTGCTCCATA TTTTCCAGTG GTCCCGTTGT | 120 |
| CAGCCAGAAT GAAGTGGGAA TGCATGCTGT TGAGAACAGT GAGCTTGCTC ATGGGATTGG | 180 |
| ACATGGTCTG GTATGGCCGG ACAACATCTC TTCCAATGAG GTCCTCCTGG TTTTCCACAA | 240 |
| TTCCCCAGGG GGCAATACCT ATGGTGCATA TCTTCTCTCG AG | 282 |

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

| | |
|--|-----|
| GAAATTCGGC CAAAGAGGCC TAGGGTGCCT GTGGTTCCGG CTAATCGGGA GTCTGAGGCA | 60 |
| GCACAATTGC TTGAACCTGG GAGGTGGAGG TTGCGGTGAG CCAANATGGT GCCACTGCAC | 120 |
| TCCAGCCTGG GTGACAGACT GAGACTCTGT CTCAAAAAAA AAAAGACCTT CCTTAATAAG | 180 |
| TGGAGTTGGA TAGACATTTT GCTTTGGAAA ACAGAAAGCTA TTTACTGTCA ATATTAGGTC | 240 |
| TACTTCATTC ATTTACAGA ATAGGCAAAG ATGTCTGGGG CTTTGCTCAC TAGGGAATTC | 300 |
| TGGCCATGGC CTTTGTCTT TCTTCTAACC AGGCCTTTT CTTCTCTTCT CCCTTTTTCG | 360 |
| CAGATGTAGA ACCACCAGGC GACTCGAG | 388 |

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAAGTTTCTA AAGATTGTAA ATTTAAAAGG AAATGCCAAA | 60 |
| TGAATTATTT GTAAAATTGT TTAATAAAT TAATAAATAA TGAGTGCGCC TCGAG | 115 |

(2) INFORMATION FOR SEQ ID NO:865:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGATTGAGAA TGCTGACTCG CCTAAAAGCT TTATGCTTAT | 60 |
| CATGCTCTGTG GTGCTTGGAG CCTGTGGCCC AGGTGATTG GGGTTTGGG ACGCCTCATG | 120 |
| GGCAGAGACG GCTCGAG | 137 |

(2) INFORMATION FOR SEQ ID NO:866:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

| | |
|---|-----|
| GAATTCGGCC AAAGTAGGCC TAAAATCCGT CCGGNAACTA TGAACAATGG CAGCTACAGC | 60 |
| GTANTCAGCT TCAAGGAGCA ATGCAGCAGT TTAACCAGAG ATTCATTTAT GGGGAATCAA | 120 |
| GATTTATTG CTACATCACA AAGTAAAGAA TTTGATCCTC TTGGTCCATT GCCACCTGGA | 180 |
| TGGGTCAATT AAATGAAAAG CCCTTACCTG AAGGTTGGNT TTTNAGATTC ACAGTGGATG | 240 |
| GAATTCCATA TTTGTGGAC CACAATAGAA GAACACCAC CTATATNGAT CCCCCGACAG | 300 |
| GAAAATCTGC CCTGTAAGTT TTCTAAACAT TGTAAGTTAA GAGTAAATA CTAGTCCTTC | 360 |
| AGATTTTGAT ATAAAGATTT GTATTAGCAA GGAGTGAAG TCTTAGTATT TCTTGAGTTA | 420 |
| GCTTGACAAT AGGTTTCTGT TCATTAAGTA TTTTGCAATT CCATCTCCCT CTTGGATATT | 480 |
| TTATCCTAGA GATTTTCATA TTTGTTACCA TTTGTTTACA CAGCACTAAA TGAACTATT | 540 |
| TAGAATTTAT AGGTATTGTA CTGCTTACCA ATTAGTCTCT GATTCTGAT TTTTCTGAT | 600 |
| TTTCATTCCC TNAACACTCG AG | 622 |

(2) INFORMATION FOR SEQ ID NO:867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT GGCAGGCGTG TTTATTGACT CTTCCAATTA ATTTTAAAGA | 60 |
| ACCTGAAGAA ATGGACAAAG ACAGAGAAAA GNCNACCAGA TGTGATTCGG CCCTTCCAGN | 120 |
| AAGCAAAGAG CTTATTTTCAT CCCATATGAT CGATGCCAGT CATGGGGANG AGTGGCTGTG | 180 |
| TGGAATTAAT GGATTTTCAA CATCCATCAC AGAGGACACA CATGTATATT AGCNAGTCTN | 240 |
| AAACCTCTTA AATAAACTGC ATTGCTTTTC ATTTTCACTT CCAGTTATAA AACCAGTGGA | 300 |
| TGATGNAAAG GCCATGTGAC NATACAGCAT GTACTCTCAG GNATGTTTGT GTGACAGGGA | 360 |
| TATTATATCT GAAGGGACAG GGCAACTGGG AGGGTGAAGT GCTCATAACT CTCAATTGTC | 420 |
| CAGGTAATGA AGCATTGGGA AAGCGACCTC GAG | 453 |

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```

GAATTCGGCC AAAGAGGCCT ACGAGCACCT CCGCCGCGCG CCTCCTCCGC CGCCGCGGAC      60
TCCGGCAGCT TTATCGCCAG AGTCCCTGAN CTCTCGCTTT CTTTTTAATC CCCTGCATCG      120
GATCACCGGC GTGCCCCACC ATGTCAGACG CAGCCGTAGA CACCAGCTCC GAANTCACCA      180
CCAAGGACTT AAAGGAGAAG AAGGAAGTNG TGGAAGAGGC AGAAAATGGA AGAGACGCCC      240
TGCTANCGGG AATGCTAATG AGGAAANTGG GGAGCAGGAG GCTGACAATG AGGTAGACGA      300
AGAAGAGGAA GAAGGTGGGG AGGAAGAGGA GGAGGAAGAA GAAGGTGATG GTGAGGAAGA      360
GGATGGAGAT GAAGATGAGG AGCTGAGTCA GCTACGGGCA AGCGGNCAGC TGAAGATGAT      420
GAGGATGATG ATGTCGATAC CANGAGCAGA AGACCGACGA GCATGACTAG ACNGCCAAAA      480
AGGGAAAGTT AACTNAAAAA AAAAAGGCCG CCGTGACCTA TTCACCTCCA CTTCCCGTCT      540
CAGAATCTAA ACGTGGTCAC CTTGAGTAG AGAGGCCCGC CCGCCCACCG TGGGCAGTGC      600
CACCCGCAGA TGACACGCGC TCTCCACCAC CCAACTCTCG AG                                642

```

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

```

GAATTCGGCC AAAGAGGCCT ACTCCTCCTC TTCGGTCTCA CCACAACCCA CCCTATCAAA      60
ATACTGCACC TCCACACAGC CGTTCTCTT TCATTGGGAA AGGCCAGCAC CTGGCCTCTT      120
TCTCTTTGAT GCTTTTGTA AATTGAGTTT GGGGAGAGCG TTCTGGTCT TTGTCTAAA      180
CCAGTGAAGA CAAACAGTGT ACTTGGTGTA AGCAGACACT GAAGGTTTGT CTAAGCTGTC      240
AGCCTGCTCT CCAACACCT GTGCCTGTGC TGAGACCTGA TGGTCCAGGA AAGGGCAGCT      300
GCCACACTGT GGATCCCCCG CCACCCACAC ACGCACCCCC CCTCGAG                                347

```

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

```

GAATTCGGCC AAAGAGGCCT ACAGAGAAGC GGGGCGAACT GAGGCGAGTG AAGTGGACTC      60
TGAGGGCTAC CGCTACCGCC ACTGCTGCGG CAGGGGCGTG GAGGGCAGAG GGCCGCGGAG      120
GCCGCGATTG CAAACATGGC TCAGAGCAGA GACGGCGGAA ACCCGTTCGC CGAGCCCAGC      180
GAGCTTGACA ACCCCTTTCA GGACCCAGCT GTGATCCAGC ACCGACCCAG CCGGCAGTAT      240

```

GCCACGCTTG ACGTCTACAA CCCTTTTGGAG ACCCGGGGAGC CACCACCAGC CTATGAGCCT 300
 CCAGCCCCCTG CCCCATTGCC TCCACCCTCA GCTCCCTCCT TGCAGCCCTC GAG 353

(2) INFORMATION FOR SEQ ID NO:871:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTCTTAG TTTGTTTTCA ACTGGAAAAT ATATAGAGAA AGATGAAGGG GCATTTTTGC 60
 CTCTACTCAT CAATTTTGG TACCAAATTT CTAAAAACC AGATGGTTTA AAGAAAATTT 120
 TTCCAAAAAT TATGTTAACA TTCTGCTCAG ACATGGCTGC TAAAAAATA GCATATACAC 180
 ATATAATACT GAACAGCTTC TGCAGTGCCT GTAAACTCTC AGCTCATTTT CTCTTTCTAA 240
 ANAAAAATA TATTATACT GATCCAGAA CTCAATCTCT ATTGTGCAGC AGTATCAAAG 300
 GTCCTTAAAT TCTCAACAAT GAAGGAAAA CAAAAACCA TTCCCGGAC CGCTTGAGCA 360
 GGACTAGGGA AGGAGGAGTC CGTGGATGCA AAGGTTGCT GCGCCGACGC CCTCAGANTC 420
 CTCGAG 426

(2) INFORMATION FOR SEQ ID NO:872:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GAATTCGGCC AAAGAGGCCT AGGGAGGGCT GAGAGGGAGG GAGGGAGGAA GGAAGGAAAA 60
 AAGGAACAAA TGCCGCCTGA CCGTTCCTTG TGGAATGACT ACACCTATGA TGAGTACCTC 120
 CATGGACCAT GCACCTGCCT TGAAACAAGG AGGCACAGCA CACAGGGCCC TCAGCTAGAG 180
 TGACAGGGAA AGGCGGGTGG ACATGGGGAA GGCTCAAACT CAAGCTTTGA AATCGGGGAA 240
 AGCCCGGAAA TCTGAACCAC TCTTGGGCCC ATCCTTCTCT CTCCCACATT CACACCTTCG 300
 CCTGCGCTCC CATAATTGCA AATTAATTCA TCCACACATT CACACATTCT CTCCCTCCCA 360
 CTCTCAANAG GCAGCCCCAA GCGCGGGGCT CTCACGAAGT CTGGGTGGAT GACCAAGCTC 420
 CTCCCTCGAG 430

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC AAAGAGGCCT ACGGGCATGG TGGTAGCTCA GGAGTTCAAG GCTACAGTGA 60
 ACTATGATTG TGCCACTGCA CCCCAGCTTG GGTGACAGAC AGTGAGACCC TGTCTCTAAG 120

```

AAATAAATAA AAATAAAAAA TAAGAGGAGC TTTTGGAAAT CAGCTATTAG GAAGTTACTG      180
GTGCCCATGG AGGGAAGTGT TCCAGGCAAG TGGTGGTGT AAAGGTNGAG AGAAGAGACA      240
TTAGCTCAGT GCTTCCCAA TAGGATANCC AAGGCGCCAA GCTGCANACT GATCTCAGGT      300
GTGGCCANT GCCTCCCCCT CAGCTGGAAC CCCAGACCAG ACTCCTGCAG TTTCAAGCAG      360
CCTCCTCCTT CTATCCCGGT GTACCTTCCA TATCTCAGTT CCACCACGGG GAACCTCAAA      420
CACTCGACAA CCCATTTCAA AAGCCTGGCT ATGGAAAGAA GAGGAAAGGG AGGAGCCGCA      480
AGTTTGGGAG AAAGTGATT TGGGATGCTG GAGTGGGAGC CTGTTTGTAG GAGCCATAGG      540
GCAGGCTTGA AGATGAATGG GAAAGAAGAT GAGNGGAAGA GGAGGTGAGA CTGAGAGCAT      600
CTCGAG                                         606

```

(2) INFORMATION FOR SEQ ID NO:874: --

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

```

GAATTCGGCC TTCATGGCCT ACTGGGGGTG AAATAATAAA GAAAAGCAAG AAGTGATTAT      60
CATAAAGAA AGTAATGAT GTTTTTTCCC TTTCTCGAG                               99

```

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

```

GATGAACAGA TACGATTGTG GGATTTTAT CATCTGTGTA GCAGGTGGTG TATGCATCGG      60
GGTACTCCTC GAG                                                         73

```

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

```

GAATTCGGCC TTCATGGCCT ACCAGAAGAT GCCTGCCTTC AATAGATTGT TTCCCTGGC      60
TTCTCTCGTG CTTATCTACT GGGTCAGTGT CTGCTTCCCT GTGTGTGTGG AAGTGCCCTC      120
GGAGACGGAG CCGTGCANGG CAACCCCATG AAGCTGCGCT GCATCTCCTG CATGAAGAGA      180
GAGGAGGTGG AGGCCACCAC GGTGGTGGAA TGGTTCTACA GGCCCGAGGG CGGTAAAGAT      240
TTCTTTATTT ACGAGTATCG GAATGGCCAC CAGGAGGTGG AGAGCCCTT TCAGGGGCGC      300
CTGCACTGGA ATGGCAGCAA GGACCTGCAG GACGTGTCCA TCACTGTGCT CAACGTCCT      360
CTGAACGACT CTGGCCTCTA CACCTGCAAT GTGTCCCGGG AGTTTGAGTT TGAGGCGCAT      420

```

CGGCCCTTTG TGAAGACGAC GCGGCTGATC CCCCTAAGAG TCGGACTCGA G

471

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACGGAAAAAT AGTTATATTC CAGTCTAAGC CAGAAATCCA | 60 |
| GTACGCACCA CATTGGAGC AGGAGCCTAC AAATTTGAGA GAATCATCTC TAAGCAAAAT | 120 |
| GTCCTATCTG CAAATGAGAA ATTCACAAGC GCACAGGAAT TTCTTGAAG ATGGAGAAAG | 180 |
| TGATGGCTTT TTAAGATGCC TCTCTCTTAA CTCTGGGTGG ATTTTAACTA CAACTCTTGT | 240 |
| CCTCTCGGTG ATGGTATTGC TTGGATTG TTGTGCAACT GTTGCTACAG CTGTGGAGCA | 300 |
| GTATGTTCCC TCTGAGAAGC TGAGTATCTA TGGTGACTTG GAGTTTATGA ATGAACAAA | 360 |
| GCTAAACAGA TATCCAGCTT CTTCTCTTGT GGTGTTAGA TCTAAACTG AAGATCATGA | 420 |
| AGAAGCAGGG CCTTACCTA CAAAAGTGAA TCTCGAG | 457 |

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

| | |
|---|-----|
| GAATTCGGCC TTCANGGCCT AATAACATCT CCCAGACCC AGAAAAACAG AAAGCTCCAC | 60 |
| AGAAATTAAA TGTGAAGAG AACTCTCAA AGGAAGTTAC AGAAGAAAAC TATCTCTTTC | 120 |
| CCAGTAAGTT CAGTGGAAAG TGCACTAGAA CATGAATATG ACTNGGTGAA TTAGATGAAA | 180 |
| GTTTTATGG ACCAGAAAAG GCCACAACAT ATTATCTCAT CCAGAGACCC AAAGCCAAAA | 240 |
| CTCAGCTGAC AGGAATGTTT CAAAGGACAC AAAGAGAGAT GTGGACTCAA AGTCACCGGG | 300 |
| GATGCCTTTA TTTGAAGCAG AGGAAGGAGT TCTATCACGA ACCCAGATAT TTCCTACCAC | 360 |
| TATTAAAGTC ATTGATCCAG AATTTCTGGA GGAGCCACCT GCACTTGCA TTTTATATA | 420 |
| GGATCTGTAT GAAGAAGCAG TTGGAGAGAA AAAGAAGGAA GAGGAGACAG CTTCTGAAG | 480 |
| TGACAGTGTG AATTCTGAGG CATCATTTCC CAGCAGAAAT TCTGACACTG ATGATGGAAC | 540 |
| AGGAATGCTC GAG | 553 |

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

GAATTCGGCC TTCATGGCCT AGGTTCTTAG GCTCTGAGAT ACTTCCTGCT TCCCTCACAA

60

ACATGCTTAT GTTTGGTGTG CATGCACATT TGCCTATCAG CACATATAAA GAGACAGTGG 120
 AAAAGTCAGA AGTGTTCCTCA GGTATTTTTC CGATTGAATT CTAGACCTGC CTCGAG 176

(2) INFORMATION FOR SEQ ID NO:880:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GAATTCGGNC TTCATGGCCT ACTTCCTCTT CCTCCTCTTC CTCTTCCCCT TCCTGGTGCA 60
 GGTACATGAC ATTCCGCACG TTCCGGACGG CCCGGGCAGT CGGAGACAGG ATCACTGTGT 120
 CACAACTGTC ATCACTGTCC CCCTCACTGT CCAAAATGTA GTCCCGGGGA ACATGATTCC 180
 ACAGCCCATG ATGTCCCCTT TGTAACAGCG TGGCCCAAAG GGTCCCCCAC ACCACCTTCC 240
 TGCCCTCATG CTCGGCTCT ATCTCTTCCC CATCCTCTTC CTCTTCTCT TCCTCCTCTT 300
 CCTCTTCCCC TCACTCGAG 320

(2) INFORMATION FOR SEQ ID NO:881:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GAATTCGGCC TTCATGGCNT AATCTGTAAC ATGAGGGAAT AAAC TAGTAT TATCTAAGCA 60
 TTCTCTAGAC TTAAATATG ATTCTAGAC CACTGAGGAG ATTAATAATG AGGTGAGAGG 120
 GATTTCAAAA TGAAGCGACC TGCCAGACAT GGTGGCTCAC AGCTGTCATC CCAACATTTT 180
 GAGAGACTGA GGCAGGGGGA TCGATTGAGC CCAGGAGTTC AAGACCAGCC TGGACAACAT 240
 CGCAAGACCC TGTCTCTACA AAATAAAAAA AATGTAAAAA TAGCTAGGTG TGGTGGCACA 300
 CACCTATAGT CCCAGCTACT CGAG 324

(2) INFORMATION FOR SEQ ID NO:882:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GAATTCGGCC TTCATGGCCT ACAGAAATTG AGAGTAAACA GAAACATTTA TAGGTCAATT 60
 GCTATTGATT ACGAACGTCT AAGTGCATTT CAGTGTTTTA TATTTACAA ATGTGTTGGA 120
 ATTTTACTTT ACTTATTCTT TTGAGACAGG TTCTCGCACT CCAGCCTAGG CAACAGAGTG 180
 AGACTCCGTC CCAATCAGTC AATCAATCAA TCAATCAATA CCACAGCGGA:GAAAATCTTT 240
 ACAACTTTTG GTTAGGTAAT GATTCTTAG GTAGGACACA CAAAACACTC GAG 293

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGGC | CTTCATGGCC | TACCTACGGA | GTGCTTCTTT | CTCACCCTGC | ATGCTCACCA | 60 |
| CCTCTCTATT | CTGCCTAGTT | GCCGTCGCTA | TATCCGCAGA | CTCCGGGCTA | TCCGGGAGCT | 120 |
| CAATAGGTAT | GTGCCATGAT | ACCGTGTCTT | GGGATTGCCT | GAGTTACCAC | TTTTTCTCAG | 180 |
| GGGCAGGCAA | TTCCATTGTG | AACAGTAGTT | TTGAATGTTG | GGGGAGGTAT | GTACGTTATA | 240 |
| TAGTGTCTTCT | GTCTGCCTCC | ACCGCCACAT | CCATGTTGCT | CAGTTGTCCA | GAGTTCTTTA | 300 |
| CCTGGTGAAG | TGATCCAAAC | CTTGATTCTT | GAGAGTTCTG | AACCCCTCGA | G | 351 |

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACCTGGTGTT | TTTTGTTTTT | GTTTTTACCC | CTTGTCTTAT | 60 |
| GCCAGTGAGT | TCCTTCGGGG | TACTCCTGCG | AGTAGGTGGA | CTATCATCTG | GGACAGTTGG | 120 |
| GGAAGCTTCG | ACAGCCCTGA | GTTCAGCAGC | CCAGGTAGCT | TTGCAGTCTC | TCTCTCATGC | 180 |
| AATGGCTTCA | GCCGAGCAAC | AGCTACAGGT | GCTGCAAGAG | AAACAGCAGC | AGCTTTTGAA | 240 |
| GCTTCAGCAA | CAGAAAGCAA | AGCTGGAAGC | CAAGTTACAT | CAGACAACAG | CTGCAGCAGC | 300 |
| TGCAGCAGCA | TCAGCAGTAG | GTCTGTTC | CAACTCTGTG | CCTTCCAACC | CAGTGGCTGC | 360 |
| CCCTGGATTG | TTCAATTCATC | CATCTGATGT | TATTCCACCC | ACTCCAAAAA | CAACACCTCT | 420 |
| TTTTATGACT | CCACCACTCA | CCCCAGCCCT | CGAG | | | 454 |

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGACGAATTT | CAAGTATTTA | TTACCTCTGT | TGAATATAAT | 60 |
| TTATTGAACT | GTAAGCTTAT | ATATAATTCA | ACTTTAAAAA | ATGGCCTGAG | TTGAACAACC | 120 |
| AGCTCACCAC | AATTCTATAA | TCTAGGAGTT | GGCTCTCGTG | GGTCGGCACA | GGTCAGCTAG | 180 |
| GGTGCCTGGT | CCTGGTGGAG | GGCAGGAGGC | CCCCTTCCCC | TGGCCTCCCT | AGCCAGTCCC | 240 |
| CACACACAGC | CCCAGTGGCC | TCCACAGCTC | CACCCTCCTT | TCATGGCCGT | TCTTTTCTT | 300 |
| AGATGCCAAA | AGCAGAAAGC | TCGAG | | | | 325 |

(2) INFORMATION FOR SEQ ID NO:886:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGGAGAATT ATTTGATATT TGTTGATACT TGACAGCAGA | 60 |
| TAATTTTTTA ACTGCAAGAC CACTAGAGGT CACCAGCGTA AAACCTTCAA CTTTGATTCT | 120 |
| GCTGGTAGTG AACTGAAAAG TTCAACTACT ATTCTGCAAT GTTTCCTTTG TTTCTTTTTT | 180 |
| TTTCTTTTTT TTGTTTTGAG ATGGAGTGTT GCTCTGTCAC CCAGGCTCGA G | 231 |

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGTTGCAGAA GAAAAAAAG AAAATCCATC CCTGCCACTC | 60 |
| ACAAGCTGCT ACCTACAGCA GATTACTATC CTAAGCCTCA ATTTTGCCAT CTGAAAAAAA | 120 |
| CAGAAAAAAC AGTTAATAAT ACCTCACCAG GTTCTTGCTA ATTCTTTAGT AACACAGAGG | 180 |
| AATCTTTTAG CCCTTCTTTT TTTGTCTTAT AGCTTAAACC ATGCTGCAGG AAATGTATCA | 240 |
| ATCCAAGATA AAAGAGCTGA AATCCAAGAA CCTCCCCCTC ACATTTTGTT TGTTTGTGTTG | 300 |
| TTTTGTGTTG TTTTGTGTTG ACACAGGATC TTGCTCTGTC ACCCAGGCTC TCGAG | 355 |

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCCACCACG CCCAGCCTCA ATTGCATTC TACACACAAG | 60 |
| GAATAATCCA AAAAGGAAAT TAAGGAAACA ATTCATTTA CAGTAGCATC AATATGAATA | 120 |
| AAATATTTAG AAATAAACTT AACCAGTGAT GTACAGTGAC AGTATGTACA CTGAAAGCTA | 180 |
| CAAAACATCA CTAACATAAA TGAAGACAAA TTAGACATCC TGTGTTAATA CATTGGAAGG | 240 |
| CTCTTAAGCT GTCAATACTA AAGGTGATCT ACAAATTCAG TGCAATCCCT GTCAAAATCC | 300 |
| CAATGATGTT TTTTGAAGAA ATAGAAAAAC TCATCTGGGA ATTCATACGG AATCTCGAG | 359 |

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

```
GAATTCGGCC TTCATGGCCT ACTAAATTGG AATAAAAGTT TTAATAATAC TAACTTGTCT    60
TTTTTTTTTT TCTAAAATTG ATTCCATTGC TACTGTTAAT AGTATAAATC TTAAAAGGGT    120
GAATTTTTTG GATGAAATTA ATGCTTATTC TTTTCTTTT AAACAGGGCA ATAAATGTGT    180
TCGTAAGTGC CAACCAACTC GAG                                         203
```

(2) INFORMATION FOR SEQ ID NO:890:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

```
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AGTTGATTGG    60
TTTTCTTAGG TCAGCAATGA GTCTTAAAGA TAAATTTCT ACTGTGTAAT CTTTAGTGT    120
TTCTTTTTTT TTTCAACTAT CTTTAAATCA GTTTCAAACA TTTCAGTGAT TAAAAGAGAG    180
ATTTGTTGTG GTTTTGTGTG GGAGCAGAAA TGGATTTCAG GGAGTTTACC TTCAGAGCTT    240
TTGTTTTTGT TACGGTGGGT CTCTCTAGTG GAAAAAAAT TTCCCCATCC CTTTGGAAT    300
ATTTTCTTTA AAGGAAATCA TGTTTTTAAA ACAAATTATC GAAATCAGCT TTCTAATCAA    360
TTGAATCAT CTCGAG                                         376
```

(2) INFORMATION FOR SEQ ID NO:891:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

```
GAATTCGGCC TTCATGGCCT ACGCTTGTC GTGGCTTCTC TGAGAAGAAA AGTTGAAAAA    60
GGGTAAAAGT TTTCAGGAAT ATTCCGGCTC TCTATTGCTA AGCATAGCGA GTGTCGGTTT    120
TCTCTCTCCA ACAGACATCG CTATTGCGGT TCCGAGGCAG TGGGAAGAGA TGCGGCCCCCT    180
GGACATCGTC GAGCTGGCGG AACCAGGAGGA AGTGGAGGTG CTGGAGCCCC AGGAGGATTT    240
CGAGCAGTTT CTGCTCCCGG TCATCAACGA GATGCCCGCA GGACATCGCG TCGCTGACGC    300
GCGAGCACGG GCGGGCGTAC CCACGGACCC TCGAG                                         335
```

(2) INFORMATION FOR SEQ ID NO:892:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTATCTTTA AAGTTAATGT CTAGCCAAGA GTTTAGTAAA | 60 |
| CGAAGAATTA AACTGCACTG TTGATCGGTG CTTTGTGTAA ATACATCTTT AACATTGGG | 120 |
| TGGAGAGGGG CCTTAAGAAG GACAGTTCAT TGTAGGAAAG CAATTCTGTA CATGAGTTTA | 180 |
| AGCATTCTTG TTGCATTGTC TCTGCAGATT CTATTTTGT TTACAATATT GAAATGTATG | 240 |
| TTAGCAAAAT GGGTGGATTT TCAAATAAAA TGCAGCTTCC CACTCGAG | 288 |

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTCATCGCT AGTCCATATT TGGCCTCCTT TTAAGCAGTT | 60 |
| AATTAACAGG TATTTTTATA GCATAATGGG TTTCCTCAAA CCACCACCCA ACCAAAACCC | 120 |
| AGCCCTTGAT GATGACCTGC GCCCACCACG CAGGGCGCCC TTGATGCACA CGCACCTGCC | 180 |
| GCCCCGCCCC TGTGACCACC GCCCTGAGTG CCGGGCTCAT CATCCCTTCC ATGCCCTTTC | 240 |
| TACATTGCTA CTAAGAATCT GTGTGTATTC ATTAAGACCA TTACTTTTCT TTCAGATTTT | 300 |
| AAATTTATTA AAGGCTTTAG TGCTGAATGT GATTTTGAGG ACTCTTTTAA AAAAATACTT | 360 |
| TTGTTGGAA TGTGGACATT TCCCACTTAG CATTGTGTTG CTCATGTTCC TCCATATTGA | 420 |
| TGTGTGTTTA GCTAGAGTAC CCCCCTCTAA CTCTGCGAAT ATGCCACACT GTGTGCACCT | 480 |
| GCATACACTC GAG | 493 |

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAAAAAGGA AATAGAATCC TATAATTAC CATGAAAATA | 60 |
| TTATGAAAGA TACAGGTCAG CATGTATTGT AGGAGCAAAC TTAGTGGTCC TGCTGGTCTT | 120 |
| TTGGGTTTTCAT TGGTTTGTGG TTAAGTTTCA AGTAAGTTCC CTCTTGGTCT GGTGTGTTCT | 180 |
| GCTGCTGGTG AGCTCCAGCA GCTCAAACCA GCTCTCTCCC ATTAGTAAGC CATGCTAAGT | 240 |
| TTAGTTTAAC ACCCATAGTA GGCCTAAAAG CAGCCACCAA TTAAGAAAGC GTTCAAGCTC | 300 |
| AACACCCACA TACTCGAG | 318 |

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```

GAATTCGGCC TTCATGGCCT ACATTGAGTC AGTCACCAGG TGTTTTTTTT TGGTTTGTGTT    60
TTATTTTGTGTT TTGTTTCTGT TTGACACCTG CAGTATCTCG GCAGGTCAGA CTGTCATGCC    120
GTGCAGGTGC CAGCCCTCTC TCTGCTGTTT TTGCTCTTGT TGCTCTCAGA GCCAAGAGCC    180
ACTCTGCACC CAGAGGGCCT CCCATCCACA CCAGCCTGCC CTTTACTCAG CTCTCACTTT    240
CGTCATCACC TGTGGGATCC TGTCTGCAGA ACCCCCTCAA AACTCTTTCC TTCACGGTGC    300
AGCTCCACCC ATCCTCGAG                                     --    319

```

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

```

GAATTCGGCC TTCATGGCCT AAGACAGGGA GGCAGACACA TTGAGAAATA ATACAAATTA    60
TTATCATCTT CATAAATAAT ATAGACAGCT CTGACGATAA AGGTGTGTAC CAGATATGAC    120
AGGAGCAGAG CTGAGGCATC CAGCACCTTC AGGGATGAGG GGTAATGGTG TTAGGAAAGG    180
TTTTCTGTAC TTCCTCTACG TGGGTGCTTT TCTCCATCTC TACTTTCAA TCCCACCCAT    240
GCTAAGGCCT TATCCAAATG ACCACTGCCA GAAAG                                     275

```

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

```

CTCGAGTTCC CCCATCAGTC TATGTGCCCC ATGAGAGCAG GCACACATAG GAACAGGTCA    60
GTCAGTTCCT GATGCCCAGC ACAAGGCCAG GCACAGAGTG GCAGGGGAGT TGTGGGGCCC    120
CACAGACCAG AGGCCAGCGC CAATTCTGCC CCTGCTATTT GCATGCCCTC ACCTCTGTGG    180
GCCCCTGTCT GTCTGCGAGG ATTCAGGGAG TAAGTCTCTG AGCACAGCGC GGGTTGGAGC    240
ATGCAGAACT GCCAGGTGCT ATCAGCACCA TCATTCTTTC CACTCCCTAC TCCCTTTAGG    300
CCATGAAGGC CGAATTC                                     317

```

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATGACCTGGA AGAGTGGTGC GAAAGAGAGG AAGGGGCAGA | 60 |
| GGCCAGGAGT GTCATGCAAT TGCTGTGCCT CCTCACGGAA TTATTGAGTG TGTCCCCTGT | 120 |
| GTCATAGACC CATCACAGTT GTCTCTTCCA GTACTTCGTG AGCTCCCTAA GGGCAGGGAC | 180 |
| TGTGTATACT TCTGGGCGCT AAAATGAGTG TGAATCCATG TCAGGCACTC TGTGCCAGTC | 240 |
| TTTATTGGAA ATATATGATT TTATCTTAAA TAGTTCCTCA ATGTAGGTAC TATCACTTGC | 300 |
| CCTGACTTTA GAGATACAGG CACTAAGGTT TGTGGAGGTA AATAACTTTC CCAAGATCCT | 360 |
| CGAG | 364 |

(2) INFORMATION FOR SEQ ID NO:899:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTGTTTAT GGATATCCTC CAGATTATTA TGGATATGAA | 60 |
| GATTATTATG ATTATTATGG TTATGATTAC CATAACTATC GTGGTGGATA TGAAGATCCA | 120 |
| TACTATGGTT ATGAAGATTT TCAAGTTGGA GCTAGAGGAA GGGGTGGTAG AGGAGCAAGG | 180 |
| GGTGCTGCTC CATCCAGAGG TCGTGGGGCT GCTCCTCCCC GCGGTAGAGC CGGTTATTCA | 240 |
| CAGAGAGGAG GTCCTGGATC AGCAAGAGGC GTTCGAGGTG CGAGAGGAGG TGCCAACAA | 300 |
| ACTCGAG | 307 |

(2) INFORMATION FOR SEQ ID NO:900:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATTTCCATC ANGAANTCNG TGAGGTTCTC AGATGTGGCA | 60 |
| ATGTCCACGC AGTTTCGCAC CANGGCATGG CGGTCTTGT CTCCCATTC TGGCTGTCCC | 120 |
| AGGTAGCGCA GATGCCAGGG TGCCCCTGCC CTGTCCATAG AGCGTCGGGC CCTGAGAACA | 180 |
| AATGGGCTGG CTTGCTGGNC CTTAAGGAGG AATACCATCT CATGGTCAAG GAAAGTCTCA | 240 |
| GGTTCCATGT TGTACACAA ACCACGAAGG CGGTGGATGA GGCTTTCCAA ACTGTGATCT | 300 |
| AAAACACTTC CCTGCAACAG GTACTCCATC ATGTTAATGG TGCCCCCAGT GACAGGGATC | 360 |
| ATGGTGA CTG GAGGTGCCTC CATGGTGTCT AAGTTGAAGA CAACACA ACT GGACTCAGAG | 420 |
| CCCCCAGTCA GGTAAGGCAC GGGATATACC TCCTTGAGGC TGTAGTGTCT TCCTCGAG | 478 |

(2) INFORMATION FOR SEQ ID NO:901:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

```

GTACCAGGCG NATCCTGAAG AGACACTACT ACNACCAAAT GGAACCCAG AAGAAATAAA 60
ATGTTTGGAT CNAATAAAGA AAATTGAAAC NACTGGTTGC NACCNAGAAA TAACATCATT 120
TGAAATTAAT CTGAAGGAAA AAAAGTACCA GGAGGACTTT AACCCGCTGG TGAGAGGATG 180
TTCCTGTTAC TGCTGTAAGA ATCACACTCG GGCATACATC CACCATCTGC TGGTGACCAA 240
TGAGCTGCTG GCCGGAGTCC TGCTTATGAT GCACAACCTT GAACACTACT TTGGGTTTTT 300
CCATTACATC CGGGAAGCAC TAAAAAGTGA CAAACTGGCA CAGTTGAAAG AGCTCATCCA 360
CAGGCAAGCA TCTTGAGATC TTGCAAATAC AAGTCTCACT CTTCACTG AGCCTGTACC 420
ACTGTTGTAA CATGGAAGA CGTGAAGAAG AAATAATCTG AGCTCGAG 468

```

(2) INFORMATION FOR SEQ ID NO:902: --

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

```

GAATTCGGCC TTCATGGNCT AGCCAGGGAT AAAAATACAA TCTTCAAAGC GGTCAGAGAA 60
AAAAATGCAAA TTATGAACAG AGGCATCAAG GTAACAATAA CAGCCGAATT CTGGTCAGAG 120
ACAATGCAAA CCACACATGA GCAGAGCGGN CCCTTTAAAG AACTCAAAGG AAAGAAAAAG 180
TGAATCGACC TGGAGCTCAG AGCCAGATAA AATATCTTGA AAATATGAAA GTAAAAAAG 240
GAGAAGAGGA GCTCATGAGG GCAGAGGGAC TAGTGTAAGG AAAGGTGTGT AGGTGGGAAA 300
AGGNCCAGTG TGTTCAAGCA TAGATAAGAA AAGNAGACCA CGCNAAGAG TAGACGAACA 360
GGCAAGGTTG GTCATCAGGT GAAAAGACAG GTTAGTGGAC GATCAAAGAG GNTCTTGACT 420
GCCGTGCTAC AATAAACTAC ATATTTTTTT TTAGGCAAA GTAAGGATTT CAGAGATGAT 480
TTTAAACATG GGATGATATA ATGCACAGTA TTTTAGAAAT ATTGTTCTAA ATCAAGAGTG 540
GAGAACCAC TGCGGAGACA AATTCTCGAG 570

```

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

```

GAATTCGGCT TCATGGCCTA CTCCATCAA ACTCCAGAGA AGAGAGTGAA TACTGGAGAA 60
GAAAGGAGGA AAATATCTGA GGAAGCAGCA AGAAAGAGAA GGCTGGAATT TATTGAAAAA 120
GAAAAGAAAC AAAAGGATCA GATTATTAGT TTAATGAAGG CTGAACAAAT GAAAAGGCAA 180
GAAAAGGAAA GGTGGAAG AATAAATAGG GCCAGGGAAC AAGGATGGAG AAATGTGCTA 240
AGTGCTGGTG GAAGTGGTGA AGTAAAGGCT CCTTTTCTGG GCAGTGGAG GACTATAGCT 300
CCATCATCTT TTTCTTCTCG AG 322

```

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAATGTATGT | AAGGTACAGA | GAGGATGTCT | GGAGGTGCGC | 60 |
| CCTGTGGATA | TCTTAAGCCT | TTAAGGGTGA | GCAAAAAACA | ATAGGTTCAC | AAAGGAAAAT | 120 |
| GAGAATGGGC | TATGAGAAAG | GTAAGAGGAA | AACCAAGGAA | AGAGAACGTT | TTGAGACAGT | 180 |
| AGTAGTGGTC | AGCAATGTCA | AATTGCTGCA | GAAATTTTCT | AAGAGTGAAA | TTGGGTTTAG | 240 |
| CAGCTGCAAG | AGGAGTTCAT | TTAATTGGTG | TAGCAGAAGC | CCATTAGATT | GCAGTGTGAT | 300 |
| GAGAAATTAT | TGGGAACAAG | GATACTCGAG | | | | 330 |

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGATGCCGCC | ATCTACCAGG | CCTCTGCCCC | AGAACAGCAA | 60 |
| GGGCATTGTG | TCCTGCTCAG | GGGTCCCTGA | GGTGGGCACC | ATGACTGAGT | ACAAGATCCA | 120 |
| CCAGCGCTGG | TCGCCNAGT | TGAAGCGCAA | GGCTGCGGCA | AAGCTGCGCG | AGATCGAGCA | 180 |
| GAGCTGGAAG | CACGAGAAGG | CGGTGCCTGG | GGAGGTCGAC | ACTCTGCGCA | AGCTCAGCCC | 240 |
| CGACCGCTTC | CAGCGAAAGC | GGCGATTGAG | CGGGGCTCAA | GCGCCGGGCC | CCTCGGTCCC | 300 |
| TACCAGGGAG | CCTGAGGGTG | GGACCCTGGC | GGCTTGCCAG | GAGGCAGAGA | CTGAGACTGC | 360 |
| TCAGCACTCA | GGTTTGGGCC | TGATCAACAG | TTTTGCTTCT | GGAGAAGTGA | CCACCAACGG | 420 |
| GGAGGCTGCC | CCCGAGAATG | GCGAGGCTCG | AG | | | 452 |

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGCCATGGAT | TTAAAGAAAT | TGTGACTAAA | CCAATGTTTT | 60 |
| AGCATTGATA | AATGGGAAAT | TGCGGAAGGA | TGTAAACGTA | GAGTTTAACT | CTACAACCTG | 120 |
| GCTTAGGGAC | TCAGGTATGG | ACAGTGAGAA | TAACTTGGTT | TAGGGACTCA | GATATGGACA | 180 |
| GTGAGACTGG | CCACATGAGT | GCCTTTCTCA | CTGTCAACT | CTTACCCAGG | TTGGAGTGCA | 240 |
| GTGGCTGTCT | ACAGGTGTGA | TCATAGCTCC | CTGCAGCCTT | GAATTCCTGG | GCTCAAGCAG | 300 |
| TCCTGCCTCA | GCCTCCCAAG | GAGGTGGGAC | TAAAGATGGT | GTGCCACCAC | ACCTGGCTAA | 360 |
| TTTTTAAATT | TATTGTAGAG | AAGGGTCTT | GCTATGTTGC | CCAGGTGGT | CTTGAACCCC | 420 |
| TGACCTCCAG | GGATCTCTCC | TGCCTTGGCC | TCCTCAGGAG | CTGGAACTAC | AGATATATGC | 480 |
| TAATGTCTTC | AATTTATGGA | AATGCAGAAA | TGCTCGAG | | | 518 |

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTTGCTGCT | GCGCTTTGAC | ATCAGCTTGA | AGAAGAATAC | 60 |
| CCACACCTAC | TTCTACACCA | GCTTTGCAGC | CTACATCTTC | GGCCTGGGCC | TTACCATCTT | 120 |
| CATCATGCAC | ATCTTCAAGC | ATGCTCAGCC | TGCCGTCCTA | TACCTGGTCC | CCGCTGTCAT | 180 |
| CGGTTTTCCT | GTCCTGGTGG | CGCTGGCCAA | GGGAGAAGTG | ACAGAGATGT | TCAGCTACGA | 240 |
| GTCCTCGGCG | GAAATCCTGC | CTCATACCCC | GAGGCTCACC | CACTTCCCCA | CAGTCTCGGG | 300 |
| CTCCCCAGCC | AGCCTGGCCG | ACTCCATGCA | GCAGAAGCTA | GCTGGCCCTC | GCCGCCGGCG | 360 |
| CCCGCAGAAT | CCCAGCGGTC | TCGAG | | | | 385 |

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACCCCTGTCC | ACTTTGGTCA | CTGTTGGCTG | GGGCCCCGTGG | 60 |
| AGCTGTCCAG | AGGGGACCGG | GGCCAGTAGA | GTAAGGACA | GTATTTGTAG | AGCAGGCATT | 120 |
| TCTTCTGAGG | TTCTTGGA | TCCCCTGAGC | TATGAAAGCT | GGAAGCAGTT | GAAAGTTTTC | 180 |
| AGGGAGAGGG | ATGCTGGAGT | CTCAGAACTT | TAGAGGTGCT | GCAGGAGTCA | GTTCTGGCAG | 240 |
| TGAGAGAACA | CTTGGGCGGG | TTTCACACAC | ACACAGCACT | TGAGCCATT | TTGGGCAGAA | 300 |
| GGGGCCTCAC | TTCCAAGCAC | AAGGAGTGTT | AACGAAAAAT | JATTAACATG | GTAAGGAAGA | 360 |
| CTTTATTTCAG | GGCCATTGCA | GTAAGCATCC | CAATAGTGGG | GAGAGATGGG | GCTCAATTCC | 420 |
| AAGTACAAGA | AGAACAAGTG | GGCACTTAGC | CAAGGAGCAG | GTGGGAGGGG | GTCAGAGGAT | 480 |
| AGAAAATTAC | TAAGAGGAGA | CGTCAAGGTT | AGGGGGATT | TTGCTGAAGT | CAGGCCAAGG | 540 |
| AGCAGGTGGG | AGGGGGTCAG | AGGATGGAAA | ATTACTAAGA | GGAGACGTCA | AGGTTAGGGG | 600 |
| GATTCTTGCT | GAAGTCAGGC | CTTGCTCGAG | | | | 630 |

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGACGGTGAT | GTTTTTGGTA | AACAGGCGGG | GTAAGATTTG | 60 |
| CCGAGTTTCCT | TTTACTTTTT | TTAACCTTTC | CTTATGAGCA | TGCCTGTGTT | GGGTTGACAG | 120 |
| TGAGGGTAAT | AATGACTTGT | TGGTTGATTG | TAGATATTGG | GCTGTTAATT | GTCAGTTCAG | 180 |
| TGTTTTAATC | TGACGCAGGC | TTATGCCGAG | GAGAATGTTT | TCATGTACT | TATACTAACA | 240 |
| TTAGTTCCTC | TATAGGGTGA | TAGATTGGTC | CAATTGGGTG | TGAGGAGTTC | AGTTATATGT | 300 |
| TTGGGATTTT | TTCGAGGGTG | TAGGGATGCG | AGCTCTGGAG | GGGACCCCTC | TTTCAGGACA | 360 |
| GCGCCCTGGC | CCCCAGTGCC | CCACTCACCT | TCCTGGGCGG | GAACCTCAAG | TGCAGCCAGG | 420 |
| CTGGGGGACA | GAGTTCCCCC | CAAGCTGAGA | CAGGAGGGGT | CTCAGGCGGC | AAAATTCCTC | 480 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCCAAGTCC | TGGTGGGGTG | GGGGTCATGG | ATGAGGGGGG | CCCCTTCCTT | CCCCAGCCCA | 540 |
| CTCAGGGCAC | CCCTGGCCCG | TCCCGCCCCA | CCTCCAGCTG | CTTCATGGTC | TCCTCCAAGC | 600 |
| TGAGCAGGTT | CTCCTGGATT | TCCTGGGTCC | GTGCTGGGCT | CAGGGGGCCG | CCCCCTGGGA | 660 |
| CCCCATCCCC | ATCTCGAG | | | | | 678 |

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGAAGAGGA | GGAAGAAGAC | GGGGCTGCAG | TTGCTGAGAA | 60 |
| ATCACATCGA | AGAGCTGAAA | TGTAGCGGCA | CCCAATTTCT | AGACAACGCT | CAGCCAACGG | 120 |
| ATTCTTTTCA | AGCTGCTCAA | ACATAAATCT | GCCTACTGAA | CTCTAGGATA | TTTAATTACA | 180 |
| AAAATTAAGA | ACTTAGACTT | TTTTAAACT | TTTGTATTAG | AAATGCGCAT | ACATTTATAT | 240 |
| GAATATATTT | TGATAACGTA | GGTCTAGAGC | TTCTTTTATA | TTCAAGCTTA | ACATGANAAA | 300 |
| GAAGAAAAAC | AATAAAGTAA | ACCTGAGCCC | CCACGTCCCA | ATTTTTTAAT | AGATTATGTG | 360 |
| ATGTTGGAAG | GCTCATTGAT | TTTGTATATG | TTTCAGCGTG | TTACCTTTCT | GGCTTCCAGT | 420 |
| TCCCAGGTGT | TCTTTGTTTG | CCTTTGATAA | AATACAGGAT | TTAAGAACAG | AGAGTACTGC | 480 |
| AAAATGCCAT | GCAGACTTTA | AAGAGAATGG | CCTGTTTACT | AATTGCTGCC | CTTCTGATGT | 540 |
| CTTTATGTAT | AGCTCTGATA | GAATTTTCAC | CAGTCTATGT | ATCTCTGGAG | TGAGATCCTA | 600 |
| TGTACAAAGT | GACATACAAT | TGGAAATCCT | CGAG | | | 634 |

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCGACCTTC | ATGGCCTAAT | GAGCTGTTTT | GTAAACGAGA | TTTGTTTTGT | GGGAAAGGGA | 60 |
| ATTTTGTTTC | AAGACTTCCC | TAAGAACTG | ATAGCATCGG | GTAATCTTA | AATTGACTT | 120 |
| ATCATAATGG | TATATCTGGA | AGGAATTGT | CAACTGATAT | GTTATAATTA | TTTTTAATT | 180 |
| TTTTTTAATT | TTTGAGATAG | GTCTTACTCT | CTTGCCCAGA | CTGGAGTGCA | GTGGTGTGAT | 240 |
| CATGGTTCAC | AGCAGCCTCA | AACTCCTGGG | CTCAAGAGAT | CCTCCACCT | CAGTCTCCTG | 300 |
| AGTAGCTGGG | ACTAAAGGCA | TGTGCCACCA | TGCTGGGCTA | GTAAATTTT | TTTTTTTTTT | 360 |
| TTAAGTAGAG | ATGAAGTCTT | GCTGTGTTGT | CCAAGCTGGT | CTCACACTCC | TGAGCTTGAG | 420 |
| CAACCTCCT | CTAGGCCATG | AAGGCCGAAT | TC | | | 452 |

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGCGGGCTAT | GTGGCTGATT | GAAGAGTATG | CAATGAGCGA | 60 |
| TTTGTAGTCT | GTTTGTGCTA | GGCAGATGGA | GCTTGTATA | ATTATGCCTC | ATAGGGATAG | 120 |
| TACAAGGAAG | GGGTAGGCTA | TGTGTTTTGT | CAGGGGGTTG | AGTTTGATGA | GTTTAGGCAG | 180 |
| GGCCTGGATC | ACCTCTTCT | TCTCCAGCCC | ATTGAGCACC | GGGATGAGGA | AGCGGACGTC | 240 |
| TGGCAGTCGC | TTGTGGTAGA | GATCCCGGAC | CCGCTTCACC | AGCTCTGGGG | AGGGTGGGAC | 300 |
| TTTGTCTGTG | AGGCTGTGCA | GACATCTCGT | GACCAGTGTC | TCTGCTCCCT | TGGGACAATT | 360 |
| TTCCACCAGC | AGGAGCAGCT | CCGGGGAGTT | CATGCCCATT | CCTCGGATCG | GCTGCTCAAT | 420 |
| GACCTCAGC | ACCGTCCGCT | TGATGTCGGC | GATGGCTTCA | GTGTACACGG | CCGCCAGTTC | 480 |
| GTGGATCAGC | TTGTGGGCTC | GAG | | | | 503 |

(2) INFORMATION FOR SEQ ID NO:913:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAAAGATATT | ATTTTAAATT | AATTTTGAAC | TATAGAAAAG | 60 |
| TAGTACAAAT | AATTCAGAAA | ACTCCCATAT | TTACTTTACA | TGGATTCACC | AATTTTAAAC | 120 |
| ATTTTGCTAC | ATTTGTTTGC | TTCTCTCGCT | GTCTCTACAC | ACACATACAC | ACACAAATTT | 180 |
| TTGGGAGGTC | TAGTGACAGT | CCCGGCCGGC | CCAGGAGGAC | AGGAAAACAT | CACTCAGGAA | 240 |
| GTCACTCTTG | GCCCCGAGCC | GCTTTGTCCT | GTCTTCTGTC | AGGAGGCCCT | CCAGGAGGTG | 300 |
| TCTTGCGGAA | TTGTAAATAT | TTGGTTTCAT | CTCGAG | | | 336 |

(2) INFORMATION FOR SEQ ID NO:914:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGACAGTCAA | TGTGGATGAG | AACTAATCGC | TGATCGTCAG | 60 |
| ATCAAATAAA | GTTATAAAAT | TGCAAAAAAA | AAAAAATAAA | AAGAAGTGAG | GATGACAGGA | 120 |
| GAAGGTAGAT | GGTGCAACAT | GAGGGTGCTT | TCTACCAACA | AGGTGTGCAG | CATTGGACAC | 180 |
| GCATGACCAC | GTGACCTGCA | GCTCTGATGG | TGCAACATGA | GGGTATGTCC | TACCAACAAG | 240 |
| GTGTGCAGCA | TTGGACATAC | TTGACCACGT | GACCTGCGGC | TCTGAAGGTC | CCACCTGTTC | 300 |
| TCGTTCTAAA | GTCAACCATTT | CTGACCGCTG | TGCTGTGGAA | GGGGAGGCAA | TCAACCAGAA | 360 |
| CTCGAG | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:915:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGCAACAAG AGCCCTGAAG TGCTCCGGGC ATTTGATGTA | 60 |
| CCAGACGCAG AGGCACGAGA GCATCCACG GTGGTACCA GTCATAAATC ACCTGTTTGT | 120 |
| GATACAAAGC CCAAGGAGAC AGGTGGAATC CTGGGGGAAG GCACACCGAA AGAAAGCAGT | 180 |
| ACTGAAAGCA GCCAGTCGGC CAAGCCTGTC TCTGGCCAAG ACACATCAGG GAATACAGAA | 240 |
| GGTTCACCCG CAGCGGAAAA GGCCAGCTC AAGTCTGAAG CCGCAGGCAG CCCAGACCAA | 300 |
| GGCAGCACAT ACAGCCCCGC AAGAGGTGTG GCTGGACAC GTGGACAGGA TCCGGTCAGC | 360 |
| AGCCCCGTGTG GCTAGAGGAA CACCACTCGA G | 391 |

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACGGGTGTTC GAGGAGTACA TGCGGGTTAT TAGCCAGCGG | 60 |
| TACCCAGACA TCCGCATTGA AGGAGAGAAT TACCTCCCTC AACCAATATA TAGACACATA | 120 |
| GCATCTTTCC TGTCAGTCTT CAACTAGTA TTAATAGGCT TAATAATTGT TGGCAAGGAT | 180 |
| CCTTTTGCTT TCTTTGGCAT GCAAGCTCCT AGCATCTGGC AGTGGGGCCA AGAAAAAAG | 240 |
| GTTTATGCAT GTATGATGGT TTTCTTCTTG AGCAACATGA TTGAGAACCA GTGTATGTCA | 300 |
| ACAGGTGCAT TTGAGATAAC TTTAAATGAT GTACCTGTGT GGTCTAAGCT GGAATCTGGT | 360 |
| CACCTTCCAT CCACACTCGA G | 381 |

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

| | |
|---|-----|
| AGATGGACTG GCTTCAGCTG GTTTTGGAGG TGCTTGTGTT TGGAANAAAT GCAGGGATGG | 60 |
| CAGANGCCTG GCTCTGCAGC CAGGANCCAC TGGTGCGCAG CGCTGAGCTG GGTTCACCGG | 120 |
| TCGACGAAGT TGAGAGCCTC ATCAAGCGGC ACGAGGCCTT CCAGAAGTCA GCAGTGGCCT | 180 |
| GGGAGGAGCG ATTCTGTGCG CTGGAGAAGC TTAAGTGGCT AGAGGAGCGG GAGAAGGAGC | 240 |
| GAAAGAGAAA GAGGGAGGAG GAGGAGCGGC GGAACAGCC GCTTGCTCCC GAACCCACAG | 300 |
| CCAGTGTGCC TCCAGGGGAC TTGGTGGGCG GCCAGACAGC TTCTGACACC ACCTGGGACG | 360 |
| GAACCCAGCC ACGGCCACCA CCATCCACAC AAGCACCCAG TGTTAATGGA GTCTGCACAG | 420 |
| ATGGAGAGCC CTCACAGCCC CTGCTGGGAC AACAGAGACT TGAGCACAGC AGCTTCCCCG | 480 |
| AAGGGCCGGG ACCTGGCTCA GGGGACGAAG CCAATGGGCC CCGGGGAGAG AGGCAGACCC | 540 |
| GGACTCGGGG CCCGGCCCCA TCTGCAATGC CCCAGAGCAG GTCTACCGAG TCAGCCCATG | 600 |
| CTGCCACCTT GCCGCCTCGA G | 621 |

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

```

GAATTCGGCC TTCATGGCCT AACATGGGTG ACACGGATGT CTATAGTGTC CACCACATTG      60
TCTGCGATGT GGAGGAAGGA GGCCAGCCCC AGGAGGCAGG ACTCTGTGCT GGGGACCTCA      120
TCACCCACGT GAATGGGGAG CCTGTGCATG GCATGGTGCA TCCTGAGGTC GTGGAGCTGA      180
TCCTTAAGAG TGGCAACAAG GTAGCAGTGA CCACAACGCC CTTGAAAAAT ACCTCTATCC      240
GCATTGGTCC CGCAAGGCGC AGCAGCTACA AGGCTAAAAT GGCTCGGAGG AACAAAGCGAC      300
CCTCCGCCAA GGAGGGCCAG GAGAGCAAGA AGCGCAGCTC CCTCTTCCGG AAGATCACGA      360
AGCAGTCGAA CCTGCTGCAT ACTAGCCGCT CGTGTCGTC GCTGAACCGC TCGCTGTCAT      420
CCAGCGATAG TCTCCCGGGC TCGCCTACGC ACGGGCTGCC GGCGCGCTCG CCCACGCACA      480
GCTACCGCTC CACGCCTGAC TCCGCCTACC TAGGCGCCTC ATCCAGAGC AGCTCCCCAG      540
CCTCGAG                                         547

```

(2) INFORMATION FOR SEQ ID NO:919:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

```

GAATTCGGCC TTCATGGCCT ANACACTCTT CCTCTTCTCC TTTTTCCTTT AGAGATATGA      60
ATCAGGTTCT TGATGCCTAT GAAAATAAGA AGCCATTTTA TCTGTACACG GGCCGGGGCC      120
CCTCTTCTGA AGCAATGCAT GTAGGTCACC TCATTCCATT TATTTTCACA AAGTAAGTAT      180
NGGATCTTAT GGCTTTTCTT ACTCTCTTAG TGAATTGAGA ATGTTGCTTA TAAACCATGT      240
TTAGAACTGA CAAGATCATG CTAGTTCATT TGCTGAGCAA CCAAGATGTC AAGAGTTGGC      300
ACTTTTTTGG CTTCCATTCA CTTTGTTCCT GGGCTCACTT TAGAGGACCA TGGAGTGATG      360
GGGAGAGCGC AGCTTTGGAG TCAGCCAGGC CTGCTCCTCT TCTCATCCTG CTCCCTGTCT      420
GCATGGCCAT GGGCCTGCTA CTTCTCTGAG CCTAAGTTTC CACATCTGCA AGATGAGAAT      480
GAAGATACCT ACCTCATAGA ACTACTGTAA AGCTTCAAAA CAAAGTGTGT AGAGCAGCTA      540
ACACAGAGCA CACAGGGCCA CCTGGTCGAT AAATGGTAGT AGACCTTATC ATTATCCATA      600
GTCCCTCGAG                                         610

```

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

```

GAATTCGGCC TTCATGGCCT ACTAACTCTC CTTCTCAAAA CACCAAAAGT AAATTTTAAT      60
ACCCAAAACG AAATTCATTT TGTTAATCAC AGCTTAGAAG GTTTCATATG ATCTGGCCAA      120
ATCTGTATCT TGCATCACTC TTATCACTCC CCCTCTCTGC TCACTGTATC TGCATGATG      180

```

GAATCAGCTC ATCTTCCTAT ACATCAGTAC TAAACAACC TCACTCCTAC CTGAGGCCCT 240
 GTGTGCTGTC TGTAGATGGT CCATCTTCTC ACTTCACTCA GGACTCAAAT GTCCCTCTT 300
 CACTCGAG 308

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GCAACCGGGT TTTGCCAGGG CCTATTGCAC CAGAGAGCAG CAAGAAGCGG GCCCGTAGGA 60
 TCGGACCAGA CCTTTCTAAG ATGATGGCCC TCATGCAGGG TGAAGCACT GGGTCTCTAT 120
 CTCTGCATAA CAGGTTCCAA CACAGCAGTA GTGGCCTACA GTCTGTGTCA TCTTTGGGTC 180
 ACAGCAGTGC CACTTCTGCA TCTTTGCCCTT TTATGCCATT TGTGATGGGT GGTGCACCAT 240
 CATCCCCTCA TGTAGACTCC AGCACCATGC TTCATCACCA CCACCACCTC GAG 293

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GAATTCGGCC TTCATGGCCT AGTGGGGCCT GTTTATAGTT GACTGACAGT AAGTTCTATA 60
 TGGTATATAA CACTAATTCT CTAGTCTTCT GGGCATATCT ACGAACAAAT ACAATCCAAA 120
 TATTATGAGT AACTGGGTTG TGACCACTGC ATGCATTACA CTGAAAGAAA CACCAACTCG 180
 AAGCACAAAT ATATTATTAT TATATTTCCG CTCAGCTCTC AGTGGGGAGA GCAGCTACCT 240
 CGGACCACAA TGCCATTTAA ACCAGATTCT TTTCAAATAA AATTCTCAAT CTAAGTGGAA 300
 AGCCCCCTCA GAGAATGCCT TATTTCCCTA CTAAGCAATC CAGGCTTGTA TAAAACGTCT 360
 GATAAGGCCT GTAGTGCCCA TTGAGTATGA GTCTGCTGTT TACATTCTGC ACAGGCCAGG 420
 AGGGGAACAG AAGGTGTGAG CCACAGGTGC TCCTGGGTCT GACCAGCAAG TCTAACCCAT 480
 GAAGATCTCG AG 492

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

AAATAACCAC AAATATNAAG AAATTATAAT CAGGGCAACA GATTAAATG AAAAGGGGTA 60
 TAGAAAGATA TATTTTAGAT AATATAAACT CCTGACAAGC TATGCCCTAG AATTGCAGCC 120
 TCCAAACCTT GCCCANGATT TCCACCTTTC CATAGCCTCA CTTCAAGTTC AAATGGAAAT 180

```

GAAAAACAAA TAAAGTGAAC AGGTGGTTGA GCCAGCCNAA GCCTCCCAAG TTATGTTAGG      240
TGGACAGTAA GACCAGGTGG ACAGCATTTG AGAAACTGGC TGGACACAGG GGAGCTGCTA      300
CTGGTAGTTA TATTTAATTT GGAGGAATTT CCAGCCCACT GATAAAGAGA GAAACCAAGG      360
AACCAAATGA CTTTTCTAGT AACATATAAT ATATGAGATG AAATATAATT CTGTTAGAGA      420
GGACATGGTG GTGAGATGGG AAAGAAAAGA GAAGAGAAAC AGGCAGACTT CGGGCACCAT      480
CTCCCTTTGT TTTCTACAAT GCATTGGTTT CTTCTGTGTG CGGAGCATTG TTTAGGATTA      540
GCTACAGACC CCAATGTCCT CTGAGTAAAT ATATGTCAGC TCAGCTCCTG ACATGATATC      600
CATGCTTATT GGCCTCCTGG AGGGCTGGGT GGTTCCTCAGG GTCCCTCGAG      650

```

(2) INFORMATION FOR SEQ ID NO:924:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

```

TGAGCTGCGC TAAACTCCAC CGTGACCTCA AACTCTTTGG ACTGTTTGAA AAAAAAAAAA      60
NTNGGAAGAA ANTCCATCCT CCAANANAAT CGGCTTAGGA GGAGATGGAA CTTTNCCCCT      120
TTCTCTNGGT TNGTCCGTC TGGTGGTCTC GAACCTGGGA TTCGGCGAAT GCGGATTCGA      180
TCATTACAT CCGAGCAATT TTGATGAAT CTGCCAAAAA GGATGATGAG GTATTTCGCA      240
CTGCGGTTGG TGACCTTAAC CAGAATGAGG AGATCTTACA GACTGAGAAA ATCACATTTT      300
CAGTGACGTT TGTTGATGGC AACCAACCCTT TCCAAGCAGT TCAAGAAGCC TGTGAACCTTA      360
TGAATCAAGG CATCTTGGCC CTGGTCAGCT CCATTGGCTG CACGTCAGCA GGATCCCTCC      420
AGTCTTTGGC AGACGCCATG CATATCCCCC ACCTCTTCAT TCAGCGCTCA ACAGCTGGGA      480
CCCCAAGGAG TGGCTGTGGA CTCACCCGGA GCAACAGGAA TCTCGAG      527

```

(2) INFORMATION FOR SEQ ID NO:925:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

```

GATTCGGCCT TCATGGCCTA GAACTTTCTA CTTGGACAAC TAACACCCAC AGTCCTCCAG      60
ACAGAAAGAC AACAGGTACA AAGCCCTAAG GATTATAAAG GTATGCTGCT TACCATCATC      120
TTAGTGACCA AGGCAGCGAA GCTGTTTCTG TACCTTGGA CAGTCTTCCC TGACAAGCCA      180
GAGAACAGTG ATAAAGCCAC CAGCCTTGGG ATCAGGACTG AAAAGGCAAG AGTGATGGAG      240
ATTCTCCTG CGCTAAGCCA AGAGAAGGTT TCAGCACTTC AGACAGCTCC CACCGAAGTA      300
GCCGATCTCG AG      312

```

(2) INFORMATION FOR SEQ ID NO:926:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGATGTTTG | TCTTTATCCA | GTAAGGTGTT | TGTATGCTCC | 60 |
| TTAAGTGGCA | GCGGGGAGTG | AGCAGAGCAG | TGAAGATAAA | CATGAAAGCT | GGTGGTAACA | 120 |
| AATCCTGATA | CCTCCTCTAT | TCCAAAAGGA | AAGGCAGAAC | TCAGAGGCAC | CATCCTCCTG | 180 |
| TTGTGTTTGC | AAGCTGTTGA | CACAACCTGG | AAAGGTAAAT | AGTTTTCAAC | AGACTTGTCA | 240 |
| GAGTTTGTGT | TCAATGGAAA | CTGACAGAGC | CTACCGGCTG | AGGGGCTAAT | TTTAATAGAA | 300 |
| ATAACCTAGG | TGCGCGCTCG | AG | | | | 322 |

(2) INFORMATION FOR SEQ ID NO:927: --

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTGGAACCTA | GACTGCCAGC | TGTGAGCCTC | AGAGCTCCTG | 60 |
| GCTGCCTGTT | GCTGAGTCTA | TCAGCTGCTG | AGCCTTTCTC | ACCNNAAAAA | AAAAAAAAAA | 120 |
| AAAAAAAAAN | TGNGCTTAAT | AAAATAACCC | TGCACAGAAA | TTTTCTGAAA | TTAAGATAAC | 180 |
| ATTCAATGGA | AAACAGAATT | TAATCTACAG | AAATACACTT | CACAGATGTT | TTAGGAACAG | 240 |
| AACCTAGAGA | AAATGAAAGT | CAAAATTTAA | TAAAAGAATT | TGTCAGGAAC | TTCAAGGTAA | 300 |
| AGACTCCATG | TATTTTGTGG | CAACTATAAA | ACACTAAGAA | GGCTTTTTTA | ATATTAAAAA | 360 |
| GCCATTTAAA | CACCTCAAAT | TAAGATTCCCT | CAATATACTT | CAGATTTCTG | TACTGAGTTA | 420 |
| CCCTCTCGAG | | | | | | 430 |

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TCATGGCCTA | CGTTAGTGTG | TGGATAGTAT | GTGTGTGTCC | GCACTCATGA | 60 |
| TAACTTGAAA | CCAGACATAG | GGTTCATTTT | TGAAAGGTTA | AACCACACTG | TTTCAGGAAC | 120 |
| TTGCTCCAAA | TACTACTTGG | TTATCCCTTC | CTTTACCAGT | TAGAACTAAA | GAGTGTGATG | 180 |
| TATGAACACA | CTGGGTTGGG | ATTTTCTGTT | GAGGATATGC | AGGGCATTTC | GGCATGAGGC | 240 |
| AAATACAGAA | GCAAGATTTC | ATTCTACTTG | GTGATTTGAA | TCATGACAGT | CCTCATTCCA | 300 |
| ATCTCTCTTT | AATTCTCTCT | GGCCCTGCCC | ACACTCTGTA | TTTGAAAATC | TTGTTTTTGC | 360 |
| TCTTTCCGGA | GCTTCACCCC | TCTACTTACA | TATTGTAAAG | TTGTATAAAT | CTATCATTGA | 420 |
| AAGGTCTCT | CTGCCAGCAG | TGGTGCCACC | CTTTGGTTTG | CTGTGGTACT | TTGCTGTGTA | 480 |
| CTCCGTGGCA | TACTCGAG | | | | | 498 |

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

```

GAATTCGGCC TTCATGGCCT AGTTAAGGGC ATTTACTCAT GTTGAACCTA GTTTTATTTA      60
CAGTATATTT GTATGCATAG AAGATGGAGG TCCACCAAAG TGTTAATTAT GCTTAGTTGT      120
AGGTCAGGTA TAGCTAACTT TCCTTTTTTA ATATATATAT TTACATTTGT GTTTCCTTTA      180
TAATTTATGG CATAGATTGC CACGATTTTC TTAAGTATAC TTTTATAATC AGAAAAATGA      240
TATTAAGGAC TCATTTTAAG TACACTAAAT CAAATATTAG AAGGCTTCTT TATTTTAAGC      300
TAATTGTGAG GATTATTTGT CATTTAAAC TTTTGCTTCT ACTTATTACC CTGAAGTATC      360
TTTGTGGTGC TTATGTTTTT CACAGACTGT ATAAATTGAT ATACTCTCCC GCCCATGGT      420
AATGTTGCTA CACATAAGCT CTAATAATTA TCATTTTAA TGTTTAAAGA TTAATTCAAC      480
TAAGTTTAA AAATAATCCA TTGGTTACAT ACATAAGAAA GTACTGTATA CAGATTCCTC      540
TGACTTATAA TGGTTCGACT CTCGAG

```

566

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

```

GTGATATGAC ACTGACAGAA TTCAAGTTCA TCTGGTACAT GGAGTACTCA CACCGAATGT      60
GGGGTCGCCT TGTAGGCCTT GTGAACATCC TGCCTGCTGC CTACTTTTGG AGAAAGGGCT      120
GGCTCAGCCG TGGCATGAAA GGACGTGTTC TTGCCCTCTG TGGCCTCCTC TGCTTCCAGG      180
GTCTGTTGGG ATGGTATATG GTGAAAAGTG GACTAGAAGA AAAATCAGAC TCCCATGACA      240
TCCCTCGGGT CAGTCAGTAC CGCCTTGCTG CCCACCTGGG ATCAGCCCTG GTTCTTTATT      300
GTGCCAGCTT GTGGACCTCA CTGTCACTGC TACTCCCTCC GCACAAGTTG CCTGAAACCC      360
ACCAACTCCT ACAGTTGAGA CGATTTGCTC ATGGAACAGC AGGTCTGGTG TTCCTTACCG      420
CCCTCTCAGG GGCTTTTGTG GCAGGGCTAG ATGCTGGGCT TGTTTATAAC TCCTTTCCCA      480
AAATGGGAGA ATCCGGATCC CTCGAG

```

506

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

```

GGGAAATTAG AAAGGGAGGG CCTGAGTTGG TTGCTATTCC TGAAAGTTTC TTTGAATGGA      60
ATACTGGATC ATCGTTTTTG AAGAGGTCTG TTGTTACTTC ATTATTACCT CCTTTAGCAG      120
CACCTTGTT TTCCTCCAAC CTCTGCCAAG ATTAGTGTCC TGTGTCTACA TTTGCCCTT      180
CTGTTTCTCA TACTCCAGA TGGAAATATT ATATTTCTTA GGACTTTTCG CTCTATTGTA      240
ATTAGTATTT TCTACTCGAA ACACCTCGA G

```

271

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACATTTACTT | TTGTTACACA | GGGCACTACT | TTGATTTCTA | 60 |
| TTAGTGCTGT | TTGTGATTGT | GTATGTCTTT | CACTTGAAAT | CCACCATGAA | GGTGAAAATT | 120 |
| TGTTTGAACC | GTGGCACTAT | ATGGCAGTGC | AGTGTAGTCA | GTTGTGTTTG | TAGTCCGGAT | 180 |
| TATCAGAGCT | TGAATTCTGG | TTCTGCTGCT | CACTAGCTTC | TTCTTGACA | CTGTTTCAGT | 240 |
| GTAATCAGCC | TCACCTTTTA | TTTTATTCT | ACAGAGTCCC | ATTGGGTGTG | TAAGCTGGTC | 300 |
| TCGAG | | | | | | 305 |

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCGGTGGCAC | GATCTCGGCT | CACTGCAACC | TCCACCTTCG | TTCAAGCGTC | CACCATGCCT | 60 |
| AGCTAATTTT | TTTGTATTTT | TGGTAGAGTC | AGGAGTTCGA | GACCAGCCTG | GGCAACATGG | 120 |
| CAAAACCCCA | TCTCTACTAA | AAATACAAAA | TGTACTCAGG | CGTGGTGGTG | CCCGCCTGTG | 180 |
| ATGCCAGCTA | CTCAAGAGGC | TGAGGTGGGG | ATCACCTGAG | CCCAGTATGT | CGAGGCTGCG | 240 |
| GTGAGCCATG | ATTGCGCCAT | TGCACTCCAT | CCGGGTGAGA | CTGAGACCCC | GTCTCCAAAA | 300 |
| AAAAAAAAAA | AAAGAAAGTG | AAATAATTG | TGGACAACAC | AGAATTACAA | ACTTTTATT | 360 |
| TTGTCTTTTT | AAAGTTACCA | CAAATTGTCA | CCACCATTCT | CTGAAAGGAC | ATTAACACCT | 420 |
| GAATATATTT | AGTTTCATGA | AAATTTCACT | TTTAACACTC | GAG | | 463 |

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGCATCCTG | GGGAGCACCC | ATTTCCTGGG | AACAAGCTGA | CCCTTTTGCG | TCCTTAAAAA | 60 |
| AAGTCGGCCA | AGATTCCATA | GTGCTGCTGA | TCTGCATTAC | AGTGTTTCTC | TCCTACCTAC | 120 |
| CGGAGGCAGG | CCAATATTCC | AGCTTTTTTT | TATACCTCAG | ACAGATAATG | AAATTTTCAC | 180 |
| CAGAAAGTGT | TGCAGCGTTT | ATAGCAGTCC | TTGGCATTCT | TTCCATTATT | GCACAGACCA | 240 |
| TAGTCTTGAG | TTTACTTATG | AGGTCAATTG | GAAATAAGAA | CACACTCGAG | | 290 |

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTTTGGCCC GGCAGCCTCT CAGGTTGGAC TTCTCAGGAT | 60 |
| TTGCCATTG TTTTAATCCC TGAGACCACA CAGTTGATGT TTAGAGCCTG CCCTGCATGT | 120 |
| GATCGTTCCA GTGGAGGATA CAGCATGGGG TCTGGCCTCC AGCAGGGTCC TCCCCAGGCC | 180 |
| ACCCCTGGGT GCCGGGAGGG CAGCCCCTTG GCCTGAGGCC CACTATGACC TGCCCCCTGC | 240 |
| AGCTGCACCG TGATGGTGGC TTGCCTTTGT GGCTCCCTGG GCTCTGGTGG CTCGAG | 297 |

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

| | |
|---|-----|
| GTTTAATGAA GAGTAGTCAG TCTTCTAGAT TGTTCTTATA CCACCTCTCA ACCATTACTC | 60 |
| ACACTTCCAG CGCCAGGTC CAAGTCTGAG CCTGACCTCC CCTGGGGAC CTAGCCTGGA | 120 |
| GTCAGGACAA ATGGATCGGG CTGCAGAGGG TTAGAAGCGA GGGCACCAGC AGTTGTGGGT | 180 |
| GGGGAGCAAG GGAAGAGAGA AACTCTTCAG CGAATCCTTC TAGTACTAGT TGAGAGTTTG | 240 |
| ACTGTGAATT AATTTTATGC CATAAAAGAC CAACCCAGTT CTGTTTGA CTATGATCATC | 300 |
| TTGAAAAGAA AAATTATAAT AAAGCCCCAA ACTCGAG | 337 |

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACATAGTTAT TCAGATTTAG GACCAGTAAG GATAGAAGTT | 60 |
| TCTCTTATTT ATGAAAAAAA ATGCTAATAA TTTTGGGGCA GTTTTTTCN TTAATTATTT | 120 |
| TTTTCAATTT CAAGTTTAA TTTATTTTAG CTGATCTGAT GTGGTTTCAA CTAACCCAAG | 180 |
| GTCTCACCAT GTTAAAANGC CGGCGGACTC TACGGCGTTT TGATAGATCCC CCCCCCCCAC | 240 |
| CCACTGTGAA GGGGTGCCAT ACTACCTTAA ATGCTAATGC TAGATATGCA ACCCTCGAG | 299 |

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

| | |
|---|-----|
| CTCGAGTGGT GTGTCATTAT AGCGGACAAA GGTCACGATC ACAAAGGTGG TGGCGATGAT | 50 |
| TCCCAATATT GCAACAAACA CAGGCACCAC AGCCCAGGGA GAATGCCACT CCAATTTGAT | 120 |
| GATGGGGATA AGCTGGCAGC CTGTGCGGTT CATGTTGGGT CTCTGATCCA GAGGGCAAAG | 180 |
| TTCACAGGAC AGCTCATCCA CCTGGTAGTT GTAACCTTCA CAGCGTTCAC AGTGCCAGCA | 240 |
| GCAAGGGACC CCTTTCACCG TTTTCTTCCT CTCCCCTGGC TTACACGGCA GGCTGCAGAC | 300 |
| AGACGCCGGG TGAGTATGTT CTCTATGAGC CCACTGCATG TCTTCCACTT TTAGATGAAG | 360 |
| CTGATTGGTC CAGTGGCCGA TGACTTTGTA CTCTGTGCTT TTC | 403 |

(2) INFORMATION FOR SEQ ID NO:939:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATTCTTTTC TGCCTTCAC ATGCATGTCA CAGTTCATCT | 60 |
| CACATTTCTG TGAGAGGGC TCCATTTCTC TGCATATGGC ATTACCATTG TGCCTGATGT | 120 |
| ATTCCAATTC AGATAAACAT AAGCTCCTTT CTGCTGCTTT CCCTGAGACC CCTGGTGTGG | 180 |
| ACTTCTCTAA TGTTCATATA ATATCTATGC ATCTCTCTAT GATTATACCA TGTTATACTC | 240 |
| TGTGTGGCCT TAGGCTTTGT GAGGAGAGGT TCAGAGTAGG TTTTGCTCTA GAGTGTGGTC | 300 |
| CTTACTCCTA AGGTGACCCC TTTGNGGTGT CTCTGCTGGT GTATGGCATT AATGTGATTG | 360 |
| CTTCACTCTC GAG | 373 |

(2) INFORMATION FOR SEQ ID NO:940:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

| | |
|---|-----|
| GCAAGCTCTA ACCTAAATCA CAGAGACATG CATGTTTCAT GCATTAACAC TGATTTCGCT | 60 |
| CTGTGGCCCA CCAGAGGGGT GGGCTCATGT CCCCTGACTC CTCACATGAG TGCCTCAGCT | 120 |
| CTAAGNCCCG TGGACGGGG GGTAGGGAAG GTTTGCGATC TGGAGCTCAG CAACTGGCTC | 180 |
| AGCAACGTTT TCTCCATTTT ATTAGCACTA AACAAGTTTC TTGCTCTCAG GAATTTGTCA | 240 |
| GAAAAAAGAA TAACATCACC TGAGACTCCA CATACCAGAT TATAAACTCT TTCTCGAG | 298 |

(2) INFORMATION FOR SEQ ID NO:941:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTTTCCGG ACACTTGGGA CACGCGTTTC CATCCTGGCT | 60 |
| CACTGAAGCC TCGATCTCCC AGGCTTTCTT TGACGGTGT CCCTCAAAGA AAGAGGCCCA | 120 |
| AAGCCCTCCC CCGCAAAAAA AGCCAGAAAG GAATGGAGGT GCCTCCGCAG AAATCCAGAG | 180 |
| CATCTGCAAG ACATCCTCGA ATTCTAGACC TGCCTCGAG | 219 |

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCAAGATG GGTCTGAGGA TACCTGTGAG AAGTAATTCA | 60 |
| ACACATCTTT CACACATGGG CCAATTGCT GGTCTAAGTT AAATNGGAGT GACAAGGACA | 120 |
| GCTGCTTAAA GAGTGAGTTC TAAAGCCCCA GGAATTAGGT GATGTCTTGA GCTGGGGTGA | 180 |
| AGCAAGNCAA GTGGGATGGG GAAGAGATGG CTGGNTTCTG CNGGAGTGAG TTTAAGGGAG | 240 |
| GAAGGCAGGG TTGCCCCGCA GCCCGCATGT TCCAGAAGAG CCCACGAGAG ATGTCTGTCC | 300 |
| CACAGGGCTT ATAGCACNTN GCANTCCNTC AAAGGGCGGT GTCTCATGTC CCNTCTGTGA | 360 |
| GGCTCTGGGT GGGCTTTTGT GACAGCTTTG ATAATGTTCT GGAAGAGATG CTGCTGGGCT | 420 |
| TCTGGGCTCC CGCGACCCCT TAGAGAAAGT GGTGCAGCTT CTCATTGGCT CTGTCTCTCT | 480 |
| CCGAACACGC CCCTTTTGA GCCCTCTGGA AAGGAAGACA CTGAGCAACC AAATAACATA | 540 |
| TTTTGACACT AATTTCCTGA GACCGTCTCG AG | 572 |

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGGAAATGT GTGTCTCTAA AACAGATTG GATTTTATTT | 60 |
| ATTTGGGACA TATAAAAGAG GAAGGAAGAG TTGATAAGA TTCTTATTTG ACTCTTCAA | 120 |
| GTCAGTGTTC ACCAGAAATT CAGAGAATCA ACATACAAAT TACAATGGTA GTTTGTTTTC | 180 |
| TGGAAGGCCA GTGAAATACA GTCCTTAAT TTATAATGAA ATTTACTTTC TAACAAATTA | 240 |
| AGTCTTTCTA ATGAGACCAA CATTGAGAAT TCAGCCCTTA CCTCGGGATG GTCTGAGAAA | 300 |
| ACCAAAAGGC CAACTGTTTT ATTGCTTTAG ATCAGTTAGG TGATGATAAC TATGAGCATT | 360 |
| TATAATAATA TTTTAAATTG GCCCTGAGAG GCTTGAAGAC ATAGAACTCG AG | 412 |

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

```

GAATTCGGCC AAAGAGGCCT ACAAAAAAAAAA AAAAAAAAAA NNACTTGAAC TGAGACCTGA      60
AANNGTAAAA CTANNGNAAC AAAACTTAGG GAGAAAGCTT CTTGACATTG GCCTGGGCAA      120
AGATTTT TTTT GGATATGGCC CCATAATGAC ATAGGACAGG CAACAAAAAA AAAAATGGAT      180
AAATGGGATT GCATCAAACCT AAAACTCTGT ATAGCAAAGA AAACAATCAA CAGAGTGAAG      240
AGACAACCTA CAGAATGTGA GAAAATATTT GCAAACCACA CATTTCATAG GAAATTAATA      300
TTCAAAATAT ATAAGGAACT TATGTAACCT AATAGCAAGA AAACAAATAA CCTGATTAAA      360
AAATGAGCAA AGGTCAGTTG AGAGAGGAAG AGAAAAACAA TATGAGTAAA AGACTTTAAT      420
AGACCTTTCT CAAAAGAAGG TATGTGCATG GCTGATCTGT GCATGAAAAG GTACTTAACA      480
TCATTAATCA TCAGAGAAAT GCAAATTAAC ATCATCTCGA G                    521

```

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

```

GAATTCGGCC AAAGAGGCCT AGGTACACAA AAGCAAACAG AAAAACTCTT AAGTTTTTCT      60
GCAATACTAA AGAAAGTGAG ATAAGACTTT AAAGTTAAAG ATCTATAGAC ACTTTAGGCA      120
AAACAGGCTC ATAAAGCAAT TAAAAAATCA ACAATTTAGT AAAACAGGC TACATAGTAT      180
TTTGTTTTTA CGTTTCATTT GTCTATTGAT CTTTAAATTA AATTAGACAT TTCTACTGTT      240
TTCCTGTACT CTTATACACA CCTGTTTTCT CCAATGTTCT CCTTTAGTAT GGCTGGTAAT      300
TGTTTTGGTG ATTGCCACCC CCTCGAG                    327

```

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

```

GAATTCAAGG GCTAGGCGAG TTATTGCAGT CACGTCCTTA AGTCAGCCGG GTCCTCTTCT      60
TTTCCCTCAA GGTGCCTGTG TTTTCTATTT CCCCGTCCAG TCGGTGGCCC CACCCAGCCC      120
CAGGGTGCTC CCTTCCCCC TTTCCGGTTT CTGCCTGGAG GGTGTGGTTT TCTCTCCAC      180
CTCGGTGCCT GCCAGTAGAC TGGAGTTCCC CGCCACGCTG TCGGTCCCAT CTCATCACCT      240
TTCCGCTTTC ACGCCCGTAG CTAGTCTTGG GACTGGCCCT GTTATAGCCC CAACTTATGC      300
GCTCTCTAAC CTTTCTGGC TTACCCGGAG TCACAGTTCA GTTCTACTTC TTTTCAATTC      360
TGTAGGGCAT TGGTCTCAAT TGGGACTCAG TTTTCTCCA CACCCGCCGT TCCTGTAGTC      420
TGGTTATATC ACAGTTCATT ATTTAATGTA GGTTTTTGAG CGCTTGTAAC ACGGCAAAGC      480
TCTCTCTGTT AATAATACAT ACTCAAAATG TTATCTTTC ATTGGTGCAT TACAATCAG      540
TTGTTTGCCT CTGAATCACT TTCCCGACTC GAG                    573

```

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGGAAGTCA | TTTATTATTT | TATAAATTGA | GAACAACCAC | ACCACCAAAT | GTCACACCTT | 60 |
| CTTATAAAGT | GTGAACAAGG | AAGGTCATGT | TTTTGTGGGT | ATTTTGTGAG | ACTTAGAGGT | 120 |
| TTCAATTCAG | GGCATAGTCA | AAGGCATCAT | CCTCCCAACT | ACCCACTTGA | TTATGTATTT | 180 |
| CAGATCCCTC | CGTGGGGGCC | TTCTTCTGAC | AGAGAATTCT | TTGAGGTACG | CAGTAGTGCT | 240 |
| TTTGTGAGCA | CAGACTGCTA | ATCTACATCT | TGCTGCGTTC | TGTTTGCTGA | GGTTGGGCTT | 300 |
| ATTCATTTAA | CACGTACCAA | CCATTATCAC | TCGAG | | | 335 |

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACGGCCAAAG | AGGCCTAGTC | GGAGGAGGAA | ACATATGTAG | 60 |
| GGAACAGCCT | GGGTCTTGTC | AATCCGTTTC | CCAGCTATGA | TGCCTATTTT | CTCAGCAGAA | 120 |
| TGAGTGTAGC | ATGTCTCCCA | GGTCTGTTTT | TTATTTGTTT | GAGAGGTGAT | TTCAAGCAGA | 180 |
| ATCTCACAGC | TTACTGTTGG | AAATGCTATC | AGTTGTAAAG | ATAGGGAAAA | TCTCTCTTCC | 240 |
| ACTACGGTGG | TAGGAAATGA | ATACATATCA | TTTCCCAGCT | TCCAGGATGT | CCTGTCATCT | 300 |
| TAAGTGTGCG | TCCCCAAGGA | CCTACAGATC | ACAGGGCAAC | AGGGGCTGTG | AAAGAGTAGC | 360 |
| CCGGGGCTCG | AG | | | | | 372 |

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTAGCATTAC | GAATCTCTTA | GGATTTTAA | GATTGTATTT | GATAATACTT | ATATTTTACA | 60 |
| GGGCACACTT | TTGGCACACC | TCAGAGCACA | CTGCTGCTAT | TTTGGGTCAT | ATCACTGTAA | 120 |
| AATACATAAT | AAGTACTACT | TAAGTGTGAC | ATGAAGAATT | GGAATCCCAG | AGGGCAACAT | 180 |
| TTGATTCGAC | TAAGATCAGG | CATAAGATAG | AATTTTGTGC | ATTTTTCCTT | GCAGTTTAT | 240 |
| TGACTTAGTT | TATGAGCTTG | GATAAAATAA | TTTTTTGATG | AATCATGTCA | ATAAAAGGAA | 300 |
| AAATAATGTA | ACTACCTCAT | AAGTCTGATA | AAAGGAAGTT | GCTAGTGTTT | TATAGAATTT | 360 |
| CTGAAGGTGG | TTAAATCAAG | TATGATTTC | AAATATCAAC | TAGTTCCACT | TTTGTGATTG | 420 |
| CAGGATGCTT | CTTATACTAA | AGTTCTCGAG | | | | 450 |

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACGTAGGCAA AGGTTGACCC AATCAAAGAT AAAAGAAAAT | 60 |
| CGACAGCAAA TCGTTCGTGC TCGAAAATAT ATGATGATT ATAGAGTTCA GTTGTGTGCA | 120 |
| AAAATGATGA GAATGAGGAC CCGGGAAGAA ATGATATTTA AGAAACTGTT TGAAGAAGGT | 180 |
| TTAAACATTG AAAAGCAAAG ATTACGAGAC CTAAGAAACT ATGCCAAAGA AAAGCGAGAT | 240 |
| GAACAAAGGA GACGCCACCA GGATGAACTG GACTCCATGG AGAACTACTA TAAGGACCAG | 300 |
| TTTTCATTGC TGGCAGAAGC CATATCACAG GAACAACCTCG AG | 342 |

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACCCTGTTTT AATCACATGA CTACCTGTCC CAGTACACGA | 60 |
| AAGGGCGCTG GTTGGCATTG TTCTTAATGT ATTTAGTAAA GATTATAAGA CATCCTTTAA | 120 |
| GAGTTTAAAT GTCTCTGAAA CAGGCATACA GGCTCTAGTC AAGAATGAAT TAGAGTGAAG | 180 |
| GAAAGCTGTG TGACACCTGG CATTCTCTCT TGTTTCATGGA GCTTCTTTGA GGCTTGAAGT | 240 |
| TTGATTTTAC TATCTAGACC TCTCTGGCTA ATACCTATTC TTCAACCACC TCGGTTACTC | 300 |
| TGACATAGGA ATTTACTTCT TTTCTTGAG TGGAAAAACAC TTTAGAAAAT AATAACAAAC | 360 |
| ATTATTATAA ACTAATATAT GTGAGAGTAC TTAGTTGAAA CAAAAAGGAA TTTTAGTAGA | 420 |
| CAGTATTATA TTATCTTTGA AAATCAAGGA GAAGTTTATG CAACTGAAAA TGTTTACACA | 480 |
| CTGTGCTACT CGAG | 494 |

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

| | |
|--|-----|
| CAAAGAGGCC TAGGGAGTGT CGCTCTGTCA CCCAGGCCGA GATTGCACCC CTGCACTCCA | 60 |
| GGCTGGGCAA CAGTACGAGA CTCTGTCCAA AAAAAATAAA AAAGAACAGC CTTTTTAGGC | 120 |
| CACAGTGACC TGCACAATGT TTATATGCTT NGACCTACTA ACTTTCTCCT AACTAAATAT | 180 |
| TTGATTTTAG GAGAGTGTGTT AAATAAATTA CAGTATGTCT ATATGATGAA ATGTTATTTT | 240 |
| GCCATTAAAA TTTGTTTAC AAAGATAATT TTTATTGACA TAAAAATNAC TTTAATGTAA | 300 |
| TTTATGTTGA AAAAGCTGAA TACAAGTCTT TATATAGAGT AATATTGAG CTGTGTTCAA | 360 |
| AAATACATAG GAAAAGACTG ATAAAATGAA ATATGGCNAA ATGTTAATAG TTTCCCTGG | 420 |
| AATAGGATAA TAGGCAATT TAAACAGAC TCCTTTAAAA AAACAAACAA ACNAAAAAAA | 480 |
| CATAGACTTC TTTATATCTT TTGAGCTCCC CCCNACTCG AG | 522 |

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGTGTTAT ACAGTTGTTG CCACTGCTGT TTTCCAAATG | 60 |
| TCCGATGTGT GCTATGACTG ACAACTACTT TTCTCTGGGT CTGATCAATT TTGCAGTAGA | 120 |
| CCATTTTAGT TCTTACGGCG TCAATAACAA ATGCTTCAAC ATCATCAGCT CCAATCTGAA | 180 |
| GTTCTTGCTG CATTGTGTCA AAAGAAATTT CCTTATTTTC TACTGCCATT CCCATAAAAG | 240 |
| TAAGTAGTCT CATTTTGCC ATATTCTGTT CATGTAACAG GCCAAGTGAA TCAATGAAGT | 300 |
| CTTTATTATT CTGATAAAAC TTGACATATG ATGCCAATTT AGCACTCACA AAAATGGTTA | 360 |
| AAAGATCATG AATAAGCTCG CCTTCCAAAA ACTTGACTGG TTTTAAAGTA AGAAGGTGGT | 420 |
| CAAAAAGAAA TGCATTGGA TCTTTCAATG CTCGTACAAT ACACCTGTGG GCATCAACTC | 480 |
| GAG | 483 |

(2) INFORMATION FOR SEQ ID NO:954:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTGCCCTC TGTGAAGCCA GTGTTCTCTG CTCCCCGGGT | 60 |
| CAGAGGTCAC AGGTCAAGTT CAGTCAGTCC GAAGAATCAT GGGCGGGTGC TCGCTGTCCT | 120 |
| CATCCAGGCG CAGGGCGCTG GCCTCGTCCT CCAGGCAGGC GGCACCCACA GCACCCAGGT | 180 |
| CGTCTGTGTA GGCTGCAAAG AGACGACGAA GTCACCCCTC AAAGGCTGGG GACACACCAC | 240 |
| AGACCCCATG ACACACACTG AGGACTGTGT TTTGGAAACA CTGGGTGATA TTTATAAACT | 300 |
| GAAGCCTGTA CTAAGACGTT CTGAATTCTG ATTGCTTTCT AATGAACTCT TTGCAGCCTT | 360 |
| AGGCAGCTCG AG | 372 |

(2) INFORMATION FOR SEQ ID NO:955:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTATTACCA TTATATATCA CCCATCTGCA ACAAGGTACT | 60 |
| GTACAGACAA GTAAGAAGTA TGTTATCTAG TTCCCTTTCC CCCAGAAGGT TGAGGCTCAG | 120 |
| GTATAGGGGT AATTCTCCTG TGCAGTCTTT ATTTATGCTG ACTCAGTGAC TTCAACAGGC | 180 |
| TTAATCATGT GGTCAAGTTT GTTGCCAGCT GCATAATGCT CCCACATCTG TAGATAGAGC | 240 |
| CGCTCTAGTT CCATTGTGTA TTGTTTGGTG TTGAACAGAG GGCTAGATAT TCTTTGCTTC | 300 |
| CAGACTTTGC CACGAACCTT CTTCAGGTAT TCTAGATCAG TTCCCAGCTT CACAGCTATG | 360 |
| TCTTCATATT CTGTGCTGTT TTTAGCAATA AGCTCAAGAC AACCTAAGCA AGTGAGCTGG | 420 |
| GATGCTGCAA CTCGAG | 436 |

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

```

GAATTCGGCC TTCATGGCCT AAGGAGATGG GAGAATGTCC GGGGAGGGGC TGGCAGGAGG      60
GGCCAGCCAA ACTGCACGGA CTTGCTGGT TAGTGAAGGA TTTAAGTCC TCTAGTGGAA      120
TTAAGTGATT AGATTTTTC CTTACAAAGG AAACCTCTCT ATGGAGAACA AACTACCATA      180
TGAAGCTAGC GGCCTAAACC AGGAGAATGT GGGGAAAGAA GAGAGGTGAG GATAACTGGA      240
GGGGTATTAT GTAACAACAG AAAGCATCAC AGTTCAATGA ACAGGGCAAG GTGGGCAAAT      300
GAAGAGGGCA GAGGAGGACT GGGCCCTCGA G                                     331

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(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

```

GAATTCGGCC TTCATGGCCT AAGACTGTGA GTTCTGGGGC CAAGAAAAGT TTTGAATTGC      60
TCTCAGAGAG CGATGGGGCC TTGATGGAGC ACCCAGAAGT ATCTCAAGTG AGGAGGAAAA      120
CTGTGGAGTT TAACCTGACG GATATGCCAG AGATCCCCGA AAATCACCTC AAAGAACCTT      180
TGGAACAATC ACCAACCAAC ATACACACTA CACTCAAAGA TCACATGGAT CCTTATTGGG      240
CCTTGGAAAA CAGGTCTGTC CTCCACCTGA ACCAGGGGCA CTGCATTGCC CTGTGCCCCA      300
CCCAGCTTC CCTTGCTCTG AGCCTACCCT TCCTCCACAA TTTCCTAGGG TTCCATCACT      360
GCCAGAGCAC ACTGGACCTA CGCCAGCAC TGGCTTGGGG TATATACTTG GCCACCTTCT      420
CGAG                                                                 424

```

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

```

GAATTCGGCC TTCATGGCCT AGATATGGCC AGGATGCTAT AGCATTGTCA GTGAGGAGAC      60
ATCAGAGCTT TCCCAGATCG GGAGGAAAAA TATGGAATGT GTTTACCGC TGAAGTGAACA      120
CAACCAATG AACTGTCCTG ACAGTAGTTT GCAAACGAGC AGCTAGCAGT TTGTCCAGCC      180
TCTAACATTG TCCAGCACTT TCCAGAGCAA ACTCACTGTT TACAAGAAGT CTTGGCCTTA      240
CGAAGTTTAT AACCTCAAGC TTGTTTATT TAAATATTC CTGCAAAAGA AAAGTACCCG      300
GCCCATGACC ATTCGTGACA GGCCCTTTGA ACGGACGATT ACCATGCATA AGGATAGCAC      360
TGGACATGTT GGTTTTATCT TTAAAAATGG AAAAATAACA TCCATAGTGA AAGATAGCTC      420

```

| | |
|---|-----|
| TGCAGCCAGA AATGGTCTTC TCACGGAACA TAACATCTGT GAAATCAATG GACAGAATGT | 480 |
| CATTGGATTG AAGGACTCTC AAATTGCAGA CATACTGTCA ACATCTGGGA CTGTAGTTAC | 540 |
| TATTACAATC ATGCCTGCTT TTATCTTTGA ACATATTATT AAGCGGTGGC ACTCGAG | 597 |

(2) INFORMATION FOR SEQ ID NO:959:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGTGTCTTCT TGCAACTTC ATTCTCTTCT CTGTTTTCT | 60 |
| ACGTCTGAGA TCTTTCTGAA CACATTTTGT TAGAGGCTGC TGTCTCCTGC TGTCTGGAGA | 120 |
| ATGATCTTTA GAGGGAACGG AAGCTTTCTT CCTGTGCGTG TGTGTCTTCC TGTGCTCTAG | 180 |
| CACTTGGGGG TGGAGAGTCT CGGGGCGGGG ACACCAAGTGT CATCAGCGCC TGTGCTGTCG | 240 |
| TGCTTCTCTT TTGCATGTTT GGAAAGCCTC AAGCGGGAGG CGGACTCGAG | 290 |

(2) INFORMATION FOR SEQ ID NO:960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTGAGTGAG TAAGACAGGT TGCTCTTTGG AAAACAAGGA | 60 |
| AAATCCCTTT ATTAGAACAA GGCATGAAAT TCTGCCACTA GGTGGCGATG CCCTATAACT | 120 |
| TTACAACCTA GTGTACATCA CACGAGCACT ATGGAAGATT TCTCCATTCT GCGCCCCACC | 180 |
| AACTCCCTCC CCTCCTTCAT TTTTCAGGAT GACAACACCT TAGAGGTTTA TGGCCATCAG | 240 |
| GAGAATTTAC TACTAAGCTA TATACTGATG TAATGAAATC TAATATATGT TGTGCTCGAG | 300 |

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATTTCCCTT CAGGATTGTG TGTGGGGTG GGGGCATACT | 60 |
| GGGGATGACA GAGGGAGAAA GAAAGATTTT TATTTTCTT TCTAATAAAT GTTCATTGAG | 120 |
| AAAGTTATAG AATATGGAGA AAATGAAATT TATAACTCTC CTGCGCAGAA ATACTGTTAG | 180 |
| CTGTGAGTTT CTTTCTATA TATGCTTATA TAGTTGAGAT TATGCATGTA TACAGTTCTG | 240 |
| CATCTTAGCT TTAATAATAA TGTCACATCT TGATAATTTC CCAGTCATTA AAATTATTTG | 300 |
| AAGATATCAT TGATGTATCA CCTTATTTTA TATTCTATTT GAATAATACA TCCAAGGTCA | 360 |
| CCAAAAGATG ACAGTGAAAT GTATTGTTTG TAATCTACAT TAGCATCAGT AAATATGGAC | 420 |

CATTAAATT GTGTTAAGTC AACCTCTCTG ATCTTATTTT ATTAAAGTTT AGGATAGGCA 480
 CTACATTTGA TGGGACTCTC GAG 503

(2) INFORMATION FOR SEQ ID NO:962:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GAATTCGGCC TTCATGGCCT AAGCAGCTGC TGCCTGCCAG AGAGGCGCCT TCAGAGACCC 60
 AGCGCTTACA CAATACCCAC CATGTCCCAG GCTGGTGCTC AGGAAGCCCC TATCAAGAAG 120
 AAGCGCCCCC CTGTGAAGGA GGAGGACCTG AAGGGGGCCC GAGGAAACCT GACCAAGAAC 180
 CAGGAAATCA AGTCCAAGAC CTACCAGGTC ATGCGAGAGT GTGAGCAAGC TGGCTCGGCC 240
 GCCCCGTCGG TGTTCAGCCG CACCCGCACA GGTACCGAGA CTGTCTTTGA GAAGCCCCAA 300
 GCCGGACCCA CCAAGAGTGT CTTCCGCTGA GAAGTGTGCG CCACTCCCCT TGCTGCCCGA 360
 ATGCTCGGAA ACAGGAGCCT TACCAGGCT CGAG 394

(2) INFORMATION FOR SEQ ID NO:963:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GAATTCGGCC TTCATGGCCT ACCCTTCATG GCCTAGGAAA CTCACAAAAT GAAATATCCT 60
 TCTCAACGTC ACTAGAGAGT GGCAGAGTTT AGAGACAAAG CCATCTGATT TTGGAGCCTG 120
 TGCTCAGCTT TTAGCAGACA CACTGATTTC CAAGAATTGC TAGGATGTTT CTCAGTGCAG 180
 TTGACCACAG GACTCTCTGG AAAGCCTTCA GGACTGAACT TCCTCCAGAC AGTTTGGGAA 240
 ACACTGCATG TGTCTATTAT GAAGCCATCA GCTGAGCTCA TCCCCCGTGC ACTCCACAAC 300
 GCTGAGGCTC TGCACATGGC TCACCACTGC CAGGTGCTGC CAGTCAGCAG TGCCGTGCTG 360
 TTTCCACAGC AGCCTGCATA CGTCTATATT GCCCAGCCTG TTTCACCTGG CGGGGTCA 420
 CAAACCACCC CCTGGTATTG TTAGCAGCTC CACATAATGG CATCTCCACA GCTGTGTCAT 480
 CCAAAAGAAA CCTCGAG 497

(2) INFORMATION FOR SEQ ID NO:964:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

GAATTCGGCC TACATCTTTT GATGACTCTG ATACCTTCAT TCATTTTCA AAGGAATTTA 60
 CTGATCATGA GGTGGAAAA TCTGTATTTT TCTTGCTTAT TATGTATTAA TAATCATAAA 120

| | |
|---|-----|
| TGTCTAGATT CACCAGAAGT CACCAGAAGG TCTGTCTCAG TGAAGAAAAC TTATAAAGCC | 180 |
| ACTTTGTGTC ATTTTGTGTT TCAGTGTTAC AGTTTGAGAT CTGTATATTT GTACACAGCT | 240 |
| ATGTGTTTTT CATTGAAATA ATGTACAAAG ACTGATCTTG ATGCTGTGTA TTTTATGAG | 300 |
| TTGTCTTAGG CATTCTGAG CTCAGCTTCA GTTGGATGGT GGGTCAGCAC CCTGCGTTTC | 360 |
| TGAACATACT AGACTTCAGT TTAACACTGC TCGAG | 395 |

(2) INFORMATION FOR SEQ ID NO:965:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATAGTAAATG CCCACTAGGC ACCCTGGAGT CATTTGTGTA | 60 |
| GAGTGGCATC TCTATACAAC TGTTGACTA ACTGTCGGAG ACACCCTAAT CACCCAGCC | 120 |
| ACAAACAAAT AGAACATTGT ATGTGTGCTG AATCCCACAA AGGCCAGACA TGATGCCATG | 180 |
| AGACCAAGAA GGAAAAGAAA TAATGTGGAA AGGGTTTGGG GTGGAAAGGT GGGGAACCTG | 240 |
| GAGGCGGGCC ACATGGGGCC CCAGAAGCCA TGTGAGGGT TTTGTCTTCA CCAAAGGATC | 300 |
| AGTGGGAGAT TAGTGTAGAA CATTAAACAG AGGTGGGGTA TGTGTCATAT TTCCATTAAA | 360 |
| AAATTCATCC TGGCCACAGT GTAAAGAATA GATTAGGGAG GAAGCCAATC AGGAAGCAAT | 420 |
| TGGAGTAGGC AATGCAAAAAG GCAAAGTGAA CTTGGACTAG TGTTCTCGA G | 471 |

(2) INFORMATION FOR SEQ ID NO:966:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 611 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCCAGCTC AGNTGCNTCA GAGATTTTGT GTGTCCTTGC | 60 |
| ATACACAAC TAATTCTCT AGGATTCAGT CTCCTCGTNT TATTTTAAA ATNATTTTAT | 120 |
| TTGTAAATAC CTCATCGTGG ACTCCAAAAG CATGTCTCCT CGTTTTAAA ACTGGCATAA | 180 |
| TACCTACCAC AAAGGTGGAT GTGAGAATTA AATAGAGCTT TATACAGAAT TCCCTCAGGC | 240 |
| ATTTTAAAGT TTATGTAATA GGGATGTATC TTACAGTTGA TGGGTACATT TAGTGTAGTC | 300 |
| CCCCTACCTC CCAAGCTAAT AATGGTGCGT CGTACAATTG ATGGTACCAA ATTGAGGTGA | 360 |
| TAATAACATA GAAAGAGTTT AATGCAACGT GAAGTACAAA ATGCATTCAA TAAGTAGCTG | 420 |
| CTATCATTTT TTTAAAAATT AAATATGGCT GCTTGTTAAG GCCATATCCC AGGAGGAAAG | 480 |
| TGTGGTCTCT GCTGGGAGGT TGGTCTACAT ACAGGAAGCC AGATGTGTGA GATGGCTCTA | 540 |
| GATAGGCAGA AGGGGAGAGC TCGTGCCCTC TAGGAACCTA TTAATAGATA TCAAGGGAGG | 600 |
| GATAGCTCGA G | 611 |

(2) INFORMATION FOR SEQ ID NO:967:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATTAAAGTT | TTTCTAGCAG | ATCGCTCAGG | TTGCTCTTAA | 60 |
| CTGGAATGTA | GTGTTTCCAG | GGCTGCAGCT | CATTGTAAAA | ATGTTTCATAG | TAGATGGAAT | 120 |
| CCTGCTTCAG | CACAACACTG | TCACCAACTA | GCAAATATGG | CAGGCGATAA | GCTGCTACAG | 180 |
| TGCCATCGAT | ATTTATTGTA | TACTTATGCT | TGAAGAAATC | AAAAAATGAA | ATATGTTTCA | 240 |
| CAATGGGACC | ATACAGGTTT | TCATCGTGTT | TAAAGAAGAA | AAAGTTGGTG | AAAGCAGCGT | 300 |
| CTATGAGTTC | TGGGTGTTTT | CTACTGAGTT | TAACCAGCTC | GAG | | 343 |

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATCGCCT | AGCCAGGANC | TTTCTCGGAC | GCCTTGCCCA | GCGGGCCGCC | 60 |
| CGACCCCCTG | CACCATGGAC | CCCGCTCGCC | CCCTGGGGCT | GTGATTCTG | CTGCTTTCCT | 120 |
| GACGGAGGCT | GCACTGGGCG | ATGCTGCTCA | GGAGCCAACA | GGAAATAACG | CGGAGATCTG | 180 |
| TCTCCTGCCC | CTAGACTACG | GACCTGCGG | GGCCCTACTT | CTCCGTTACT | ACTACGACAG | 240 |
| GTACACGCAG | AGCTGCCGCC | AGTTCCTGTA | CGGGGGCTGC | GAGGGCAACG | CCAACAATTT | 300 |
| CTACACCTGG | GAGGCTTGCG | ACGATGCTTG | CTGGAGGATA | GAAAAAGTTC | CCAAAGTTTG | 360 |
| CCGGCTGCAA | GTGAGTGTGG | ACGACCAGTG | TGAGGGGTCC | ACAGAAAAGT | ATTTCTTTAA | 420 |
| TCTAAGTTCC | ATGACATGTG | AAAAATTCTT | TTCCGGTGGG | TGTCACCGGA | ACCGGATTGA | 480 |
| GAACAGGTTT | CCAGATGAAG | CTACTTGAT | GGGCTTCTGC | GCACCAAAGA | AAATTCCATC | 540 |
| ATTTTGCTAC | AGTCCAAAAG | ATGAGGGACT | GTGCTCTGCC | AATCCGACTC | GAG | 593 |

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCAAGGCCT | AGTTTGTTTG | TTTTCGTTTG | GTAAAGCTT | ATTGCCATGC | 60 |
| TGGTGGCGCT | ATGGAGACTG | TCTGGAAGGC | TTGGAATGGT | TTATTGCTTA | TGGTAAAATT | 120 |
| TGCCTGATTT | CTTACAGGCA | GCGTTTGGA | ACCTTTTATT | ATATAGTTGT | TTACATACTT | 180 |
| ATAAGTCTAT | CATTTAAAGA | CATGTACTGA | AACAAATGTA | TTTGTTTCAT | AAGCATCTTC | 240 |
| CTGTAATCTA | TTATAAAATT | GAAATTAAAT | ATAGAGAATG | TTTAAACAAT | TTTTTAATCT | 300 |
| AAAATTTGTC | AATCATTTTT | AATAGTTCTT | TTTTTATAAA | AAGAAAAAGG | AATTTAAGGA | 360 |
| CAGGCAGTAG | TCTCTTTTAA | AATTTATTCA | CAAAACCCAT | TAACTCGAG | | 409 |

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

```

GAATTCGGCC TTCATGGCCT AAGATTATAT AAGATTATGC CAATAAAACT CATGCCTGAG      60
GAAGTGGTTG CTCCTTTTCT ATGGGTCAGT ATTGGTGCAA GAACTGGAAA CCAGCCCTTG      120
GAGAATAGTT ATACATGGC CATGATTTTC CACAGCCCTG GAAATGCACA ATTCTATCCT      180
CCTACCAGGA TGATTGTAA GTTTTAGCTA ACATTGATT ATAAAAGGCC GTAAGTATGA      240
GTATCTCTGA GATAATTTGT GTATTGGAAA GAGGTGTGTA ATAGCACTTT TTTAAAAAAA      300
CCTAGGTGTG AAGGAATTAC AAGTCCAGAA GGCTGAAAT CTATAGTGA AGGAATCATA      360
GAGGAAGCTC GAG                                     373

```

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

```

GTGGAAGTCC TGACCTCAGG TGATCCGCC ACCTTGGCCT CCCAAAGTGC TGGGATTACA      60
GGCGTGAGCC ACCACGCCCG GCCTATCTCT TGTTTTAAA TCAGTCTAGG GTGCCAAAGC      120
ATCAGGGTTC CCGGCCTGCA AGAAAGGGAG ATTCCTGTTC ATGTTAAAGT GTCATATTTA      180
TGAAACTGCC CTTTTTGAA TCTTTGAGGT TGTCTGTACT ATAGGACTGG GGAAATGCAA      240
GTGACTCTAA GAAGAAACCC AGATGTGTCC TACCCTGGCT GGCAGTAGTG AGAAGGGAGG      300
AAGTCTTCC TTGGACACTA GTACTATTGG AAAGTTCCTT ATGTCTGGTT CACTGATGAA      360
GCTTGAGGAT AGAATTGGTG AGGAGGGAGG GGAGAACAGG TCACAGCTGG AGGGGAGCCT      420
GGGCCCTATA GGGTGTGAGG CAGAGCAGAG TGGCAGATAG GACATGTGGA CGGTGGGGAA      480
AATATTCCTC ATGGGACAGA AGATACCTGG CACATGTACC CACAACCTGT ACACAGATGA      540
TCTGTACTGG ACACACGTGG AGATATGGCC ATGCCACGCA TGTGCAAACA GAGGTGTACA      600
CACAGGAGTG CAGTGATACA GGACACAGAT AAACAGAATG TACACAGCTT CTCGAG      656

```

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

```

GCAGGAATAG AGTTGGAGCG GTGCCAGCAG CAGGCGAACG AGGTGACGGA AATTATGCGT      60
AACAACTTCG GCAAGGTCCT GGAGCGTGGT GTGAAGCTGG CCGAACTGCA GCAGCGTTCA      120
GACCAACTCC TGGATATGAG CTCAACCTTC AACAAAGACTA CACAGAACCT GGCCCAGAAG      180
AAGTGCTGGG AGAACATCCG TTACCGGATC TCGTGCGGCG TGGTGGTGGT TGGTGTCTCT      240
CTCATCATCC TGATTGTGCT GCTGGTCGTC TTTCTCCCTC AGAGCAGTGA CAGCAGTAGT      300
GCCCCACGGG TCCTCGAG                                     318

```

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

```

GGAAAAATAC AAAAATTAGC CGGGTGTGGC GACGTGCGCC TG TAGTCCCG GCTATTCAGG      60
AGACTGAGGC AGGAGAATCG TTTGAACCTG GGAGGTGGTG GTTGCACTGA GCCAAGATTG      120
CGCCATTGCA CTCCAGCCTG GGCAACAGGG TGAGANTCTG TCTCCAAAAA AAAAAAAAAA      180
AAAAGCTGGA TTACAGGCGT GAACCAACGC ACCCAGCCAA TTCATAGGTG TTTTAAGTGT      240
GACACTTGGA TGGTTTAAGT CTGATAGAAC TTTTACATT ATTATACATT TAAATATATA      300
CCAGGGGCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:974:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

```

GAATTCGGCC TTCATGGCCT ATTCTTCGCA GATTATGAAG ACTACATTAA ATGCCAGGAG      60
AAAGTCAGCG CCTTGTACAA GAACCAAGA GAGTGGACGC GGATGGTGAT CCGGAACATA      120
GCCACCTCTG GCAAGTTCTC CAGTGACCGC ACCATTGCCC AGTATGCCCG GGAGATNTGG      180
GGTGTGGAGC CTTCCCGCCA GCGCCTGCCA GCGCCGGATG AGGCCATCTG AGCCTCCAGA      240
CCAGACCCCA AACCAGCCCT TGAGTCTGTC AACTCTCTT GGGCCAGCCC CAGCACCTCA      300
TGCAGAGGGT GGGGTACTGG AGTTAGATCT CTAAGCCCCT CCTGGAACCC TCATTTTCCC      360
CACGTGCTCG AG

```

(2) INFORMATION FOR SEQ ID NO:975:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

```

GAATTCGGCC TTCATGGCCT AAAGGATTG ATTGAGAGTG ACATAGCTGC TCTCCATCAC      60
TTTTACTCCA AGCATCTCGA ATTCCCTGAC AATGATAGCC TCGTAGTACT CTTTGCACAG      120
GTAACTGTA ATGGCTTCAC AATTGAAGAT GAAGAACTT CTCATTGGG ATCAGCGATA      180
TTTCCTGATG TTGCATTGAT GAATCATAGC TGTTGCCCCA ATGTCATTGT GACCTACAAA      240
GGGACCCTGG CAGAAGTCAG AGCTGTACAG GAAATCAAGC CGGGAGAGGA GGTTTTTACC      300
AGCTATATTG ATCTCCTGTA CCCAACGGAA GATAGAAATG ACCGGTTAAG AGATTCTTAT      360
TTCTTTACCT GTGAGTGCCA GGAGTGTAAC ACCAAGGACA AGGATAAGGC CAAGGTGGAA      420
ATCCGGAAGC TCAGCGATCC CCGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:976:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

```
GAATTCGGCC TTCATGGCCT ATAGTGTCTT CCTNGGCGCT GCGACAGCCA ATGTAATGGC    60
CTTCTGTGTT CTCATAAGCA GTTTGTACA GATAATCACT GGCAATATCC CTGGAAGCCT    120
TGGCATGCTG GATCCCAATG GCATCAAAC CGAG                                154
```

(2) INFORMATION FOR SEQ ID NO:977:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

```
GAATTCGGCC TTCATGGCCT AGAAGAAATC TCTCTTCCAT TCCTGAAAAC AATTTTAGTC    60
CATTCCTCTT CATTAAACCTA AGTATAAAC TACTAATATC TTTCAAGTGC CAGAAGTTCC    120
TCAAGAAGCC GCAGAAAAG AAATTCCCGT GGCTCCACCC AAAAAACCAG AAGCTCCGAT    180
TGTCCCAGGT AACTTTAGC CCTGACTTCA TTCTGCAGAA GAGATATCTC CTCTCCTACT    240
GTAAACAATT TTAGCCCAT TCTCTTCATT AACTTAAGTC TAAAACTACT AATATCTTTC    300
AAGTGCCTGA AGCTCAAGAA GTTGTCCAG AAAAGAAAGT TCCTAAGGCT CCTCCCACAA    360
AACCAGAAGC CCCACCTGCC ACAGGTATTT TTTACCCCTG TCCTTTTCT GCAGAAGAAA    420
TATCTCTTCT GATCTTAGAA ATATTTTACT CCATTTGTCT CATTAACCTA AGTAAAAAC    480
TCGAG                                485
```

(2) INFORMATION FOR SEQ ID NO:978:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

```
GAATTCGGCC TTCATGGCCT AGAAGATTCT ACAGTGGGC GACGAGGCTC AGAGCAAGAG    60
AGGTATCCTG ACCCTGAAGT ACCCTATCGA GCACGGCATC ATCACCACCT GGGATGACAT    120
GGAGAAGATC TGGCACCACA CCTTCTACAA CGAGCTTCGC GTGGCTCCCG AGGAGCACCC    180
CACCTGCTC ACCGAGGCCC CCTCAATCC CAAGGCCAAC CGCGAGAAGA TGACCCACCA    240
ATCACCTAGG CCATGAAGGC CGAATTCGGC CTTTCATGGC TAGCGCGACC GGCGAGGGAG    300
GAAGAAGCGC GAAAAGCTCG AG                                322
```

(2) INFORMATION FOR SEQ ID NO:979:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

```
GAATTCGGCC TTCATGGCCT AGCCGCATCT TCTTTTGCCT CGCCAGCCGA GCCACATCGC      60
TCAGACACCA TGGGGAAGGT GAAGGTCGGA GTCAACGGAT TTGGTCGTAT TGGGCGCCTG      120
GTCACCAGGG CTGCTTTTAA CTCTGGTAAA GTGGATATTG TTGCCATCAA TGACCCCTTC      180
ATTGACCTCA ACTACATGGT TTACATGTTC CAATATGATT CCACCCATGG CAAATTCAT      240
GGCACCGTCA AGGCTGAGAA CGGGAAGCTT GTCATCAATG GAAATCCCAT CACCATCTTC      300
CAGGAGCGAG ATCCCTCCAA AATCAAGTGG GCGGATGCTG GCGCTGAGTA CGTCGTGGAG      360
TCCACTGGCG TCTTCACCAC CATGGAGAAG GCTGGGGCTC ATTGCAGGG GGGAGCCAAA      420
AGGGTCATCA TCTCTGCCCC CTCTGCTGAT GCCCCCATGT TCGTCATGGG TGTGAACCAT      480
GAGAAGTATG ACAACAGCG                                     499
```

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

```
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT ACTTGCCTCC      60
TTTGCTGTTT TAGGAACAAT TCCATGGGAG GGTCTATTCT GGATTAGGAA TTCTTTCTTG      120
AGTAATTTTT ATTACCTTTT AATTGTGTCC ATTCTTTTGG GAAATAGCAA GCTCTCCCTG      180
CTCCCGCCAA TCTCTCCTCT TACTTTTTGG ACCAGTTCTT GTACCTCTTA GCTCACCTCA      240
TTCAGTGAAA ATTGACAAAA GAGACGTGAG TTTCTGTACC TGTGAGACAG CTTATTTTGG      300
TGTCTTTATG GTTCTAAGC CAAAAATCTC GAG                                     333
```

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

```
GAATTCGGCC TTCATGGCCT ATCGAGTAAT CCTGATGTTT TCACTTTCTC TAATCACTTC      60
TTCCTATTTT TGTCCAGTGG CTTTCTCGA G                                     91
```

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

```

GGCCGCTCGT GGCTGCGTTC CCGCTGATGC TTGTGCCTGC AGAGCCTCTC CAGGCTGCTG      60
GTGGGGGAGC ACTCCCTTCC CCGAGGTCTG GACGCTGATC TCCTTTTCTT CTTCTTCCTA      120
CTCTCATAGT GCTCATAGGA AGAGCTGCCA GGGCTCCCCG ACCGCGACCG GGACGTCCTC      180
CGGCTGTGGC CCCAGGGGCC CCGCTGTGTC TCCCTGCTCT TGTCTTGGC TTTCTTCTC      240
TTAGCTCGCT CTCGGCTGCT GGAGCGGTCA CTGGAGGACC GCCGGCTCTT GGCCTTGGAC      300
CGCTGCCTCC TGGGGCGCTC CTCACCCACT GATGGTGACG CCGACCTCGA G      351

```

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

```

GAATTCGGCC TTCATGGCCT ACACAAATAT TGCTGTTCCA TGTTCTCCAC TTTCATTTTC      60
CACTACAAAT GAAAAGCAAT TTTTGAGACT GAATCTGTTG CTATTTTAAA GGTTATTGTG      120
GGAAACTGAG CTAAAGGAGT TAGCATCTTT ATTTTGTAT CAAAAATAAA GGTTATTTTG      180
AAATTATTAG GATTTTACA CAATTCTGAA ATCTGTTGCT TTTGTAAACA AATTGTTTGA      240
TCTTAGTGAT CCCCTACTA CTACCACCAA TTCAC TTCAC AAAGTCAGTT ATGAGTCTAC      300
CAGACTTTGT TCTGAAAAAT AGAAACAAAA CACCTGATTA AGCTCTTGAG TATGGCATAG      360
GAATTTTTTA GAAGAATGCA TTCAAGGATT CTTTTCCTTT CCTTCAGTGT CATTAATGTT      420
AAAAGAGCAG CCACTGTTTT GTTGAAACAA ACAGCTTAAC TTCAGAAATA AGAACTAGCA      480
CACTCGAG                                     488

```

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

```

GAATTCGGCC TTCATGGCCT ACCTCCTGGC TCAGCAGGCT CCCTCCTTTT ACCAAGACTG      60
CTGGGACGTT GAACTCCGGT GTCTGATCAT CTCACCTACT CTCCTCCTAA CTCCCAACTG      120
AAATCCATCT CCTCTCTTCC TCCCCAACAT CCATCTCTTT CCAACATGC CTTTGCACCT      180
AGAGCAGGTG AAGAAAGCCC ATGACTAAAA CTAAAGACTC AGAATGAAAC AAAAGGTGTG      240
ACAAGTTATT TGTGGGAAG GTTTTCAGAT ATGTTCCAAG AGAAAATAAG GTAAAACAAC      300
CTTGTTTCATC AGACCAACAG TGCTGGAAG GGCTCGAG                                     338

```

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACCTGAATTG | GGTGGCGAGT | TCCCTGTGCA | GGACCTGAAG | 60 |
| ACTGGTGAGG | GTGGNTTGCT | GACAGTGACC | CTGGAAGGGA | TCAACCTCAA | ATTCATGCAC | 120 |
| AATCAGTGT | ACCTTTTATC | TCTCAGTGGA | CATTCTTAA | GCTAATTCCT | TTCTGAGGCC | 180 |
| AGCGCATCAT | CCCAGGACCG | GAAGGTTTC | ATAGAGCTGA | ATCACATTAA | AAAGTGCAAT | 240 |
| ACAGTTCGAG | GCGTCTTTNG | TCCTGGAGGA | ATTTGGTAAT | TACACTATT | TGCTCTTAGG | 300 |
| TCTGGACTCA | CATGGCAGTA | ACTCAAACCT | CGGACTCTCCA | GAGGAGGGTC | TAGGGGCAGG | 360 |
| GAGAAGAAGA | ACCTCTGTAG | AGAAGTCTGG | AGGAGCAGGA | GTGACAAGGA | AGAAAAGGGA | 420 |
| CCCCTGAGAT | GAGAGCCGGG | ATGTGGAAGG | GAAAGATAGA | TAATGGATCG | CAGAAGAGCA | 480 |
| AATGGGGCCT | CNGGTGGTAC | TCGAG | | | | 505 |

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACACCTTCAC | ACCTGTCCTT | ACCTCCATTC | TCACTTCCAC | 60 |
| TGTCTTCACT | AACTCCACCA | TCATCACTTC | AATCTTCCCT | TCCATTCTCA | CTCTCTTCTC | 120 |
| ACTCACTGTC | CCTCTTTCAC | CTCCATCCTC | ATCTCTGTCC | TCCCGTCTAT | TCTCCTCTCC | 180 |
| AACCTCACTT | CTGTCTCTCC | CTTCTCTCTG | CTCTCCATCC | TCACCTCCAT | CCTCACCTTC | 240 |
| AACCTCACCT | TTATCTCTAC | CTTCAACCTC | ACCTTTATCC | TCACCACTCG | AG | 292 |

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCGAGTATC | CACTTGCCTC | GGCCTCCCAA | GGTGCTGGGA | TTACAAGCAT | GAGCCACCAT | 60 |
| GCACGGCTGT | AGATGTAAAT | TTTGGAAAGA | GGAAGGCATC | AAATTAGGGG | TGGGGGGATG | 120 |
| GAGGTACATC | CAGCTTAGCC | TTGAGACCTT | AATGGAAATG | CTTTCTAAAC | TAGCGATCCC | 180 |
| AGAGCAGTTG | ACTCTCCTGA | AATAAAACAG | GATCTGAGTA | GGCCATGAAG | GCCGAATTC | 239 |

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGCAGACTGC | AATACCTGCG | TGGAAATAGA | AGACAGAAAG | GTTTCAAGAC | AACAGATGAA | 60 |
| TTGTGAAAGA | GAGCAGCTAA | GGGTAATCA | GGAAGCAGCC | GCTGCCCCTG | ACACAATGGC | 120 |
| TCAGCCTTAC | GCTTCGGCCC | AGTTTGCTCC | CCCGCAGAAC | GGTATCCCCG | CGGAATACAC | 180 |
| GGCCCCTCAT | CCCCACCCCG | CGCCAGAGTA | CACAGGCCAG | ACCACGGTTC | CCGAGCACAC | 240 |
| ATTAAACCTG | TACCCTCCCG | CCCAGACGCA | CTCCGAGCAG | AGCCCCGGCG | ACACGAGCGC | 300 |
| TCAGACCGTC | TCTGGCACCG | CCACACAGAC | AGATGACGCA | GCACCGACGG | ATGGCCAGCC | 360 |
| CCAGACACAA | CCTTCTGAAA | ACACGGGGCT | CGAG | | | 394 |

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTTCCGGGC | TTTGACTCAA | TTCATGGGAA | ACAGGAAAAG | 60 |
| CAAAACTAGT | TGATCTTGCT | ACTAAGGCGG | ACTGAAGTTT | CTGTCTTCA | TTGCTAAACA | 120 |
| ACTTCCAAAT | CACTTTGACT | CTTTGACCAT | ATTCATGTCT | ATTTCCCAT | AAAGCATCAC | 180 |
| AAAATAATGA | AGGAATTCTT | AGGAAGAGCC | TCAAGATGCC | CATGTGGCGT | CTGTGTGGGC | 240 |
| TGCCTCGTCT | GGTAGTTCAG | GGACCCACTG | GGCCATTGTA | AGGGCAAAGA | GAAAGCCCCA | 300 |
| GGTCTCATGG | CAGGAGACAA | GACTTCCACA | GTGGTGAGCC | AGTAAGGAAC | AGGGCACGTA | 360 |
| CTCGAG | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACATGTTTCAT | TATGAAGTTA | TTAGTAATAC | TTTTGTTTTT | 60 |
| TGGACTTATA | ACTGGTTTTA | GAAGTGACTC | TTCCTCTAGT | TTGCCACCTA | AGTTACTACT | 120 |
| AGTATCCTTT | GATGGCTTCA | GAGCTGATTA | TCTGAAGAAC | TATGAATTTT | CTCATCTCCA | 180 |
| GAATTTTATC | AAAGAAGGTG | TTTTGGTAGA | GCATGTAAAA | AATGTTTTTA | TCACAAAAC | 240 |
| ATTTCCAAAC | CACTACAGTA | TTGTGACAGG | CTTGATGAA | GAAAGCCATG | GCATTGTGGC | 300 |
| TAATTCATG | TATGATGCAG | TCACAAAGAA | ACACTTTTCT | GACTCTAATG | ACAAGGAGCT | 360 |
| CGAG | | | | | | 364 |

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCGG GGAAGAAGAC AAGAAAATTA ATGAAGAACT GGAGTCTCAA | 60 |
| TATCAGCAAA GTATGGACAG TAAATTATCA GGAAGATATC GGCGACATTG TGGACTTGGC | 120 |
| TTCAGTGAGG TAGAATACCA TGATGGAGAA GGTGATGTGG CTGGAGATGA TGATGATGAC | 180 |
| GATGATGATT CACCTGATCC TGAAAGTCCA GATGATTCTG AAAGCGATTG AGAGTCAGAG | 240 |
| AAAGAAGAAT CTGCTGAAGA ACTCCAAGCT GCTGAGCACC CTGATGAAGT GGAGGTCTCG | 300 |
| AG | 302 |

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTGCAGCA GGTCTCTGG GAAGTGTCGC ACAAAGGAGT | 60 |
| CGCCCACTGG AAGGTTCTGG GCAGGCGAGA TGCCAGAGG TGATCCCTGC CCGCCCCTCC | 120 |
| CACCTCCCTT CCCACACAGC CCATGGAGGT GTTTGTGGAC GACGAGACCA AGCTCAGCT | 180 |
| GCACGGCCTG CAGCAGTACT ACGTCAAAC TCAAAGACAGT GAGAAGAACC GCAAGCTCTT | 240 |
| TGATCTCTTG GATGTGCTGG AGTTTAACCA GGTGATAATC TTCGTCAAGT CAGTGCAGCG | 300 |
| CTGCATGGCC CTGGCCCAGC TCCTCGTGGG GCAGAACTTC CCGGCCATCG CCATCCACCG | 360 |
| GGGCATGGCC CAGGAGGAGC GGTGAGTNCG AACCGCCCGC CAAGGCTGCA GGGNGCACCA | 420 |
| CCAGGAGCCC AGTGTCTGAC GGCCTCCACT TGTCTCTCT GCACCCCNCC CCATCAGCT | 480 |
| CGAG | 484 |

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAAGGAATTT ATCTATTTAA TCATTGAATG TATTGAACAT | 60 |
| TCATTTGTTT ATAATTTTGT TTTGTTATTG AAAATGTCTG TAAGATTAT AGTGATGTTT | 120 |
| CCTTTTCTAT TCCTGACATT GTTAATTTGT GTTCTCTCTC CCTCCATCCC TCTCTCAT | 180 |
| CTCGAG | 186 |

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

```

GAATTCGGCC TTCATGGCCT AGTGTTCCTCA TAAAGGGGTT GAGGCCACCA GTACTGCAGC      60
GAATTTTCCTT TTCTTCTCCC TCCTCCTTCC TTCTCTGAGC TTGCTTTTAG GGAAGGTAA      120
TCTTACAGGC TACCTATGTT TCTCTCCACC TTAATAAAAT CTAAATAATG ATAGAAATTT      180
TAAGTTTTTA AATTGAGTAG TTCTGAGTAA TCCTAGAATA TTTTCCAAA TTAAATAATC      240
CTTATTATT TGCAAGTTGG GCCAAATTT TTTTTTTGTG GAGACGGACT CTTAACAATC      300
TAAGATTGTT TCAACAGGAC TTTCTTATTC CCATCCCTC GAG                          343

```

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS: ..

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

```

ATCTTTAACA GAATTATTAT TATTTAATAT AGAAGCACAA GCAGGGGAAA AATACGTCA      60
CAAAATTTTC AAGTAGTCAA CTCATTATTG GAGCCATTTT ATTTTATAAT TTTATTATC      120
AGCTGGTTCA GAATTCAAAA GGGCATGTAA TGAAGTCGCT ATCCTGCTTC TGTTCCCGAG      180
CTATCCAGCT TCCCTCCCTG GAGGCAACA GTGTCATTGG TTTCAATAT ATCCTTCCAG      240
ATGTATGTTA TCCGTAATC TCGAG                          265

```

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

```

GATTCGGCTT CATGGCCTAC AGCAGACACC CTCCTGCCCA CACCTACTTG TCCGCGCGGT      60
CTGAGGTTTG CTTGAGG                          77

```

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

```

GAATTCGGCT TCATGTCGCT CTTCTGCGAG GTCAACATGT ACAGCAGCGT CTTCTTCCTC      60
ACCTGGATGA GCTTCGACCG CTACATCGCC CTGGCCAGGG CCATGCGCTG CAGCCTGTTC      120
CGCACCAAGC ACCACGCCCG GCTGAGCTGT GGCCTCATCT GGATGGCATC CGTGTCAGCC      180
ACGCTGGTGC CCTTACCGC CGTGACCTG CAGCACACCG ACGAGGCCTG CTTCTGTTC      240
GCGGATGTCC GGGAGGTGCA GTGGCTCGAG                          270

```


(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID No:998:

```

GAATTCTAGA CCTGCCCCCA GGCCACAGTC ACACCCCCCA GGAAGGAAGA GAGAATGGAT      60
TCTGCAAGAC CATGTCTACA CAGACAACAC CATCTTCTGA ATGACAGAGG ATCAGAAGAG      120
CCACCTGGCA GCAAAGGTTT TGTCACTCTA AGTGATCTTC CAGGGTTTTT AGGTGATCTG      180
GCCTCTGAAG AAGATAGTAT TGAAAAAGAT AAAGAAGAAG CTGCAATATC TAGAGAACTT      240
TCTGAGATCA CTCACAACT CGAG                                         264

```

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

```

GAATTCGGCT TCATGGCCTA GCGGATTGTA ACTGCCTATG AGAATAGCTC TCAGCATGAT      60
CCCAGTTCAA ATAACGCTAT GCTTGGGGTT CATGCATCAG CTTACGCGAT CATCCAGTAT      120
GGAAAAATCG CCCGGAAACA AGGACTGGTC AATGTAGCTC TGGATATATT AAGTCGGATT      180
CATACTATTC CAACTGTTCC TATCGTGGAT TGCTTCCAGA AGATTGACA GCGTACTCGA      240
G                                         241

```

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

```

GAATTCGGCC TTCATGGCCT AGAATTGAAT TTAGACTTTA CAGAGTTACT GGTTTGTAAG      60
TCTTTGAGTT GTTTAAATTT TAATGTTAGA GTTTTACTGT TTGATCAGCA CATTTTTTTT      120
CTCTTTTGTC TATAGGCCCG AAATGTTTGA GACGGCGATT AAGGAGAGCA CCTCCTCTAA      180
GAGCCCTCCC AGAAAAATAA ATTCATCACC CAATGTTAAT ACTACTGCAT CAGGTGTTGA      240
AGACCTTAAC ATCATTGAGG TGACAATTCC AGATGATGAT AATGAAACAC TCGAG          295

```

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGATATTTAG AAATTTTGTG TATTATATGG AAAAAGAAAA | 60 |
| AAAGCTTAAG TCTGTAGTCT TTATGATCCT AAAAGGGAAA ATTGCCTTGG TAACTTTTCAG | 120 |
| ATTCCTGTGG AATTGTGAAT TCATACTAAG CTTTCTGTGC AGTCTCACCA TTTGCATCAC | 180 |
| TGAGGATGAA ACTGACTTTT GTCTTTTGA GAAAAAAAC TGTACTGCTT GTTCAAGAGG | 240 |
| AGCTCGAG | 248 |

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

| | |
|--|-----|
| GAATTCGGCC TTCATGGAGT CAGCCTTCCA GTCCTCATCT CAGAAATTGA CTAGCCAGAA | 60 |
| GGAACAGAAA AACTTAGAGT CTTCAACAGG CTTTCAGATT CCATCTCAGG AGTTAGCTAG | 120 |
| CCAGATAGAT CCTCAGAAAG ACATAGAGCC TAGAACAACG TATCAGATTG AGAACTTTGC | 180 |
| ACAAGCGTTT GGTTCCTCAGT TTAAGTCGGG CAGCAGGGTG CCAATGACCT TTATCACTAA | 240 |
| CTCTAATGGA GAAGTGGACC ATAGAGTAAG GACTTCAGTG TCAGATTCT CAGGGTATAC | 300 |
| AAATATGATG TCTGATGTAA GTGAGCTCGA G | 331 |

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACAGTATTGG ACTTTCAGAA GCTGAACAGA TGATGGGTGA | 60 |
| GCAAACCTGGT TTAGCAGACC CAAGAGAGCT GAATCCTAAG CCAGCAAATA GAGAAATCCA | 120 |
| AGATTCAGCC CAAATTATGC TTTAGAATTC CTCAAAGGCT CAGAACTGG CTGCACTAGT | 180 |
| TCCCCCGACA GGAAGCATGG ATTGAGGAGG TACCAAACCC ACTCCCCACC AAAAACCCAA | 240 |
| AACTCGAG | 248 |

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

```

GAATTCGGCC TTCATGNCCT GGNGAAGAGN AACAAAGAGAA CAAAAAAN ANAAGTCGAG      60
AGTCAGTAAT TTTCTTACTT AATATTGNGG GGATNTTACT TNATACATAA AGTTANTGAA      120
ACTAGAAATA GTGGTTTAAAT ATATTACTTN TAATTCAAAA ATTAACCTAT ATTTACAGAT      180
GCTCTACACA GTTTCTTTGT GAATCCACCT ATGGTTTTAT TTTNATTAAT TTTTNTTNC      240
ANAGCNATGA AATGTTGCTT TGTGGNGCCA GCGCACTCGA G                                281

```

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

```

GAATTCGGCC TTCATGGCCT ACATAACCA TCACATTTAA TCTGGCAGCT GCCCTGTTTT      60
TGAGGTTTTT TTTGTATTTA TCTTTCTTTG GTAAATGAAA GCTCTCATCT TTGTTTACAG      120
GCCAGAAAAA CTGAAAAAGA CACAGGCTCT TCCACTTACT GGATGTTTGA CAAATGATA      180
TTTTGGGGCC AAAACATTGG CATTACTGGT AAACCTGGTA GAGATTGAGT AACTCAGACT      240
TTATTTTCTG TCTCCTGAAA AAATAATCTG CATTAACTG ATGACTCGAG                    290

```

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

```

GAATTCGGCC TTCATGGCCT AAATTTTCAC ATATATGTAT ACTTAATTTT CAGCAATTAT      60
GACACAATAA AAAGAATATG CAAATTTATT GTTGTTCAG AAGGTTTTC AGGACTGGGA      120
ACGCTTTAGT GTCATCAACA GTAAACCTCA GATACTGTTT TGCACAGTTC AGAAGTACCA      180
TACCAGGTAT TGTGAGTGGC AAGAACGCCA GGGGACAGAG ATGCTTCTGG TAGATGAGGG      240
CCAGAGAAAC CAGCTCTCCT CCATTTTGAC AGCAATTCTT CACTGTGGCC ATTTGGCCTC      300
CATTATGTTT TGAGAGGAAC GCTCGAG                                           327

```

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

```

GAATTCGGCC TTCATGGCCT AAAAAAAT ATAGTGTTTT ATGCCACAGA GAATCAAGTT      60

```

GCATTGTGTA TACTAAATGG TCAAGCATTT TCAAGAACAT GACAAAATAA AAACATACAA 120
 ATTTATATCT CAAAAGGAAA GTATCTTCTT TCATGTCAGA TCATCAGCAC AGAAGCCCTC 180
 GATGCATGCA AAGGCAAGCA CAGGCTCTGC AGATGAGATG TGAAGAAGCA ATTAGGGAAA 240
 TTCTCGAG 248

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GAATTCGGCC TTCATGCCTA CATCAAACCC TTTTCTTGTA GCAGCACAGG ATTCTGAGAC 60
 AGATTATGTC ACAACAGATA ATTTAACAAA GGTGACTGAG GAAGTCGTGG CAAACATGCC 120
 TGAAGGCTG ACTCCAGATT TAGTACAGGA AGCATGTGAA AGTGAATTGA ATGAAGTTAC 180
 TGGTACAAAG ATTGCTTATG AAACAAAAAT GGACTTGGTT CAAACATCAG AAGTTATGCA 240
 AGAGTCACTC TATCCTGCAG CACAGCTTTG CCCATCATT GAAGAGTCAG AAGCTACTCC 300
 TTCACCAATT TTGCCTGACA TTGTTATGGA AGCACCATTG AATTCTGCAG TTCCTAGTGC 360
 TGGTGCTTCC GTGATACAGC CCAGCTCATC ACCATTAGAA GCTTCTTCAG TTAATTATGA 420
 AAGCATAAAA CATGAGCCTG AAAACCCCCC AGAAGTCGAG 460

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

GAATTCGGCC TTCATGGCCT ACGACAAGTT TTTAAATTTA CTCTTGAGTA TGGTTCAGT 60
 GATTACCAG AAAAACCAAG AAGACAGGCA CAAAAAGCA AACGGCATTG GGCAAGATGG 120
 ATTATCAACT GCAGTACAGA CTTTATAGTAA TAGATCTGAG CAACACATGG AGTATCACAG 180
 TTTCTCAGAG CAGTCTTTTC ATGCCAATAA TGGGCACGCA TCATCAAGCT GCAAACCTCGA 240
 G 241

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

GCGATTGAAT TCGACCACCT TGTTCAAATT TGTTATTATT TTTCTACTTT TGTATTGATT 60
 CTGTTAATTC TTATCTATTG GTTCAGCTTA CTTTTTATG TTGGTCACAT TTCTCTTCAT 120
 TGATTGTGTT AATTTTCTA TGTGATAGA CACATTTTAT GTTCATCACT TTTTCTCTC 180

CTCCTTCAAT TATTATCCTT CTGATTTCTT TTTGTTTTCT CATAGTGTTG GCCATCTCGA 240
G 241

(2) INFORMATION FOR SEQ ID NO:1011:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

GAATTCGGCC TTCATGGCCT AGGCCACAAC TCAAAAGCAT TATCTTTTTT AGGGTTAGTA 60
 GAAATTGTTT TATGTTGAT GGAGGTTTGT TTGATTGTCA AAATGTACAG CCACAGCCTT 120
 TTAATTTGGG AGCCCCGTGT GTCAATCAAA TGTGTACCTC TACAGTTGTA AAAAGTATTA 180
 GATTCTACTA TCTGTGGGTT GTGCTTGCCA GACAGGTCTT AAATTGTATA TTTTGGGAA 240
 AAGTTTATAT ACTCTCTTAG GAATCATTGT GAAAAGATCA AGAAATCAGG ATGGCCATTT 300
 ATTTAATATC CATTCAATTC ATGTTAGCGG AACTCGAG 338

(2) INFORMATION FOR SEQ ID NO:1012:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

TGAATTCTAG ACCTGCCTCG AGCTCCAGCT GCCAACACCC TTGGACACAA TATTCCAGTC 60
 TCCACTGCCC ATCTCATGTG GTTGCAGGNT CCTCGAG 97

(2) INFORMATION FOR SEQ ID NO:1013:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

GAATTCGGCC TTCATGGCCT ACACATTCTG GGGGAAAAAA ACTGGAATTG TTTGTATTTT 60
 GTTTTTTTGG GGGGGATCT TTATGTGAAA AATCAGAGCT ACTTGTTACC ATAAGCCCTT 120
 ACTATCAACA AGATAATTAT TTGTAATCAC TTTTATATCC CAGGTTGGAA TTGCTTTCCC 180
 CTTCTAAGTT ATCTTCCCTT AATAATATT ATGATACCAG GACAGTGAGG GTATAAGAGC 240
 AAATGTAGTG AGGTATTCAA AAATCCTGCA TATATGGACT CAAAAGTTCT TTAGTTATTT 300
 GAATTATATA TAGCTATATT ATTTTATTAG CTTGGGTTGT CAGAAGATTG CCAATTTTAA 360
 GAGTAAAGAG GAGAGAGATA AGTAATAAAA ATAGAGGAGG GGTACTCTCG AG 412

(2) INFORMATION FOR SEQ ID NO:1014:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

```
GAATTATGTC TCCCATCTGT GCTTTTCCTA AGTGGGGCTC CCGTGCCGTT CACCTCACAT      60
TCCTGGTGTG TTA CTGGCA GGC ACTCCCA CCACTCCGAA AGGGAGGCC TTCCTGGGAG      120
GGAGGCAAGA AGGCTCCCA GCCCCTTTC CCCCTTTCCT GGGCCTGCGT TCCAGGGCC      180
TCCCAGCCC CTCTGGCTAC CCCGTGACCT GCCTCGAG      218
```

(2) INFORMATION FOR SEQ ID NO:1015:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

```
GAATTCGGCC TTCATGGCCT ACCTTATTAC CAGACAACCT TAACCAAACC ATTTACCCAA      60
ATAAAGTATA GGCGATAGAA ATTGAAACCT GGCGCAATAG ATATAGTACC GCAAGGGAAA      120
GATGAAAAAT TATAACCAAG CATAATATAG CAAGGACTAA CCCCTATACC TTCTGCATAA      180
TGAATTA ACT AGAAATAACT TTGCAAGGAG AGCCAAAGCT AAGACCCCG AAACCAGACG      240
AGCTTCGGGG GAAGTATGTA GGAGTTGAAG ATTAGTCCGC CGTAGTCGGT GTACTCGTAG      300
GTTCA GTACC ATTGGTGGCC AATTGATTG ATGGTAAGGG AGGGATCGTT GACCTCGTCT      360
GTTATGTAAA GGATGCGTAG GGATGGGAGG GCGATGAGGA CTAGGATGAT GGCGGGCAGG      420
ATAGTTCAGA CGGTTTCTAT TTCCTGAGCG TCTGAGATGT TAGTATTAGT TAGTTTGT      480
GTGAGTGTTA GGAAAGGGC ATACAGTCTC GAG      513
```

(2) INFORMATION FOR SEQ ID NO:1016:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

```
GAATTCGGCC AAAGAGGCCT ACCAAAATAA AAACAGAAAT TATGAGATTG CCTCAACTCC      60
CACATATGCT CGAG      74
```

(2) INFORMATION FOR SEQ ID NO:1017:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

```

GAATTCGGCC AAAGAGGCCT AAAGACCTGA GGTCCAGGAT GAGCTCTTTC CCACAGAAAC      60
TTTGACAAAT GTGTGGACAA TAAAGNAGCA CTGCTTCCCT CATTACCAT AGCTCAGCTG      120
GATTTATAGA TTAAATCTT TTAACGAAAA AGTTCATGTT GAGGTATTTA GATACTTTT      180
AGAGGGTTAA ATACCAAGTT ACAGTGACAT TTAACCGAG TGTCTAGAAC ATGAAGGCAA      240
AGAGTCTGCT ATTCGGAGGT AAATTTTATC AGTGTTTGAA AGGTGAAGCA TTTGCTCATG      300
AAATGTTGAA TGAATTTCTG TGACATGGCA CGAGGSGTGT AAGAAAAAGT GGGAACTCGA      360
G

```

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

```

GAATTCGGCC AAAGAGCTAC GAGAGTGTCA TGAAATATCT CCGAGAGTCC TTCAGTGAGA      60
GGTTGTTTTT TTTTCCTATG GCTGGTGTCA CTTCTCTGAG AGCATCTTCA TCGTTTCATC      120
ACAGTCACCT TCTAACTGGA GTCAGTAAGT TCACCTTCTT TAAGCTTCCC AGGCTGCAGA      180
TACAGAGAGT GTCCACATTC CACAGTCAGC TATTCTACG ATCACTCCAT TTACGCTTGG      240
TTCAAATTC ACTCCAGTG TTACCACTTC TCATTCTTTT GCTGTGTTTC ATCTGGGCCA      300
TTTGCTTCTT ATGATTACCT GTTTTTGTAA ACTGTCATGT GGGTTTATCC CTGGGAGACA      360
AGGAGACAGC ACAACCCCTT GGTGCTGTCT CTGTGAGCGA ACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

```

GAATTCGGCC AAAGAGGCCT ACTAAGTTCT GTGAAGTGTA TGTAGCATCT GGGCTATAGA      60
TTTGAGGCTT TTAAGTACTC TNGAGAGTGG TGAAGGAGTA TCTGCAGCTC TGATGACAGG      120
NACAGAGAGA GAGAGAGAGA GATGGGTATG CCATCCGTGG ACACCAGGAA GAGTACCGAG      180
GACTGCTGTA GGCTCCTTCA GTTCTAGTTT CCAACTCAA GCAATTTTAA AGTTTTTGTT      240
TAATTATGNN TCGGCTCTGC TAAGANANNA AGGTACCTTA CATAAGTCCC TCAAAAGACT      300
TGTTGTTTGG AAGATGGCGC CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATGAATGCTA TATACCTTTT TTATATCAAA AGTCTCAAGC | 60 |
| ACTTATTTTT ATTCTATGCA TTGTTTGTCT TTTACATAAA TAAATGTTT ATTAGATTGA | 120 |
| ATAAAGCAAA ATTACTCGAG | 140 |

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

| | |
|---|-----|
| GAATTCGGCC AAAGAGCTAC GGCCAAAGAG GCCTAGACTC GCCGCTGNTC TCACACCAGT | 60 |
| GTGGAACGTC CCCGCCNTC CCCTGGGGTC CTTATCTTA GGGGACCGGG ACGTCCATCC | 120 |
| CTTCTGCAGT GGCAGCNTCT GAGCCAAAGC GCCTCTCCA GAAGCCGGAC TTTCCAGGAC | 180 |
| CCTCACTCCC AGCCACACCC TGACACGGCC TGACTGGGGT CTCTGTGAG TCCCATGCTC | 240 |
| GGCTTTGTCT GACACCTCCC AGGACAAGAC CGTCCCTTCT CCCCAAATG GGCTCTCCAC | 300 |
| CAAGAGCCGC GTTCACCCAC GGGGGAGTGG GCTCCACACA GGCCAGTCCT CGAG | 354 |

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

| | |
|---|-----|
| GAAAGAGGCC TAATCGTCAC ATCCATCAGA GGATTGCTGA TCACTCTTAC CAAGTTCCTT | 60 |
| TATGCCATCT CTAGCAGTAA GTCCTCCAAT GTCATTGTCC TGCTATTAGC ACAGATAATG | 120 |
| GGCATGTA CTGTCTCCTC TGTGCTGCTG ATCCGAATGA GTATGCCTTT AGAATACCGC | 180 |
| ACCATAATCA CTGAAGTCCT TGGAGAACTG CAGTTCAACT TCTATCACCG TTGGTTTGAT | 240 |
| GTGATCTTCC TGGTCAGCGC TCTCTCTAGC ATACTCTTCC TCTATTTGGC TCACAAACAG | 300 |
| GCACCAGAGA AGCAAATGGC ACCTTGAAC TAAGCCTACT ACAGACTGTT AGAGGCCAGT | 360 |
| GGTTTCAAAA TTTAGATATA AGAGGGGGGA AAAATGGAAC CAGGGCCTGA CATTTTATAA | 420 |
| ACAAACAAAA TGCTATGGTA GCATTTTCA CCTTCATAGC ATACTCCTTC CCCCTCAGGT | 480 |
| GATACTATGA CCATGAGTAG CATCAGCCAG AACATGAGAG GGAGAACTAA CTCAAGACAA | 540 |
| TACTCAGCAG AGAGCATCCC GTGTGGATAT GAGGCTGGTG TAGAGGCGGA GAGGAGCCAA | 600 |
| GAAACTAAAG GTGAAAAATA CACGAACTC GAG | 633 |

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ATCTTGCAG | TGGAGTGTCC | GCTGTGCCCC | GGCCTGCACC | 60 |
| ATGAGCGTCC | CGGCCTTCAT | CGACATCAGT | GAAGAAGATC | AGGCTGCTGA | GCTTCGTGCT | 120 |
| TATCTGAAAT | CTAAAGGAGC | TGAGATTTCA | GAAGAGAACT | CGGAAGGTGG | ACTTCATGTT | 180 |
| GATTTAGCTC | AAATTATTGA | AGCCTGTGAT | GTGTGTCTGA | AGGAGGATGA | TAAAGATGTT | 240 |
| GAAAGTGTGA | TGAACAGTGT | GGTATCCCTA | CTCTTGATCC | TGGAACCAGA | CAAGCAAGAA | 300 |
| GCTTTGATTG | AAAGCCTATG | TGAAAAGCTG | GTCAAATTTT | GCGAAGGTGA | ACGCCCCGTCT | 360 |
| CTGAGACTGC | AGTTGTTAAG | CAACCTTTTC | CCACGGGATG | GATAAGAATA | CTCCTGTAAG | 420 |
| ATACACAGTG | TATTGCAGCC | TTATTAAAGT | GGCAGCATCT | TGTGGGGCCA | TCCAGTACAT | 480 |
| CCCAACTGAG | CTGGATCAAG | TTAGAAAATG | GATTTCTGAC | TGGAATCTCA | CCACTGAAAA | 540 |
| AAAGCACACC | CTTTTAAGAC | TACTTTATGA | GGCACTTGTG | GATTGTAAGA | AGAGTGATGC | 600 |
| TGCTTCAAAA | GTATGGTGG | AATTGCTCGG | AAGTTACACA | GAGGACAATG | CTTCCCAGGC | 660 |
| TCGAG | | | | | | 665 |

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTTGATTG | GATTCACATT | GCTTTCATTT | CTTAAAATGC | 60 |
| TTCACTTCAG | GTTCTTGGTC | TTGGAAATAA | ATTTCAAGGT | GCATTGTATC | CATTTTAAGC | 120 |
| TGCTTTATTT | TATTTTCACT | TGTATGAGCA | AATTCCTGGG | GGAGCTTTGC | TTTTCTTCTG | 180 |
| CCAGAAAAAC | AAAAGGGGGA | AATGAAAATC | TTTTTTGGAA | TGAGTTCTGT | GGGTTTTCTT | 240 |
| AACAGCCACC | ATGTTTATTA | GTTACATTGT | GTTTTGGCCA | ATCAGTGCAA | TGTAACAAAT | 300 |
| TTTACAGTTA | ATTGCTTTCA | ATTGAGTCAG | TAAACCTGTG | ATAGATAATT | TATTTAACTG | 360 |
| GAAAACCTAG | GTACCCATAA | GAAAAAAGAT | TCATTCTCTG | TGAAAACCTG | AGGAATCTGT | 420 |
| TGTTGTTTTT | ATTGTAATAT | GCTCTACTTC | TGCTCTAGTA | TTGGTTTGG | AATATATTTT | 480 |
| GTGGCTCTAA | TTACTGTATT | TTTAAAAACC | CTACCTCCAT | TAACAGTTGG | TAAAGGCCCC | 540 |
| CTTCTCGAG | | | | | | 549 |

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| GAATTCGGCC | AAAGAGGCCT | AGTTAAGTCT | GAAGTAGTCT | TTTCCTTTGT | GATGTGGTTG | 60 |
| GAAAGTCTTC | CCTGTTCCAA | GGACTCCTCG | AG | | | 92 |

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTTAAAAAC TAATATTTAT ATGACAGAAG AAAAAGATGT | 60 |
| CATTCCTGTA AGTAAACATC ATCATCTTGG TCCTGGCTGT TGCTCTCTTC TTAGTGGTTT | 120 |
| TGCACCATAA CTTCTCAGC TTGAGCAGTT TGTTAAGGAA TGAGGTTACA GATTCAGGAA | 180 |
| TTGTAGGGCC TCAACCTATA GACTTTGTCC CAAATGCTCT CCGACATGCA GTAGATGGGA | 240 |
| GACAAGAGGA GATTCCTGTG GTCATCGCTG CATCTGAAGA CAGGCTTGGG GGGGCCATTG | 300 |
| CAGCTATAAA CAGCATTGAG CACAACACTC GCTCCAATGT GATTTTCTAC ATTGTTACTC | 360 |
| TCAACAATAC AGCAGATCTC GAG | 383 |

(2) INFORMATION FOR SEQ ID NO:1027:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACATGTGGAC TGCAGTGTG ACTTTTGGTT GGACTGGGAC | 60 |
| AATTGGGGA ATATCTACTA TGTTATTCT TCAAGAACCC ATCATCCCAT TAGATGGAGA | 120 |
| AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT GCAGATTCT TAGGAGTTTA | 180 |
| TTATGCCTTG GACAAATTCC ATCCAGCTTT GGTTAGCACA GTACAACATT TGGAGATTGT | 240 |
| GGTAGCTATG GTCTTGACAG TTCTCGTGCT GCACATATTT CCTAGCATCT ATGATGTTTT | 300 |
| TGGAGGGGTA ATCATTATGA TTAGTGTGTT TGTCCTTGCT GGCTATAAAC TTTACTGGAG | 360 |
| GAATTTAAGA AGGCAGGACT ACCAGGAAAT ACTACGACTC GAG | 403 |

(2) INFORMATION FOR SEQ ID NO:1028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

| | |
|--|----|
| GAATTCGGCC AAAGAGGCCT AAAACCGAAA CTTGATGAA AATGAAATTC CTCAAGAGAA | 60 |
| TGGCACTCGA G | 71 |

(2) INFORMATION FOR SEQ ID NO:1029:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGAAACATGT | CTAAGGTNGC | ACACAGCTAG | TANGCGTTAG | 60 |
| AAACGTGTCT | CAAACCCAAG | AGGTCTGGCT | CTGGCATCCG | TGATCATAAC | CACTNGCTTT | 120 |
| GCCTGATCTA | ACAGTAAAGA | TGGATGAAAA | AATAAATCAA | GTGTGATGAG | TGTTATATAA | 180 |
| GAAAGGGGAA | ATAGCAGGGT | TCAGTGTGGA | ACATAGGAGA | GTGGGCCTTC | ATTCCCTCCA | 240 |
| GTTGAGGGCC | AAATAAGGCA | TCCCTGAGGA | AGAGACATTA | AGCTGAGATC | TGAAAGGTGA | 300 |
| GCCTGAATAA | GTTAGGTGAA | GGAGCATGAG | TAAAGGGAAG | CCGCTCGAG | | 349 |

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTGATGATA | ATAAAACAGA | GCTTTACTTG | GGAGAAATTA | 60 |
| GCCTTGAAGG | TGTGACATCC | AAAACAATTT | TTTTAAAAAA | ATTTAGACAA | CTAAAAAGGG | 120 |
| AAATGTCAAA | AGGGAGAAAC | TTAAAAAACA | AAAGGAAAGT | AGTCAGAGAA | TCAGAGAGAA | 180 |
| AATATGAACA | GAACACAGTA | AAAAGGAATG | GCTACAAGAG | GGATCAGCAA | CTCGAG | 236 |

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ATTAGAAATA | AATATCTTCC | TTCAATAGAT | GAAAATGAAA | 60 |
| ATACAGAAAA | AAGAGAGCAG | TTGTCAAATT | TAAAAGTTTT | GAATCACTCC | CCAATGTCTG | 120 |
| ATGCCTCTGT | CAATTTNGAC | TACAAATCTC | CATCCCCATT | TGACTGCAGC | ACTGATCAAG | 180 |
| AAGAGAAAAT | TGAAGATGTT | GCTAGTCACT | GTCTGCCTCA | GAAGGACCTG | TATACTGCTG | 240 |
| AAGAGGAAGC | TGCTACCCTT | TTTCTAGGA | AAATGACATC | CCATAATGGG | ATGGAGGACA | 300 |
| GTGGAGGAGG | AGGTACTGGA | GTGAAGAAGA | AACGGAAGAA | AAAGGAGCCA | GGAGACCAAG | 360 |
| AGGGTGCAGC | AAAGGGAAGC | AAGGACAGAG | AGCCCAAGCC | AAAGAGGAAA | CGAGAACCGA | 420 |
| AAGAGCCAAA | GGAAGAGCTC | GAG | | | | 443 |

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

```

GAATTCGGCC AAAGAGGCCT AATAAAGAGC AAAAAAATGT TAATGTCAAG TCAAATTGCC      60
TGTAATGAC  TTAAGGAATA TGTTAATGAT CTTGCTCCAA ATGAATAATT ATAAAGCAGG      120
TGCCTGGAG  ATATGATCAT TTAAGTAAA  GAAACAGCT  TCTAATGGCT TCAATAACCA      180
AGATAATGGT GATATTGGAG AAGCCTGTTA AACTCATTGT TCATGCCATT CATTTAATAC      240
ACAAGAGAAC TTCAGATGGA ATCTCCCTGT GGACTCATTG CCCTGCTTAT TTAAATAGCA      300
GTTAATTAA  ACACACACC  AAGTCAAAAC TGCATTATT  CTAACACACC TCTTTCTAAT      360
AAACTATGTT CTCCAATAAC AGAACCCCTG TCTCGAG  --                               397

```

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

```

GAATTCGGCC AAAGNGGCCT ATTTTAAAAA TCACTTTAAG NATCCAATAG AGAACAACAA      60
AGCCATATTG AGATGCAGGT TTTAGGAATT TGCTAGTAAT CCCTCACAAG GTCAGACTTG      120
ATCTCCTGGA CAATCAGGGC ATGCTAGTCA GCTTTTCATGA CTCAGCAAAG CTACAAATTA      180
TGTATTTTGG CTTTTTGTGG AAATTGCCAA CCCTACAGAT AGCAAACGTC TCCTCGGTTG      240
TCAAAAAGTA AGAGTAGTTT TTAGAATTCT GCCTTTGGGT CTGTAGAAT  GAAATATTTA      300
CAAGATTTGC TATTTGTAA  CATTTTAGCT CCTTCCTTGT TCCTTCAGTC TTGCTGCTGT      360
GCACACCACC AG                                         372

```

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

```

GAATTCGGCC AAAGAGGCCT AAATATGTTT TTTCTGCTT TTATAACTGT AAAATGGAAT      60
GTTCTTCTTA CCTTAACTT TATGATTGAG CTGTCCATAT CAGGTTTTTT TTTCTACTGA      120
CTATTTATTG GGACTAGCTC ACTTATTAA  TTATGCATCC TGATATCTTA TAGAATGGAT      180
AGTGATTTTC AATATTATTA ATTAAGTGGG CCTTTGTTAG ATATAAGCA  AGATACCTCC      240
AGTAGGTCCT GTTAGCAGTA AGTTTTATAT TGTGGAGGTG AACAAGGTAT TTTTGTGTAA      300
ATCAGTTTAC TAAATTGTAT TATTTTCAAG CTAGATTGTG ACGGTAAGGC TCGAG      355

```

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

| | |
|--|-----|
| GAAATTCGGCC TTCATGGCCT ACGTCTCAGC ATTATGCATT CCAGTTGGTT TTTCCCCATG | 50 |
| CTTTTCCTGA GCTGTATCCA AGTGAGTCGT ATTAATTTCA GAGGAGTATT T | 111 |

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

| | |
|---|-----|
| GAAATTCGGC CTTTCATGGCC TANATGAACA AACTCCAGA TACCATTGAT AAGAAATTTT | 60 |
| GCATCAAGAA GGGCTTCTGA AAAGACCCAC GTGCTCCAGT CCCAGCTCCA AAAGCCACTG | 120 |
| ATGACAAGGG CCCCACTGTG GAACCTAAGT CTGGGAGCCC CCTGACTTCT GGCTGGCCAG | 180 |
| AGCTGCGGTC CGTCAAGGGC TTGCCTCGCT TCAGAATCAG TAACATAGAT CTTAAGTGCA | 240 |
| ATTGATTAAT AAGCAGTGAG TTACTGTAGC TTCCTTTAGC TCTACCGAAC TCTTTTAA | 300 |
| AACTCAAAC TGAAGCAGCT TAGAAAAGGG GTTGGGGGGT GGAACCACAG GCCATTCTC | 360 |
| TAAGTGGGCT GCTGTGAAGT TTAAATGAA AGCTCTAGCT TTAGGAGCTT GAGCCATTTC | 420 |
| CTGACTGCAC TGGCCTGGCA GTCTGGCTGC TGCAGAAGAG TTTTAAAGA GGGGTCGGAG | 480 |
| CCCGCCCGTG AGAGCGGGTC TTCTACCAT GTGGGGCTGT ACTACGTGGT GGTCTTGGTT | 540 |
| TCTCTTCACA GAAATGCTCT | 560 |

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

| | |
|---|-----|
| AAATTGGGCA GTGGTAGCAC CTGACCCAGG GCTGCTGTGA GGCCCCCTG GGCTGAAGCA | 60 |
| CATGTGGTGC AGAGGGCCAG GTTGGGGTGT GAGTGCCAGT TCCCACTGGC CTTAGGCCCC | 120 |
| ATCCACTGCT GTCCTCAGG CCATGGGTGA GCCTTTCCAC TTCTTATAAA GTAGAGAAAA | 180 |
| GTATTTATAG TATCTTCTT GGTAATCCT TTTTCTTGGT GATGTTATC TGCAGTTCTG | 240 |
| TACATTTTCT CAGATCTTCT GATGAACAAA TTCCTTTAAT TTGTCATGTC AACTTGTTA | 300 |
| ATATTTTCCT TTGTGACTCG AG | 322 |

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

| | |
|---|-----|
| GAATTCGGCT TCATGGCCTA CACTGTAGCA AATTGCGTTG GAAAAGAACT AGCTCCACAT | 50 |
| GTCAAGAAGC ATGGAAGCAA ATTTGTTCCA GAATCTCTTA AAAAAGACAA AGATGGGAAA | 120 |
| TCTCCTCTGG ATGGTGCTAA TGGTTGTAGC AGCAAGTAGT GTTCAAGGAT TTTCAACTGT | 180 |
| CTGGCAAGGA TTGAATGTG CAGCTAAATG CATCGTTAAC AATGTTTCAG CAGAAACTGT | 240 |
| ACAAACTGTC AGATACAAAT ACGGATATAA TGCAGGAGAA GCTACCCACC ATGCGGTGGA | 300 |
| TTCTGCCGTC AATGTTGGCG TAACTGCCTA CAATATTAAC AACATTGGTA TCAAAGCAAT | 360 |
| GGTGAAGAAA ACTGCAACAC AAACAGGACA CACTCTCCTT GAGGACTATC AGATAGTTGA | 420 |
| TAATTCTCAG AGGGAAAATC AAGAAGGAGC AGCAAATGTC AACGTGAGAG GGGAGAAGGA | 480 |
| TGAGCAGACG AAGGAAGTAA AGGAGGCCAA ACTCGAG | 517 |

(2) INFORMATION FOR SEQ ID NO:1039: "

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAGAATGAA GAAAGCAAGC AGGAGTGTG GCTCAGTGCC | 60 |
| TAAAGTGTCT GCAATAAGTA AAACGCAAC AGCAGAAAAA ATTAAACCTG AAAACAGCTC | 120 |
| TTCAGCATCT ACGGGAGGCA AACTTGTGAA ACCTGGAACA GCAGCATCAT TGTCAAAGAC | 180 |
| CAAGAGCAGT GATGACCTT TAGCTGGAAT GGCCGGAGGG GTAACGGTGA CTAATGGTGT | 240 |
| TAAAGGAAAG AAAAGCACCT GCCCATCTGC AGCACCTTCA GCATCTGCCC CTGCCATGAC | 300 |
| CACCGTGGAG AACAAATCCA AGATTAGCAC AGGCACAGCT TCTTCAACCA AGCGGAGCAC | 360 |
| TTCTACAGGT AATAAAGAAT CCAGTTCTAC TAGAGAAAGA TTACGTGAAC GTACCCGATT | 420 |
| AAACCAGAGC AAAAACTAC CTTCTGCAGG TCAGGGAGCT AATGACATGG CATTGGCCAA | 480 |
| ACGTCCCCGC AGTCGAACTG CTACAGAATG TGACGTTCGT ATAAGCCTCC CTATAGTGAG | 540 |
| TCGTATTA | 548 |

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

| | |
|---|-----|
| GAGGAAATGG CCAAACAGAA AGCAGCTCCT GAAGCCAAGA AACAGAAAGT GGAAGGCACA | 60 |
| GAACCGACTA CGGCTTTCAA TCTCTTTGTT GGAAACCTAA ACTTTAACA ATCTGCTCCT | 120 |
| GAATTAAAAA CTGGTATCAG CGATGTTTTT GCTAAAAATG ATCTTGCTGT TGTGGATGTC | 180 |
| AGAATTGGTA TGACTAGGAA ATTTGGTTAT GTGGATTTTG AATCTGCTGA AGACCTGGAG | 240 |
| AAAGCGTTGG AACTCACTGG TTTGAAAGTC TTTGGCAATG AAATTAAACT AGAGAAACCA | 300 |
| AAAGGAAAAG ACAGTAAGAA AGAGCAAGAA CTCGAG | 336 |

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGGCTTCCCG | AGCAGTCTCC | AAACATATAT | TACATTCGAA | 60 |
| GGTCGCGCCC | GCCCCGCCCC | GCTCGCGATT | TGGCCCTTCG | GGGCCCCCGT | CCTCCACCTC | 120 |
| CTTCTCTCCC | ATGATGCATT | GTCTCTGGC | TTTTATCACC | TGTTCTGCCC | TTGAATTGGA | 180 |
| ACATGCCAAA | GATATAAGTA | TTGGATTGCA | GTCTTGCACT | ATTATTTGGT | GAGTTTTTTT | 240 |
| TTAATGCATA | CAGCTTTTTC | ATAAGTGCAT | AAATGGGATT | ATATAAACAA | TGTTTAGAGT | 300 |
| AGTTTTCTTT | TTTACCCTTT | TGCCTGGTTT | GCTGFTCTTC | CCTATCACAT | CCCTTCCAAT | 360 |
| CCATCTCGAG | | | | | | 370 |

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACGCCATCTT | CCAGTAATTC | GCCAAAATGA | CGAACACAAA | 60 |
| GGGAAAGAGG | AGAGGCACCC | GATATATGTT | CTCTAGGCCT | TTTAGAAAAC | ATGGAGTTGT | 120 |
| TCCTTTGGCC | ACATATATGC | GAATCTATAA | GAAAGGTGAT | ATTGTAGACA | TCAAGGGAAT | 180 |
| GGGTACTTTC | AAAAAGGAAT | GCCCCACAAG | TGTTACCATG | GCAAAACTGG | AAGAGTCTAC | 240 |
| AATGTTACCC | AGCATGCTGT | TGGCATTGTT | GTAAACAAAC | AAGTTAAGGG | CAAGATTCTT | 300 |
| GCCAAAGAGAA | TTAATGTGCG | TATTGAGCAC | ATTAAGCACT | CTAAGAGCCG | AGATAGCTTC | 360 |
| CTGAAACGTG | TGAAGGAAAA | TGATCAGAAA | AAGAAAGAAG | CCAAAGAGAA | AGGTACCTGG | 420 |
| GTTCAACTAA | AGCGCCAGCC | TGTCACCCC | AGAGAAGCAC | ACTTTGTGAG | AACCAATGGG | 480 |
| AAGGAGCCTG | AGCTGCTGGA | ACCTATTCCC | TATGAATTCA | TGGCATAATA | GGTGTTAAAA | 540 |
| AAAAAAATAA | AGAGACACTC | GAG | | | | 563 |

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGCTTGATTG | TTAGAGAAAT | AATGTTGGAA | GAAGAACCTT | CAATAACATC | AGGTGAAAGC | 60 |
| CAGACTACCT | ACTCTACTTT | CAGTGCTCCG | TTAAATAAAG | CAAATAGAAA | AAAGTTAATT | 120 |
| GAAAGTCTTT | CCCCAGATTT | TTGTCACCAA | AACAAAGGGC | TCTTGCTGAC | AGTTAATACC | 180 |
| AGTAGTCAGA | ATGGAAGGCC | TGGAAGAACA | CTTATTAAAG | AAATCCAGAG | TCCTCTGTCT | 240 |
| AGTATCTGTG | ATGGCTCCAT | AGCTCTAGAT | GCTGAGCCTG | TTACCCAGCC | AGCATCGCTG | 300 |
| CCCAGACACA | GCAGCACACC | AGACCACACC | AGCACACTGG | AGCCTCCTCG | TTGCCTCAA | 360 |
| AGAAAGAACT | TACAAAGTGA | AAAGGAAACT | CTCGAG | | | 396 |

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAACTGGAAA | TCCTCTAAAT | GTCTGTCAAT | GAAGGAATAG | 60 |
| ATAAATTGTA | ATATGTTTAT | ATAAAATGCT | GCATAAATAA | GTGAAATTTA | TAAATATACT | 120 |
| AACGAATGAA | TCTTGGAAAC | AGAGTTGGGA | GATAAAAGCA | AGCTGTTGAA | GAACATGGTC | 180 |
| AGTATCCTCT | CACTTATGTA | AGTTAAAAAC | TCCAAAGAAC | ATTATCTATA | TTGGTAATGG | 240 |
| CATAGACATG | TGTGGTAAAA | TATAAAATA | TTAACTAAAA | GTTCTATACG | CTTCAGGATA | 300 |
| TTGTTAGTAT | AATAAGGCAG | GAAGTGGATA | GCATTGGGAT | GAGAACTCGA | G | 351 |

(2) INFORMATION FOR SEQ ID NO:1045:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GATTCGGCCT | TCATGGCCTA | AGCAGCTCGG | GGTTCGGCAG | CAGCGGTCCC | ATCGGCTGAA | 60 |
| GTTCGGGGGG | GGTGGGGCGC | CGAGCGCGCG | GGGTGGGGGG | GGTCCTGGTC | TTTGGCTTCT | 120 |
| CGACTCGGTC | CTGTTTCGAC | AGCGAACATG | TCGCGGCCTG | TCAGAAATAG | GAAGGTTGTT | 180 |
| GATTACTCAC | AGTTTCAGGA | ATCTGATGAT | GCAGATGAAG | ATTATGGAAG | AGATTCGGGC | 240 |
| CCTCCCACTA | AGAAAATTCG | ATCATCTCCC | CGAGAAGCTA | AAAATAAGAG | GCGATCTGGA | 300 |
| AAGAATTCAC | AGGAAGATAG | TGAGGACTCA | GAAGACAAAG | ATGTGAAGAC | CAAGAAGGAT | 360 |
| GATTCTCACT | CAGCAGAGGA | AGCTCTCGAG | | | | 390 |

(2) INFORMATION FOR SEQ ID NO:1046:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ATGAAGCATC | TGGATGGGGA | AGAGGATGGC | AGCAGTGATC | 60 |
| AGAGTCAGGC | TTCTGGAACC | ACAGGTGGCC | GAAGGGTCTC | AAAGGCTCTA | ATGGCCTCAA | 120 |
| TGGCCCGCAG | GGCTTCAAGG | GGTCCCATAG | CCTTTTGGGC | CCGCAGGGCA | TCAAGGACTC | 180 |
| GGTTGGCTGC | TTGGGCCCGG | AGAGCCTTGC | TCTCCCTGAG | ATCACCTAAA | GCCCGTAGGG | 240 |
| GCAAGGCTCG | CCGTAGAGCT | GCCAAGCTCC | AGTCATCCCA | AGAGCCTGAA | GCACCACCAC | 300 |
| CTCGGGATGT | GGCCCTTTTG | CAAGGGAGGG | CAAATGATT | GGTGAAGTAC | CTTTTGGCTA | 360 |
| AAGACCAGAC | GAAAACTCGA | G | | | | 381 |

(2) INFORMATION FOR SEQ ID NO:1047:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGGGTAGCC CTTGACCGCC TCCTGCTGGC ACAGGTCTTG | 60 |
| GTTCTTGCTT TTGACGCAGT CAACAGCGGC ACAGGCAATC TTTCGGTCAT CTTGAAGGC | 120 |
| ATCAGCAGTA GCAGTAAAGT GCGGAATGAC CTTCTTACAG TGTGGGAACC AAGGGGCGTA | 180 |
| GAACATGACC AAGGTGTGTT TCTTCTTCTT CAGGGTCTCC CGGAAGTTGT CCCCCACCAG | 240 |
| GTGCAACACG CTTGTCTGCT GCTCTTCCCA CGTGGGCTCT GGGGGCGGGG GGGCCTCAGG | 300 |
| GTTTTGCATC CACTCGAG | 318 |

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCAAATTAT TCTTCAAAAT GATTATAACC AGTTGCACCC | 60 |
| TGTATTTCTT TTTGCAGCCA GCACAATGTG ACCCAACTTA AAATTTGGGG GAAAAAGAAT | 120 |
| GCAGGAGTGA AATAACCAAG TCAAAACCAT GTACTATCTC CTTGGGGGTT AGGGATGCTA | 180 |
| AGAAGAGCCC ACAAATAGAG GATTACTCTT CCCCTGAATC TCTAAACTCA GAAACAATTA | 240 |
| CCAAAAAATA CATAACTCTT CCTTGTAGGG CCCTTTCCTT ATTCATTTAG GTAGTGTGAA | 300 |
| CATTAAGTAT AAAATAAATT ATGTTCTTAA TGCCTCTTAA ACCACTTACA TTCAAAGGGG | 360 |
| AACAGAAATC ATTCTAAGCG GGAAAACTT CCACCTTTT TTTTTCCTCA GTATCTCTCT | 420 |
| AATAACTAA TGCCACTTAT TTGCATTCTC CTTGTGGATT TTTGTGCACC TAAGGAAATG | 480 |
| CATTTGATGA GTGCTGGAAA CTTCTTAAGT GCTTTACAGT TTGTTTTCAT TGTTTGACGC | 540 |
| GGATCACTGG ACATCAAAGA TTCATTGCAC TTATGAACAA GGAACCTCGA G | 591 |

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTTTCTTG GTGTTTTTGT TTTCTGGCAG GCAGTGAGAG | 60 |
| GAGGGGTGAA GGAGGAGTTT GGTGCCATTT CTCTTTCTGC TTTTCTCTCT TCTGATGTCA | 120 |
| AACAAATGAT GAAATCCTG CTATGGGAGC CCGGGAGCCT GGGGCCAGGC TGCTGGGGGG | 180 |
| ACGGTAGAGG GTGCTCTGCT GACTTGGGGG GTTAGGGGGG TTCTGGGGCG TTGGAGTCCG | 240 |
| ACTGGCCTTG GGCCGAAAGA GGCTGCCCTG CTGGGTGCTG GTGCTGTTGG TGACGGTGGT | 300 |
| GTGGTCTGGC TCACCCGAGT CGCTCTCCGT GTAGCTGTAG GCCTGTGCCC TCGAG | 355 |

(2) INFORMATION FOR SEQ ID NO:1050:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATGTGTTAG AAGACTCCCT CTACCTACCT GTTAAAAAAA | 60 |
| AAATGACTTT TTTTGCAATT TTTTGCTGTT TCCTTAAAC TAAAGCTGTG TTCTTCTGTT | 120 |
| TTGAAGGGTT TCCGCCCCCA ACATATGTGA TCCCCCGCC TGTGGCATT TCTATGGGCT | 180 |
| CAGGTTACAC CTTCCCAGCT GGTGTTTCTG TCCAGGAAC CTTTCTCAG CCTACAGCTC | 240 |
| TCGAG | 245 |

(2) INFORMATION FOR SEQ ID NO:1051:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 548 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

| | |
|---|-----|
| AATTCGGCCT TCATGGCCTA GGGAGTTTGA GGGAGTTCTT TGGTATGCCC GCATCCCGGG | 60 |
| GTTGTTTGCT GGTATTATTCT GCCACATTAT CACCTTGTA CGTTTATGGT ACCGGAGATT | 120 |
| GTAGGTAAAG TTTGTTTATG CTTCCACGA CCTCCCTCTG TGCGGTCCGG ATGGTTTGTA | 180 |
| ATTGGGGTTT GCTTTATAGC AGCGAGGCCT GATAGGTAAA GTCTGCTGGC TTTACTGTGG | 240 |
| CGCCTAGATA AGGGCTTAGA AATGTAAAAA GGCTTGGGGC AGCATGGAGA GGAGTTGCAG | 300 |
| AGTGGGGAGG GGCAGGCAGC ACCAAGAAGC TTCTTGAGGC AGTTTGTCCC TAACAGATT | 360 |
| ATTTTCGGAA AGGAATTCTG AACTCTGAGA CCAAATCAGT ATATTGTGT ATATTTTTC | 420 |
| ATATACTTCC AAAGTCTTTT AATTCTTAAT TAACCTGATA TTTAAGTGAA AAGGGTTTAC | 480 |
| TCTTTATCCT AGTTAATTAC ATATTCCATT TGTTAATGAA ACTATCCTTT GCTCACTGCA | 540 |
| TACTCGAG | 548 |

(2) INFORMATION FOR SEQ ID NO:1052:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACATAATACT TGCTGCTCTT GGGGTTGAAG CCGTTGTTAT | 60 |
| TTTCTTAGGA GTTAAGTTGC TTTCCAAAAA GATTGGCGAG CGTGCTATTC TACTGGGAGG | 120 |
| ACTCATCGTT GTATGGGTTG GCTTCTTAT CTGTGTACCT TGGGGAAATC AATTCCCAA | 180 |
| AATACAGTGG GAAGATTGTC ACAATAATC AATCCCTAAT ACCACATTG GGGAAATTAT | 240 |
| TATTGGTCTT TGGAAGTCTC CAATGGAAGA TGACAATGAA AGACCAACTG GTATGCTCGA | 300 |
| G | 301 |

(2) INFORMATION FOR SEQ ID NO:1053:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

```

CGGAGGCCCT GAATGCCCCA TGGCACCACC ACAGCTCGCG CTCCTGCAAG TGTTCTTTCT      60
GGTGTTCCTCC GATGGCGTCC GGCCTCAGCC CTCTTCCTCC CCATCAGGGG CAGTGCCCCAC      120
GTCTTTGGAG CTGCAGCGAG GGACGGATGG CGGAACCTCC AGTCCCCTTC AGAGGCGGACT      180
GCAACTCGCC CGGCCGTGCC TGGACTCCCT ACAGTGGTCC CTACTCTCGT GACTCCCTCG      240
GCCCCTGGGA ATAGGACTGT GGACCTCTTC CCAGTCTTAC CGATCTGTGT CTGTGACTTG      300
ACTCTGGAG CCTGCGATAT AAATTGCTGC TGGCAGAGGG ACTGCTATCT TCTCCATCCG      360
AGGACAGTTT TCTCCTTCTG CCTTCAGGC AGCGTAAGGT CTTCAAGCTG GGTTTGTGTA      420
GACAACTCTG TTATCTTCAG GAGTAATTCC CCGTTTCCTT CAAGAGTTT CATGGATTCT      480
AATGGAATCA GGCAGTTTGT TGTCCATGTG AACAACTCAA ACTTAAACTA TTTCCAGAAG      540
CTTCAAAAGG TCAANGCAAC CAACTTCCAG GCCCTGGTTG CAGAGTTTGG AGGCGAATCA      600
TTCACTTCAA CATTCCAAAC ACAATCACCA CCACTCCTCG AG                                642
  
```

(2) INFORMATION FOR SEQ ID NO:1054:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

```

GAATTCGGCC TTCATGGCCT ACCTGTGAGT ACCTGGATGA AGCATACCCA GGAAGAAGC      60
TGTTGCCGGA TGACCCCTAT GAGAAAGCTT GCCAGAAGAT GATCTTAGAG TTGTTTTCTA      120
AGGTGCCATC CTTGGTAGGA AGCTTTATTA GAAGCCAAAA TAAAGAAGAC TATGCTGGCC      180
TAAAAGAAGA ATTTCGTAAA GAATTACCA AGCTAGAGGA GGTCTGACT AATAAGAAGA      240
CGACCTTCTT TGGTGGCAAT TCTATCTCTA TGATTGATTA CCTCATCTGG CCCTGGTTTG      300
AACGGCTGGA AGCAATGAAG TTAAATGAGT GTGTAGACCA CACTCCAAAA CTGAAACTGT      360
GGATGGCAGC CATGAAGGAA GATCCACAG TCTCAGCCCT GCTTACTAGT GAGAAAGACT      420
GGCAAGGTTT CCTAGAGCTC TACTTACAGA ACAGCCCTGA GGTCTGTGAC TATGGGCTCT      480
GAAGGGGACA CTCGAG                                496
  
```

(2) INFORMATION FOR SEQ ID NO:1055:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```

GAATTCGGCC TTCATGGCCT AATGTGCTTA ACCCTCAAGA AATTGTCACA ACTGAAAGAC      60
GGGAGCAAGC TGACACTGCA AGGAACACAT GATGCTTTGG AATGGGTGGC CTGCGTATTC      120
AAACACATCA AAGCAGCAGT TACTTGAACA ATCGGAACTT CTTCAAATAC TGGCCCACTT      180
  
```

CTTCCTTGGG GTAGGGCCGG AGAGCAATAC AAGTGGCGAT ATTCTCTGGT TGCTCAAGCC 240
 ACAGCATGTG GTCAATGTTT TTCTGTTGCA GGGTCTCGGC CAGCTCCTTT AGGGTGGTCT 300
 CATCTGGGGC CTCGAG 316

(2) INFORMATION FOR SEQ ID NO:1056:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double --
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

CGGGTTAAGG TAGCATCAGA ACCCTGGACG CGGAGTCAGG GCTGGCAGAT AGCAAGGCAT 60
 CTCTCGGAGC GTTCTTGGA GCGCCATCT TGCCCGACTC CATGTTATCC AGCCACTCGT 120
 CATCCCGCGG AGACAGAGGA GAGAGGAGAG CTCGCGGGGA AGCAGAATTC CCAACCGTTC 180
 CATCCAACAA TGAATCGGT ATCAGGATGT GGTAGCTCC CTGTACCAGC GAGTGTACAG 240
 TCAGAGACTG GCCAGTCCCC TTGTTACAAA CACTGTAGAA GAATGTGACA GCAGCTGCTG 300
 TGGCCAGTAG ATTGTCTACC TGTAGTTGCA GAGAAGCCCA AGAGTTTGAT GATGAGGCAG 360
 TTCCTCGAG 369

(2) INFORMATION FOR SEQ ID NO:1057:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

GAATTCGGCC TTCATGGCGT ATCTCATTCT GTCTCCAGG CTGGAGTGCA GAGAAACAAT 60
 CTTGGCTCCT GCAGCCTCAA CCTCCAGGG TCAAGTGATC TTGTTGCCTC AGCTTCCCAT 120
 ACAGCTGGAA GCACAGGTGC ATGCCACCAC ACTTGGCTAA TTTGTATTT TTTGTGGAGA 180
 TAGGATCTCT CTATGTTGTC TAGGCTGGTC TTGAACTCC CTGACCCCGT GATCCACCTG 240
 CCTCGGCCTC CCGAAGTACT GGGATTATAC GCATGAGCCA CCGTGCCAG CCGTCATTCT 300
 TATATTATTA TTTCTAGGT GTCTCTCCTG AAGACTATCT TCTGGTCTCG AAATGGACAT 360
 GATGGATCCA CGGATGTACA GCAGAGAGCC TGGAGGTCCA ACCGCCGTAG ACAGGAAGGT 420
 ATGGCTCTGT TGGAAATCCG ATAGTGTGGA AATGAGTTTG CCCTGGAAAG GGAAAGAACA 480
 GCTTCTTGCC CTCAGGTTTC TCACCTTCTC CTCTCCTCAC TCTACCAAG GACCTCGAG 540

(2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 430 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

GAATTCGGCC TTTATGCNAN NTTCTTTCA AAAAAAAAAA AGAAAAGAAA TTGCAAAAGT 60

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCTTCTAAAG | TTAAATCCAA | GGTGGTTTGT | CTAGCAGAGA | GCCAGGAATT | CTTTCTAATA | 120 |
| GTGGGCAGAG | CCCAGAGACA | AGGGGAAGAA | AGATGACCTT | CTCCCCAGTC | CTTCCCAGCA | 180 |
| CCATTTTGT | TTCACACCAG | GCTTGTGGCA | TTTTGGTGCT | CACAGGGGTT | TTGCCTTCTG | 240 |
| ACCTCTCCTT | GGAGTAGGCC | ATTCTCATGC | AGGGCTCACC | CTGAGGCAGG | AGGACCAAGG | 300 |
| GCTCCCTGCG | TCCACGGACC | ACGTATGCCT | TGGTGTGCAC | TCCCATCGGG | GCTATCAGTT | 360 |
| CTGCACTGTG | CCCTGGTGCG | GATTTTAATG | CATATTTTAA | TATATAAATG | TTCCCAAAGG | 420 |
| CCGTCTCGAG | | | | | | 430 |

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AACATTAAGG | AAAAAGCCTT | AATGGCCATG | AATAACCTGA | 60 |
| GTGAGAATTA | TGAAAATCAG | GGCCGGCTTC | AGGTGTACAT | GAATAAAGTG | ATGGATGATA | 120 |
| TCATGGCCTC | TAACCTGAAC | TCAGCAGTTC | AAGTAGTTGG | ACTAAAATTT | CTAACAAACA | 180 |
| TGACTATTAC | TAATGACTAC | CAACACCTGC | TTGTCAATTC | CATTGCAAAC | TTTTTCCGTT | 240 |
| TGCTATCTCA | GGGAGGTGGA | AAAATCAAGG | TTGAGATTTT | GAAAATCCTT | TCGAATTTTG | 300 |
| CTGAAAATCC | AGATATGTTG | AAGAACTTC | TCAGTACCCA | AGTGCCAGCA | TCATTAGTT | 360 |
| CCCTCTATAA | TTCTTACGTG | GAATCAGAAA | TCCTTATTAA | TGCCCTTACT | CTATTGAGA | 420 |
| TTATCTATGA | CAATCTCAGA | GCAGAAGTGG | CCTCGAG | | | 457 |

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACAACCCCGC | GATAACCACT | GCCGAATGCC | TGAAGGCGCT | 60 |
| TGAGCACGTG | TTGGGAGCG | TTGAGAGCTC | TACGGATGCC | CCGATCAAAT | TTCTGAACAC | 120 |
| TTATCAGAAC | CCGGGAGAAA | AATTGTCTGC | TTATGTCATT | CGTCTGGAGC | CTCTGCTACA | 180 |
| GAAGGTGGTA | GAGAAGGGGG | CCATTGATAA | AGATAATGTG | AACCAGGCCC | GCCTAGAGCA | 240 |
| GGTCATTGCC | GGGGCCAACC | ACAGCGGGGC | CATCCGAAGG | CAGCTGTGGC | TTACCGGGGC | 300 |
| TGGGGAAGGG | CCAGCCCCAA | ACCTCTTTCA | GTGCTGGTG | CAGATCCGTG | AGGAGGAACC | 360 |
| CAAGGAGGAG | GAGGAGGAGG | CTGAGCCAC | CCTTCTGCAG | TTCGGCCTGG | AAGGGCACTT | 420 |
| CTGAGTGCCA | GGAAAGGCAG | CTTTAGTGCA | GACCTAGATC | ACAGCTACCT | CGAG | 474 |

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCAGCCTCT GTTAGATATG TCCAGAGATG GAAACTCACT | 60 |
| CCCCTACAAA AGATGGAGCT TAATGGAGAA ATTGCAACTT TCATTAAAAA ACAAAATCAG | 120 |
| ATGAAATATC AGTAACTGTC TTGGACAGTG CTGAAATCAG GTGGTTAAAC GGGTAAACAA | 180 |
| AATATACTGT ATTTTGAGAA ATGGCACAAA AACAGGCAGT CATCTTTAAT GGCTATGCCT | 240 |
| AGGCAAACTA CTAACATGCA TTGTGAGAAT GCCGTGTATA CCTCACGTAC TGTGTACTTT | 300 |
| GTACATATAT TTTACCTTTT ATACCTATGT TCGATTTTGT TTTGTTTTGT CCTGGCGTCC | 360 |
| TCGAG | 365 |

(2) INFORMATION FOR SEQ ID NO:1062:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGAGCCGCA GGGCCGTAGG CAGCCATGGC GCCCAGCCGG | 60 |
| AATGGCATGG TCTTGAAGCC CCGCGTCGGG TCCCATCCGG CCCATCGTGC GCTGCCCCAC | 120 |
| GGTTCGGTAC CACACGAAGG TGCGCGCCGG CCGCGCTTC AGCCTGGAGG AGCTCAGGGT | 180 |
| GGCCGGCATT CACAAGAAGG TGGCCCGGAC CATCGGCATT TCTGTGGATC CGAGGAGGGC | 240 |
| GAACAAGTCC ACGGAGTCCC TGCAGGCCAA CGTGCAGCGG CTGAAGGAGT ACCGCTCCAA | 300 |
| ACTCATCTC TTTCCCAGGA AGCCCTCGGC CCCAAGAAG GGAGACAGTT CTGCTGAAGA | 360 |
| ACTGAACTG GCCACCCAGC TGACCGGACC GGTATGCCC GTCCGAACG TCTATAAGAA | 420 |
| GGAGAAAGCT CGAG | 434 |

(2) INFORMATION FOR SEQ ID NO:1063:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTTAATTC AGAGCCGGGT TCGCCGTCGG ATCAACCTCC | 60 |
| AGGAGCTAGC AGCGGGCGCG GACCGGGCAG TTTCCGCGCT CAGCACAGGC AGCTCGCGGT | 120 |
| CATGGGCGGC TCAGCCTCCA GCCAGCTGGA CGAGGGCAAG TCGGCTTACA TCCGAGGGAA | 180 |
| AACTGAGGCT GCCATCAAAA ACTTCAGTCC TTAACAGAT TTAACGTCAC AGTTTTTGAA | 240 |
| CTGCAATCAC GTGCGCACTG AAGTAGAACA GCAAAGAGAT TTAACGTCAC AGTTTTTGAA | 300 |
| GACCAAGCCA CCATTGGCGC CTGGAAGTAT TTTGTATGAA GCAGAGCTAT CACAATTTTC | 360 |
| TGAAGACATA AAGAAGTGA AGGAGAGATA CGTTGTAGTT AAAAATGATT ATGCTGGGGA | 420 |
| GAGCTCGAG | 429 |

(2) INFORMATION FOR SEQ ID NO:1064:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

```

GAATTCGGCC TTCATGGCTT AGTCTTGGTC ATGCCTGGGG AGCTCAGAAC GCCCGGCTT      60
GGGCCCCCAGG CCCATGGACT CCCTCCCCCA TTCTGCCCTC CCATATTCCC CTTTTTGGT      120
CCCAGACACC AGCACAAGA AAGGAGGGTT CACAGAGGAA GGCCAGGGCA GAGCCTGGCC      180
CCAGGGAGGG GATGAGGACA TTTCCGGTCC AGGTAGCTGC CGGCTGCTCT GGGAGGAAGA      240
GCCATGCGTC TGTAAGTGC TGGGGCTGGC GGCCCGCCCC ACTGCAGGGC CCAGCCTTGA      300
CCCCTGCACG TGGCCATCCA GCTGCCCTCT GGCTGECCTT GGCCTTGGCA CAGGCATCGA      360
GCCTCGAG                                     368

```

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```

GAATTCGGCC TTCATGGCCT AAGATGGTTG CCAAGCAAGG AAAAATTATT TTATATTTTT      60
ATACTGTATC CAGGCTATGC CTGGGTGTGG AGGGCTTACT CGAG                      104

```

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

```

GAATTCCTGG CCTTTGGGAA CTCATATCCT GACCTCAGAT TGAGAAGACC ATCTGTCAAG      60
GCATATTAGT AATCACCTCC GGTAGAAAAG ATTTCACGGG TAACAAGTAG GCCATGAAGG      120
TCGAG                                     125

```

(2) INFORMATION FOR SEQ ID NO:1068:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

```

GAATTCGGCC AAAGAGGCCT AAGTTCAAAT AATTCAGAA TGGTGTCTGT TAGGAATGGT      60
CCAGAGGTTG GTTGGGGGAT GAAAGGAGGA CAGGGACTAC AAGGGATATT GCAAATGACT      120
GCCTTAAAT ACCAACATAA AGCAGTGGAT TCCCAGAGTC CTCCAATCTG TTATCAGACA      180
CAAAGATTG AACAAAAATA AATGAAAGAT AGAAATCAAA AGGTTTCTT TGAAGTCTCA      240
GGGTTATTG CTTCTGAAAG CAAATGTGTT GTTCTTGCCT CATAGCAAAG TACTTTTCCT      300
ATTGATGCAT CACTTTATTG CTTTCTGTC TTCTCTCGAG      340
  
```

(2) INFORMATION FOR SEQ ID NO:1069:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

```

GAATTCGGCC AAAGAGGCCT AGACGGGACC TGTTCGAGA CAAGATGCAA GGAACACAGC      60
CTGCAGTGAT TCACAGCTTT GTTCAACCC ACAAAACAGA AAATTAGCTC TTGGGTCTGT      120
GGGCCCAAAG TGAACTTTAA AGCAATAAAG ACTGGAAGCA GGTCTGGGAA GGCAATACAA      180
AATGTGGAGA GTTGAAAAGG AGGCAGAGCT GGCAGGAATG GGTAGGGAGA GTGTTTGGTA      240
AATAGCACCT TTGAGTCAAA ATTGAGCAGT TTAGAAATCC AGGAAAGGGG ACTGGCTGTG      300
GGGAGGAGAA CCTGGGGGTA GAGGAAGTGG GGTGAAGATT CCTCACTAAG GGGCAACAGC      360
AGGAGGGTGG CCATCCTGGC CAAATGCCCT AGCCCTGTCC TTCTTAAGGT GATTTCGGTTT      420
GGGAAACTCG AG                                     432
  
```

(2) INFORMATION FOR SEQ ID NO:1070:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

```

GAATTCGGCC AAAGAGGCCT ATTCTAGACC TGC GCAAGCA CGCTGAGGAG AAATTCATTG      60
AATTTGAAGA CTCTCAAGAA CAGGAAAAAA AGGACTTACA GACCCGAGTG GAATCTTTAG      120
AATCTCAAAC AAGACAACTT GAGCTGAAAG CGAAAACTA TGCTGACCAG ATTAGCAGAC      180
TTGAAGAAAG AGAAGCAGAA CTGAAGAAGG AATATAATGC ATTACATCAA AGACACACTG      240
AGATGATCCA TAATTATATG GAACATTTAG AAAGAACAAA ACTTCATCAG CTCTCAGGGA      300
GTGATCAACT AGAATCCACA GTCATAGTA GAATTAGAAA AGAACGCCCT CGAG      354
  
```

(2) INFORMATION FOR SEQ ID NO:1071:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

```

GAATTCGGCC AAAGAGGCCT ATTCTGTCTT ATCAAAGGAA GTAAAGAAGT AAAAAACAAA      60
AATGAACGTA TACAAGCACA GATTTTGTGAG CTTGATTGT AGAGAAATGG TAGTTATGTG      120
GCTTGCCAAG AAAGTGCATC ACCTACTTCT GCTTCTGGGG ACAGAGGTGA AGGGGTCTGT      180
TCTGGAACCT TCTAAGGAGG CCATCTTCGT TATTACATCA GGAAGTTTC TAGTCAAAAT      240
GTTATTCCTG TCTACAGGGA AAAACAAAAG CAAAACACAA AAGAACACTG CTTCTAATGG      300
CATCATAGCA AGGAGTTTAT CTAGAAAGAT GATGCCAGCA GTCACCTCTT TTCCAGGAAG      360
ACAGAAACAA AAACCGTTCT CCTCGAG                                         387
  
```

(2) INFORMATION FOR SEQ ID NO:1072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

```

GAATTCGGCC AAAGAGGCCT AGAAAGTGCC AAGAGGGAAA AAAGGCACTC TGAGAAGTTA      60
CGGCAAAGAA TTGGGAAAGT TGCAAAACA AACAAACAAA AAATAATAGA TTTGTTTGTAG      120
CAAACGACTT GGCTAAAAGT TACAAACCTA ATATATGTAA TACACAAGAC TACTTCATCA      180
TCTTCTTTC TGACAGTCTC ATGTTCTTTT TCAAGCCAAA AAGGGACATA TTCTTATAGC      240
TGGAAGTTTA AGGGAAAGAC TTCCAACCTA ACTCTGTGTT GAGGGTGCAA ATCATGTGAT      300
GAAGGCTCGA G                                         311
  
```

(2) INFORMATION FOR SEQ ID NO:1073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

```

GAATTCGGCC AAAGAGGCCT ACGAAGAAAA AATATTTTGT AGAGAATTTC CCAGATTGAA      60
AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC      120
CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT      180
GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC      240
CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT      300
GGAACGCTCC AAAAATAAAG AAGCCCAAGC ACGGGCGGAA GACATACTGC CCCCATGAC      360
CCTCGAG                                         367
  
```

(2) INFORMATION FOR SEQ ID NO:1074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

```
GCTTTATCTA TTTCATTTAA TCTAAATGTT TTCTGCAATT GTTTTTCCTT TAAACTTTGC      60
TTCAAAACT CTTCATCTAC TTGAGATCTG GGCATTGTGG TTTTGGTCT CGCATTTC      120
CTGCCTTCTG ATGGCTTAGC AGGGGACCCT TTCTTCTTTG GCTGGTGGGG CTCTCTGGA      180
TCAGTAATGT CCACATGCGG CTTCTGCAGC AAGGTTTTCT CTTTGCTGA TACTGTAAC      240
CGGGGGGCTC TGTTTTCAA GGAATGAGAG GCCTCTGGTT TTCGAAGCCC CCCTCTGCCT      300
TTGCTCACCA CTCGAG                                     316
```

(2) INFORMATION FOR SEQ ID NO:1075:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

```
GAATTCGGCC AAAGAGGCNT AGAACTCGGA GACCAGAAAG TGAAGTCTG GGCAGAGATG      60
GNCCTGCAGA GCCAGGTGTG GTCTCTGGCC ACACCCATGC CCATGGCGGA GAGCTCCNTC      120
TACCGGCAGC GGCTAGAAGT CATCGCTGTA AGTGACGCCC TCCCCGCGCC CTGGGCACCC      180
CCAAACTTTC CACCATGCTC CTTTCTCGTC TCTCCGTCAT CTGTGCGGAG AGCGCCCTCA      240
GCTCCAGCCC CGCCAGGGC TCCCCACACC AATTCTCCAG CCCCCTCTGC CCCCAGTTT      300
CTGTCTGGTC ACTACCACCC TCAGAAATGGG GAGCTGTGGC CCCCACACTT CCAGAGCCTG      360
CATCGGCTAT GCCTCATTCC TGAACCCAG CCTCCCAAAA ACCCCATGCC TGAGCCGCAT      420
CTCCCGGACC TCGAG                                     435
```

(2) INFORMATION FOR SEQ ID NO:1076:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

```
GGAATTCGGC CAAAGAGGCC TAGTGGGAAA AGCTTGGATT ATCAAACAC ACAACAAATG      60
ATAGAACCAA ATATATAGAT GATACAGTGA AGCACAAGGT CAAAATTTA AAACGGGTGA      120
GCTCTTCATT AATGCATTAT TTTGTTTATT TAAGAGCTTT TTGTATGGAC TGAAGTCAAT      180
AATTTTGAAG TTTCTCTTTA GAAGTTTTAA TGTTCTTTTA CATTTTCAA TTTAGTTTTT      240
CATGAAAGTG AATAGGTTTT TATTTAAAT TTTTGTCTAG TCTTGGTGAA ATCAGATGGT      300
GACTCTCGAG                                     310
```

(2) INFORMATION FOR SEQ ID NO:1077:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

```

GAATTCGGCC AAAGAGGCCT AGGAAAACAA ATGGCTTCTT CAAGTCCTTG ATTTTGGAT      60
ACACAGGATG CAGGGCTGTG TGTAAGGAAA GGCAGCGTTT TCCTCTCTTA GAGCCTCTGA      120
CTGACCTGAG GCGCAGGTGT TCCTGGGAGA CTGGAGGGTG GGCTCCATGG GGGTGTCTGG      180
GCCCCACCTG GCAGGGCTCT TGGCAGTGAG CCAGTGGAGG TTGCCTCCCA CGTGTGGCTG      240
GCCCTGTAGC CTGGCTCTGG AGAACCTGCA ATTCAGGCTG GAAGAGACTT TGGAGCAGCT      300
GGAGTGTGAG GTCTGCCTGG GTCTGGTGGG GAGTGTTTT ACTTTGCCAG TGATAGACTG      360
AAATGCCCTC TTTGAGGACA AGGTGGCTAT CTCGAG                                396

```

(2) INFORMATION FOR SEQ ID NO:1078:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

```

AGTGTTTTCC TGTATTTTCAG CATATTCCTT GAAACTCTGC TGAAAGGAGG CTGTCAGTCA      60
GGGTTGTATA AATAGAGTCC TGGGTAAATC CTGAAGCTT GTCATTCCAC AGCAAATCCA      120
CATGTTTCTT CAATGGCTGT TAGCAGCTTT TCATATAGCT TTTCATAGCT TTCATAGGGT      180
GGAATGTCTA TTCGATTGAA GCAAGTGTGG GCTTTCGGCA GGTGTGTAGT GCAGGCATCA      240
ATCTGGTGTA TGGTAAAGAG TCTCGGCCT GCAGCACCTT GCAATGCTTT GAAGCCCTGC      300
AGAGGCACTC GAG                                                         313

```

(2) INFORMATION FOR SEQ ID NO:1079:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

```

GAATTCGGCC TTCATGGCCT AAAAATGAAC TATAATAGTT CTAATTTACC TCAAGTTTTT      60
CTAAGATAGC AAATAAATG TAGTGTACA TTAGCTTCCT AAGTAAGGCA AATTGACCTG      120
CAATAAAAGG TTCTAGTGTG AGACAAATTA AACCTTCAAC TTCCAACCTC GATTTCATAT      180
ATAATCAAA TTGTCACTGA AGCTTTTATT AAGAATAAAA ATATATTTAG TCTTTATTAT      240
TTTCTGTAAA TGACTTATTT TCAGATGCAC AATCGTGAAA TAATGAAGAT TTTGATCAGT      300
TGTTTTTGTC TTTTCTCTT GAAAGGTATT TTCGCAAGAC CATTAAAACT CGAG          354

```

(2) INFORMATION FOR SEQ ID NO:1080:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

```

GAATTCGGCC TTCATGGCCT ACTCCGGTGG CTCCCCCATC TCTCAGGCGC GATGGCTACG      60
GGCGCGGATG TACGGGACAT TCTAGAACTC GGGGGTCCAG AAGGGGATGC AGCCTCTGGG      120
ACCATCAGCA AGAAGGACAT TATCAACCCG GACAAGGAAA AATCCAAGAA GTCCTCTGAG      180
ACACTGACTT TCAAGAGGCC CGAGGGCATG CACCGGGAAG TCTATGCCTT GCTCTACTCT      240
GACAAGAAGG ATGCACCCCC ACTGCTACCC AGTGACACTG GCCAGGATA CCGTACAGTG      300
AAGGCCAAGT TGGGCTCCAA GAAGGTGCGG CCTTGGAAGT GGATGCCATT CACCAACCCG      360
GCGCGCAAGG ACGGAGCAAT GTTCTTCCAC TGGCGACGTG CAGCGGAGGA GGGCAAGGAC      420
TACCCCTTTG CCAGGTTCAA TAAGACTGTG CAGGTGCCTG TGTACTCGGA GCAGGAGTAC      480
CAGCTTTATC TCCACGATGA TGCTTGGAAT AAGGCAGAAA CTGACCACCT CTTTGACCTC      540
AGCGCGCGCT TTGACCTGCG TTTTGTGTT ATCCATGACC GGTATGACCA CCAGCAGTTC      600
AAGAAGCGTT CTGTGGAAGA CCTGAAGGAG CACTGCTCGA G                                     641
  
```

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

```

GAATTCGGCC TTCATGGCCT AGCCCTTTT GGTCTTCTAA TTAGGAATAT AGCATCTGCA      60
AATAATGACA GATTGTTTCT TCTTTTCTAA TTCTTACAAC TTTTGTACT TTTTCTTGTC      120
TAATATGCTG CCTAGAACTG TAGAGCTTCC TGCTCTTGT CCTCCCTTTT TTTTATTCTT      180
ATTTTATAGGA GCAACCCTAT TAACTAAGCC TCACTCTTAA AGGGGAAGTT TTCACCACTA      240
AGTACCTTTC TAATCTAGGT TTTTGTGGA TACCTTTTAT CAGACTAATG AAGTTTAAATA      300
TTGTTAAATA CTTTGAATTG TCTATATTAT GATGATAGTA TGCTTTTTTC TTTTATTAT      360
TAAATGGTCC CCAGGAATTT GTGAACAGCT TGGGCAATAC AGTGTGACGC TCGAG          415
  
```

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

```

GAATTCGGCC TTCATGGATC CTGATACCAA ACTCATCGGA AACATGGCAC TGTGCTTAT      60
CAGAAGTCAA TTCAAAGGAC CTGCCCCCAG AGAGACAAAA GATACAGATA TTGTGGATGA      120
AGCCATCTAT TACTTCAAGG CCAATGTCTT CTTCAAAAAC TATGAAATTA AGAATGAAGC      180
TGATAGGACC TTGATATATA TAACTCTCTA CATTTCTGAA TGTCTGAAGA AACTGCAAAA      240
GTGCAATTCC AAAAGCCAAG GTGAGAAAGA AATGTATACG CTGGGAATCA CTAATTTTCC      300
CATTCTGGA GAGCCTGGTT TTCCACTTAA CGCAATTTAT GCCAAACCTG CAAACAAACA      360
  
```

GGAAGATGAA GTGATGAGAG CCTATTTACA ACAGCTAAGG CAAGAGACTG GACTGAGACT 420
 TTGTGAGAAA GTTTTCGACC CTCAGAATGA TAAACCCAGC AAGTGGTGA CTGCTTTGT 480
 GAAGAGACTA CTCGAG 496

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GAATTCGGCC TTCATGGCCT ATTCACAGGT TTATTGGCTT CTTCTTGAAA TGCCTGTTCA 60
 TGTCTTTTGG CCACTTTTTA TATGGGTCAT TTGTCCCTTA TTGATTATA AGGGTTCTTT 120
 ATTTTTTCC TAGATATTAA TAGTTTGGC CAGATGTTT CAGATGTCTT TTCTCAATAT 180
 GGCTTGTCTT TTCAGTTTGT GTGTCTTGAT GATCAGAAGA AGTTCTTCAT GTAGTTGATT 240
 TATTGACCTT TTCCATTATG GTTTCACTC TTTGACTCTA GGAGCTTAAT AAAAGCATGA 300
 AATATTTATT GATTGTCCAT TGCTAATCCG AAAACCCTCG AG 342

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GAATTCGGCC TTCATGGCCT AACTTACTGA ATGATAAAAC TTGCAGCTAA ATTTGTCTTC 60
 AACACACCTT TCTCAGAGCA TCAATTACAT TATTCATTAA GGAATAAATA GCATCTCTAA 120
 AGCATGTATC AACATCAGAA CTAAGCTTTA TGAATTATAC AGTGCATCTA GTGATTCCTT 180
 ATTCTAAAAG ATCTCTGGTG CCATCTACTG AATGCTTTT AAAGGAAAAA ACATGAAATC 240
 AAATAATAGA TTTTCACTTA ATTCAATTTT TTGTTTTGTT TTAATTTTCA ATTACTAGAC 300
 AGATCTAGGT TTATAAAAGA ACTAAACAGG AAGTACAGAA TTCCCATATA ATCACTTTTC 360
 CCCCAGACT CGAG 374

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

GAATTCGGCC TTCATGGCCT ACTGGAACAC CTTCTCGCTG CCGCCATACC CTGCCTTCTC 60
 CAGCGACAGC CGCCCGTTCA TGAGCTCCGC CTCCTTCTC GGCAGCCAGC CCTGCCGAGA 120
 CACCAGCTAT GCCCCGTGG CCACCGCTC CAGCTTGCCA CCAAAGACCT GCGACTTTGC 180
 TCAGGACTCC TCCTATTTTG AGGACTTCTC CAACATCTCC ATCTTCTCCT CGTCCGTGGA 240

CTCCCTGTCG GACATCGTGG ACACGCCCCG CTTCCTGCCG GCTGACAGCC TCAACCAGGT 300
GTCCACCATC TGGGACGATA ACCCTGCCCC CTCCAACCTC GAG 343

(2) INFORMATION FOR SEQ ID NO:1086:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 531 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

GAATTCGGCC TTCATGGCCT AGGGCTGACG CGCCACTATG TAGCGGGTTT CGGGCGGGCC 60
 ACGCGTGCGG GACAGGAACC CAACCCAGC CGACCTTGAG CTCCAGGAGT TCGTCTCTTA 120
 CGTCTGCGGA AGTGCAGCTG CCTCAGTTCT TAGCGCAGGT TGACAACTAC AGGCACAAGC 180
 CATTGAAGCT GGAATGTCCT GTTGCTGGTA TTTCAATTGA CTTAAGCCAA CTATCCCTTC 240
 AGTTACAATA GGAAAGTGCC TCTAATAAGG CCAAATATGC GTACTAACTT GTAGCAACCA 300
 CGTGTCGGTG CAGTGCCACA GGAGCTAGAG CAGTGACAAT GCTGGTGGCA ACAGGGCAGT 360
 GTAGCAGGTG CTTTCATGTT ACCTTTTCAA CCTTTTCATT TAATTGTCAC AACTCGGAGG 420
 TGGATTCTGT TAGGGACAGG CTGCCCCAGG ACCACTCCGC CCCCCTAAC TCAATGCAGC 480
 TGACCCTTAC CCTGAATACT CTGCAGCTGC ATTCCTGAAC CATATCTCGA G 531

(2) INFORMATION FOR SEQ ID NO:1087:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

GAATTCGGCC TTCATGGCCT ATGACTAGCC ACCAGGAAGG ACATTCCCTG CTCAGCTGTC 60
 CCATTAACGT CACCTGCTCC TCTCCTCCAC GTTAGTTTTT TTCTAGCCTG TTTATTCCTC 120
 CCTGTAAGAG AAAAAGAGAA AAGCCTATTT CTATCTGATC TTGAGATGC TTGCAGATCT 180
 TACCTTTGAA GCATTCTCCT TATTGCAATA GTCTCCCTGA CCCTATTGCA ATAGTTCCTC 240
 TCTCCCTGTT TGTATTCACC CATTGAGGCT GCTATATATA GCAAATACC ATAAGCTGAT 300
 AGCTTATAGA CAATATAAAT TTACTTCCCA CAGTTCTGAA GCCCGGAAG TCAAAGATCA 360
 AAGTAGGCCA TGAA 374

(2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

GAATTCGGCC TTCATGGCCT AGGAATGTTT CCTTTTGGTT CATTGTAGGC ACATCTGAAA 60
 AAGAAGTTAT GAGTCACTCG TAGTGAGGTT TTAGTTGACC TGTGACTTGG GATCTCTGGG 120

GATCATTGGC AGTCTGTCTT AACTGTGTTAT TTATAATTCA TGTCTGATCA TCTTCTTAAG 180
 GAAGTCTGCA TCGTTTGCTT TATGTAGAGC ATTAAACACA AGGATCTGNC ACATTACTTC 240
 TGTGGCATT TTTGCTTCTC ATATCCCTGA CCACCACCA CACTCGAG 288

(2) INFORMATION FOR SEQ ID NO:1089:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

GAATTCGGCC TTCATGGCCT AAGTAGTTAA ACTCATAGAG TTGCAAACCTA GAAAGGTGGC 60
 CCCCAGGGGT GGGCAAGAGA GAGGAGTGA GAGCTTGGTG AATGGGTGCC ATTTCCATTT 120
 TGAAAGATAA AACTGTTCCG GAGACGATGA CGGTGATGGT TGCTAAACAA TGTGAACGTA 180
 CTTAATGTCA TGAAACTGTA AACTGAAAAA CAGTGGAAAT TGTAATGTT TATACTGGCC 240
 ATTCTATATG AACTAATATA TATTTATAAT TTTTAATATT TATACATGGT ATATTTTCCC 300
 ACAATAAAGA TGAAATTAA AGCAGTTGGT CTCGAG 336

(2) INFORMATION FOR SEQ ID NO:1090:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GAATTCGGCC TTCATGCCTA CAGAGGCGAA AGGAGAGTCC AGTGAGAAAC CAGCCATTGT 60
 CTTCAATGTAC AGGTGCGACC CTGCTCAAGG CCAGCTCAGT GTGGATCAGA GCAAGGCTAG 120
 GACAGACCAG GCAGCAGTCA TGGAGAAGGG TAGAGCAGAG AATGCATTAC TACAGGACTC 180
 AGAGAAGAAG AGGAGTCATT CTTCTCCATC ACAGATTCCT AAAAAGATTG TCAGTCACAT 240
 GACCCATGAA GTAACAGAGG ATTTTCTCC TCGGGATCCA AGAACTGTTG TTGGGAAGCA 300
 AGATGGCAAG GGCTGCACTT CAGTCACAAC AGCATTGTCC CTACCTGAAC TGGAAAGGGA 360
 AGATGGAAAA GAAGACATTT CAGATCCTAT GGACCCGAAC CCTTGTAGTG CAACATACAG 420
 CAACTTAGGG CAATCTAGAG CAGCCATGAT ACCTCCCAAG CAGCCACGAC AGCCCAAGGG 480
 AGCTGTGGAC GATGCCATCG CCTTTGGAGG GAAAACAGAC CAAGAAGCAC CCAATGCTTC 540
 CCAACCTACA CCACTCGAG 559

(2) INFORMATION FOR SEQ ID NO:1091:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

GAATTCGGCC TTCATGGCCT ATTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTACG 60

AAGAGGATTA TTATACACCA CAAAAGGTAA AATCAGAAGC AACTTATTTT TAAAACCTAT 120
 CTTAAGTCGC ACAGACTCCA TAATATGTCC TCTTTCCTTG GCTCTGTTGT ATCAAGGTGT 180
 TTATTCCGA AGTGTTCCT GTTTGGGAGA CTGACAAATT AGGATTCCTG ATTTAGCACC 240
 CTGTGGTCTT GTCATCTGAC CAAATCACAG AAAATTGAGA AAGTGGATAC AGCGACTGTG 300
 GACATTGTGA AGTCACATCT TACTCAGGGA TGACAGCTAA AATCAGCGTG TACAGCAGAA 360
 AAGTCACATA TAGCTACAAA TACCCTGGAA AACTCGAG 398

(2) INFORMATION FOR SEQ ID NO:1092:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GAATTCGGCC TTCATGGCCT ACGAGTTTTT TGCAAGTCAG CCATGAAGTC TATGCTCTGC 60
 TTCAGGCTCT GAATTCCTTC CTGGCTAAGA ATTTTCATTC CTGAGTGCAA CAGCTTCTTT 120
 GCAGCTTTAT AATAAATGGT CTCTGGTTTA TTGTAAATCA TGGCATTAGT ACACATTAGT 180
 TTGAAGTTAT CCTTTAGTTC TTCTATGGAC TGATAGTCAT TGTTCTTGAT CTTTCTTTTC 240
 ATGGTACTAA AATCCATTGG GTGTTTAATG ATCATGGAGT AGCCAGGAGC AATAAAATCA 300
 GTCACAGGAA ATGAAAAGAA AGCACTTGA TCTTTTCTCT GCAATTGTCT CATCAGTTGA 360
 TTCAAAGCTT CTTGAAGGGG TGTCTGTCT ACTTCTTCTT GTTTGGCTAA AGAGCTTGTG 420
 AGAGGCTTCG CTCGAG 436

(2) INFORMATION FOR SEQ ID NO:1093:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGGGCAGGGA GCCTGGCCAG GCCTGAGACA CAGAGGCCCA CTGCGAGGGG GACAGTGGCG 60
 GTGGGACTGA CCTGCTGACA GTCACCCTCC TTCTGCTGGG ATGAGGTCCA GGAGCCAACT 120
 AAAACAATGG CAGAGGAGAC ATCTCTGGTG TTCCCACCAC CCTAGATGAA AATCCACAGC 180
 ACAGACCTCT ACCGTGTTTC TCTTCCATCC CTAAACCACT TCCTTAAAAT GTTTGGATT 240
 GCAAGCCAAT TTGGGGCCTG TGGAGCCTGG GGTGGATAG GGCCATGGCT GGTCCCCCAC 300
 CATACCTCCC CTCCACATCA CTGACACAGC TGAGCTTGTT ATCCATCTCC CCAAACCTTC 360
 TCTTCTTTG TACTTCTTGT CATCCTCGAG 390

(2) INFORMATION FOR SEQ ID NO:1094:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

| | |
|---|-----|
| AATTCGGCCT TCATGGCCTA GAGGGATTTG TTAACCACTG CCACCATGTA GTTCTGGAAA | 60 |
| CGGAGGATGC GGTGGTAGAT GTCCAGTTCT GTCAGCTCAC GTTTGTGGAT GCAGATCTGG | 120 |
| TGCTCCTTCT GCGTCTGCAC GATCCGGGCC TGCACTTCTT GCCACGTGCA ATACGGAAGG | 180 |
| GCAGACATAG GGATGCGCAG AGCGTGCAGG TAGAAGGAGT GGATCTCCCA GTAGCAGCAA | 240 |
| ATGTTATAGA TGAACCTGAT AAGCCGGTGG ATCCAGAAGA CACCAGCAAT GACCAGGATG | 300 |
| GTGATAAGGG AGCCATTTC CTGAATCCTG GCACTACAGA CTTGAGCAGG CAAAAAGGCG | 360 |
| TCTGGCAGAG TGACCTTGAC GGGTTCAGTA GGGTGAAGAC TGTGGTTCAC CATCTTGTG | 420 |
| GCAAATAGGA TGTATAGTC CACGCAGCTG ACCAGGAAGG TAGTGAAGGC AACCACAAAG | 480 |
| AGGAACTGCA TGAGCTCAA GATCTCCCCG ATGAGCATAC ATGTGAAGCC ATTCTTCTGG | 540 |
| TGCAGATTAT AAACCTCGAG | 559 |

(2) INFORMATION FOR SEQ ID NO:1095:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGTTTGGAA AGTAAGACAT ACTGGCTTCC TTTATTCA | 60 |
| TTAGCATTTT CCTATTATT TGGAAACCAAC AATTCCATGT TCATTGAATT TCCTTTTTTT | 120 |
| TTTTTTTTT AAAGACTGCA AATTTTGGCT GGGCACAGTG GCTTGACTCT GTAATCCTAG | 180 |
| GTACTTAAGA GGCTAAAGCA TGAGGATCAC TTGAGGGACT CGAG | 224 |

(2) INFORMATION FOR SEQ ID NO:1096:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTTCTCTCT GATTGGTTT GTTCTGTCTC AGGCTTCTGT | 60 |
| GGCAGGACTG GCCCAGGGAG GAGGAAGCCA GCAGCACACC TGGGGAATGG GGTCCCGGCC | 120 |
| GGGAGGCTTG GCCTCTGGGC GACCTCGTCC TGTTTTGTTT GTTTGTTTGT TTGTTTTTTT | 180 |
| AAAGGTAAAC CTCCTGGGCC GCAGATGGCA AAGGGAGTGC CTGGGCCTGG TGACCCAGGG | 240 |
| CTGGATCCAC CCCTGCGGAG CCCTGGGCCA GGCAGGTGTC TGCTGCTCAC CTGGCTCTGG | 300 |
| AGGGCTGCCC TGCAGCTGGG CCTGGGGACA GGTCCGCTGT GGGGCAGCTC AGTACCCTCC | 360 |
| CTGAGGCTCA CGGTGGCTCC GAGCATGAGC TCTGCCTCCT GGGCGAGACC CAGCAGTGA | 420 |
| CAGCACGTC CTCACACCA GCTCCCTGCA CACCCAGGCC AGCCACCCCT CCCGCTCGTG | 480 |
| CACAGGCAG CAGATGCGCT CACACGTACA CACACACAA TGCAACGCCT CGAG | 534 |

(2) INFORMATION FOR SEQ ID NO:1097:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTTTATTGG | TGGACATTAA | GAATGGAGGA | ATGTTTCAAC | 60 |
| AAAGGAACAA | TCAACAGTAT | CAAATACTG | CAGAGGGGTC | AATTTGGGGA | CTAAGAGGGG | 120 |
| AGCCACTGGA | TTTGACAACT | AGGAGATAAA | TTTTAGTGCA | ACGATGAAGG | CAGAATCCAG | 180 |
| AGTATAATGA | GCTCAGTGAA | AAAAGGTGAA | NACATGTAGC | TTATTCTCTC | AAGAAACTAG | 240 |
| GCTATGATAA | ACTGGCAGAG | GCTCTAAGAG | TGGGAGGTGA | GTTGTTTTCT | CCTTCATGTA | 300 |
| AATATATTTA | CCTTTTAAAC | ACTAGGCCCA | ATTITATATC | CTATTTCATT | TAACTTTATG | 360 |
| AACATATTTA | TGTATGTATG | CATGTATGTA | TGTATCTCAT | GTGATGTTTT | AGACACTGAA | 420 |
| AAATAACTCA | TTTCTATTAT | AAAACGTGATA | TCTTTAGATG | TTTCAGAAGC | AACTTCCTAA | 480 |
| AAGGAGGTAG | CAGTAATGGA | GCTATGTCTA | TCATTCTTTC | CCATCAACCC | CCTTGATGGA | 540 |
| GATGTAACA | TGTGTCCATC | AAGCCTTTAA | TTTTTACNTC | TTATCTTCAG | GGCTCTGCCG | 600 |
| CTCGAG | | | | | | 606 |

(2) INFORMATION FOR SEQ ID NO:1098:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGCAGAACAT | GGATATTTTT | CCTTTAATAT | TTAGTACTTG | 60 |
| GGCTATCATG | AAACAAGGTT | AGCATAACCA | TCCAAAACCC | CAAGTGCTCC | AAAATCCAAA | 120 |
| ACTTTTAAA | CACCAACACG | ATGCCCAAAG | TGGAAGATTC | CATACTTGAC | CTCATGTGAT | 180 |
| GGGTCTAAGT | CAAAATGTAG | GCAAACTTT | CACGCACAAA | ATTACTTAAA | ATATTCTACT | 240 |
| GAGCCAGGCA | TAGTGGTTCA | TGCCTATAAT | CCCAGCACTT | TGGGAGGCTG | AGATGCCAAT | 300 |
| TGCTCGAG | | | | | | 308 |

(2) INFORMATION FOR SEQ ID NO:1099:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGATG | ACCGCAGCAG | GCTGGTCAAG | CAGATGGAGG | ACAAGGTGTC | 60 |
| TCAACTGGAG | ATGGAACCTG | AAGAAGAGAG | AAACAACCTCA | GATTTGCTGT | CTGAGAGGAT | 120 |
| CAGTAGGAGC | AGGGAACAGA | TGGAGCAGTT | GAGGAATGAG | CTACTTCAGG | AGAGAGCTGC | 180 |
| GAGACAAGAC | TTGGAGTGCG | ACAAGATTTC | CCTGGAGAGG | CAGAACAAGG | ACTTAAAGAG | 240 |
| CCGGATTATC | CACCTGGAAG | GTTCTACAG | GTCCAGCAAA | GAGGGGCTGG | TTGTGCAGAT | 300 |
| GGAGGCCAGG | ATCGCGGAGC | TGGAGGACCG | CCTGGAGAGT | GAGGAGAGGG | ATCGGGCCAA | 360 |
| TCTTCAGCTC | AGCAACCGGC | GGCTGGAGCG | GAAAGTGAAG | GAGCTGGTGA | TGCAGGTGGA | 420 |
| TGATGAGCAC | CTGTCAATTGA | CTGATCAGAA | GGACCAGCTG | AGCTTGCGTT | TGAAACCCCT | 480 |
| CGAG | | | | | | 484 |

(2) INFORMATION FOR SEQ ID NO:1100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

| | |
|---|-----|
| GCAGATTGAG GACCTCCAGA AATCTTTACA GGAACAAGGT TCCAAGTCTG AAGGCGAAAG | 60 |
| TTCCCAGCAA ATTAAAGCAG AAGTTGGAAG CTCATATGGA AAAACTCACA GAGGTCCATG | 120 |
| AAGAATTACA GAAGAAACAA GAACTCATTG AAGATCTTCA GCCAGATATA AATCAAAATG | 180 |
| TACAAAAGAT CAATGAACTT GAAGCTGCTC TTCAGAAGAA AGATGAAGAT ATGAAAGCAA | 240 |
| TGGAGGAAAG ATATAAAATG TACTTGGAGA AAGCCAGAAA TGTAATAAAA ACTTTGGATC | 300 |
| CCAAGTTAAA TCCAGCATCA GCTGAAATAA TGCTACTAAG AAAGCAGTTG GCAGAGAAAG | 360 |
| AGAGAAGAAT TGAGATTCTG GAGAGTGAAT GCAAAGTAGC AAAATCCCGT GATTATGAAG | 420 |
| AAAAACTCGA G | 431 |

(2) INFORMATION FOR SEQ ID NO:1101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 557 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTGGGAATC TCTCAGCAGC TTTTGGCCAA ACAGATGGGC | 60 |
| CAGGAGCCGC GGAACCAGGC TGAGGAATGT TGCCTCACGA TCTCTCATAT CCATTCTCTGG | 120 |
| CACCCACCAG CCCAGGGAAT GCCTCTACCA GTTGTACGCG AGAGGCTTAC ACAGCATCTT | 180 |
| AAATAAAAGG GATTATTGAA CCAAGAGGCC AGGGACTGAT GGAATGCCC ACCTTGCTGG | 240 |
| CTCATTGAAA AAGTTTGGCA AGGTTGTCAG GAGACATGAA TTAGATGGGC TTGGGTCTTG | 300 |
| TGCCCTTTGC TAAACCAAGT GCTGTATTGG GAAAGAGACG GGGAGAGAAG TGTTGGAGAT | 360 |
| GCTCTTTAGT CAGGCCTGAG TCACTTGCCC AACCCTGGAG TTGGAGTTGG GGATGGAGCC | 420 |
| AGGATCTCCA AACCATGTC CCCTAGAGTT TCAGGGAAAA TATGGATTGT GAATTGAAGA | 480 |
| TGGGGGGTGA TGTAAGGCAG ACAAGGACAG AAAATCCCTC TTCCAGCTGT GATTGGCTG | 540 |
| TGAGTTTGGC GCTCGAG | 557 |

(2) INFORMATION FOR SEQ ID NO:1102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGTTTTTCTA GAGTGAATTA TAGTATTGAC GTGAATCCCA | 60 |
| CTGTGGTATA GATTCCATAA TATGCTTGAA TATTATGATA TAGCCATTTA ATAACATTGA | 120 |
| TTTCATTCTG TTTAATGAAT TTGGAAATAT GCACTGAAAG AAATGTAAAA CATTTAGAAT | 180 |
| AGCTCGTGTT ATGGAAAAAA GTGCACTGAA TTTATTAGAC AAACCTACGA ATGCTTAACT | 240 |
| TCTTTACACA GCATAGGTGA AAATCATATT TGGGCTATTG TATACTATGA ACAATTTGTA | 300 |
| AATGCTTTAA TTTGATGTAA ATAACCTCTG AACCAAGAGAA AATGTTTTTA ACTTAGAGTA | 360 |
| GCCCTAAAAT ATGGATGTGC TTATATAATC GCTTAGTTTT GGAAGTGTAT CTGAGTAACA | 420 |

GAGGACAGCT GTTTTTTAAC CCTCTTCTGC AAGTTTGTG ACCTACATGG GCTAATATGG 480
 AATAAAAA TACTACATTG ATCTAAGAAG AAAGTAGCCT TGTGGAGTAT ATAGATGCTT 540
 TTCATTATAC ACACAAAAAT CCCTGACTGA CCTCGAG 577

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GAATTCGGCC TTCATGGCCT ACATGGACCT CCTGCACAAG AACATGAAAC ACCTGTGGTT 60
 CTTCCTCCTG CTGGTGGCAG CTCCAGATG GGCCCTGTCC CAGGTGCAGC TGCAGGAGTC 120
 GGGCCAGGG CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC ACCTGCACTG TCTCTGGTGC 180
 CTCATCAGT AGTGGTGGTT ACTACTGGAG TTGGATTCTG CACCACCCAG GGAAGGGACT 240
 GGAGTGGATT GGGCGAATCT CTCACAGCGG GCACACCAAC TACGACCCCT CCCTCGAG 298

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

GAATTCGGCC AAAGAGGCCT AGTCATCTTC AATATCTCTC TCTCTCATCC CTTCATTAAA 60
 TCATTCACCA AGTTTGGACA GTTTTCCTTT GCAATGTGTC TCCAAATGGT CATCCTCTTC 120
 TCCTTTTCA GATTAGGATT CTTGTTTCT TTAATCATTG GTAAAACAAG TTTGGGAAAT 180
 GCTAGTTACG CAGTTAATGG TGTAAGTTACC GCAGGACTTG ACAAACCTC TAATGAAAGA 240
 ATAAACATT TGCTATATTT GTTTGATCAG AGAACTTTT TTCCATCTCA GGGGATCATT 300
 CTCGAG 360

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGTCT AAATGAAATG ATTGCACTGC 60
 ACATACTTCT AAAACTGTCC TGCGATTGTA TAGCTTCCAT TTCATGGCGC TTCTTCTGGA 120
 TGTCAGGCAC TAAGTCGGGC GCTTTATTCT GTAGTTCTCC TAGCAATCTG GTGAGCTCCA 180
 CTCTACAGAT AAGGAAATCG AGGCCAAGGA CAGCTAAAGA AGCGAGGTGC GCAAGGTGCC 240
 CAGGTCCGAA GTGTTTCCGC TGCTTTCAGA CTGCAGTCCC AGGGCTCAGG AGTCCATGCT 300
 TTCTGCGTAT CTTACGCTG GCCACGGATC ACCTCATCAT TAGATGTCTG AGTTGAACAA 360

| | |
|---|-----|
| GTGGTGTTCATTTCGGACG TGTGTTAGGT AGAAGTGTGT GTGCACCTGC GTGTGCGTGT | 420 |
| ATGTTCCACA CGCTGATGCA GGAGGTATAC GCACAGATAT AATTGTCTTT TAGAAGATTG | 480 |
| ACTATCACTA ATTTGAAAA ATTTCTTGAA TGACCTTTCC GNCCCGGCGC TCGAG | 535 |

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

| | |
|---|-----|
| GAATTCGGCC NAAGAGGCCT AGAAAAAATT AAAAAGGGAT ACAGACGAGC TGCNAGCTAT | 60 |
| GGAACATAGA TATTAACCCC CAAAGAGTCN TAACCACAGC TGAATCTTAG CTTCACAAGC | 120 |
| AGNCCTCNGA ANGTGGTAGC TTGTTTAAAG CAGAGGCCAT GCAGAACCCA TGAAACCAAA | 180 |
| GGACAGAGCC AGTAGGGCTG GAGTCTGACC AGAAAGTTCC ATGCCCTCTG CTTTCTGCAT | 240 |
| GGAAAATGAC CTGGTAGGTT TTAACCTATC CAAGACTACA GAGGATTTC GAATTTTCAGT | 300 |
| TTGAGGTATG CCTCAAAACA TTCCAGCCTT GATCATGAAA GAAAGAAGTG ATCAAAATAC | 360 |
| CATATGTCAC AATGGAAAAC CCAAGCGGCC CCAGAGCTCT TCTTCAGTAA TGAGATTTAG | 420 |
| TTGATCTGNA CAGTTATTTA TGCATTGAGG TCATATTTTG GCCAATCTTT TGCTTACAGC | 480 |
| TGTCGCCAAA TAAAGCCTTC TGTNTTAGCA TTTCTTTTAC CAAAATCAGG TTGAGAGATG | 540 |
| GTTCTTTGAG AGGACTGTTT TGTGAGGAA TACAGGAAT CTCGAG | 586 |

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGACTTAAA AGAACAGCTA GAAAAGATGA AAGGTGACTT | 60 |
| AGAAAGTAAA AATGAAGAAA TACTACATCT GAACCTAAAA TTGGACATGC AGAACAGCCA | 120 |
| GACTGCTGTC AGCCTCAGAG AACTTGAGGA AGAGAACACG AGCTTGAAGG TCATATATAC | 180 |
| CAGAAGTTCT GAGATTGAAG AGCTGAAAGC CACTATTGAA AATCTGCAAG AGAATCAGAA | 240 |
| ACGATTACAA AAGGAGAAAAG CAGAGGAAAT TGAACAATC CATGAAGTCA TTGAGAAGCT | 300 |
| GCAGCACGAG CTGTCCCTCA TGGGGCCTGT GGTGCACGAA GTCAGCGACA GTCAGGCTGG | 360 |
| CAGTCTGCAG AGCGAGCTGC TCTGCTCCCA GGCCGGGGGC CCTCGTGGGC AGGCCCTACA | 420 |
| GGGCGAGCTC GAG | 433 |

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

```

GAATTCGGCC AAAGAGGCCT ACGTGAATAT TTTTCCATCT GTGTTCATTG ATGTTAACAA      60
TAAAAATCTT GTTTATGTGT ATAAGCCTAA CATATGCCTG TGGGTCTTAT AACTGCCTGT      120
TCAAACTCAA TGGGATACCA AAAATGTATC TGCTTACTTT GGGGGTCTAA CTTTAATTCC      180
GTACATATAA ACATCTCTGG AAAAAAATGT AGTTTTTTTC TTCCCCTGC TGTTTTCCCC      240
AGGCTTTCTC CTTTGACCTG GCCACGGTTC CCATAGACTA CAAGACGACT TAGAGACATT      300
GCTGTGACAT CTCGAG                                     316

```

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

```

GAATTCGGCC AAAGAGGCCT ACTAACATTT TCCTAATCTT ATGTGTTTGG CTCCTCTCAT      60
TTACTCCCCA CAGCAGCCAC ATGAAGTTGG AATTTGGAAC TCTTATTTAG GTATGCAAAA      120
GGGTACCAGT TCTCTTAAG GCTTTAGTTC AGGAGTGGTG TTAATGTATT AATGTGTTGG      180
GGCGCGAGAG GAAGGCGGTG CTTATTTTCA ATCATGGTAG GTAAAGATAA TTTCAACTCT      240
GACACTTCCA CTAATAAATT TTCGCATCTA GGGAAAATGA CGTAAGCTTC CTAGATCACA      300
GATTTGTTTT CATCCAAAAC CCGAAGTCTG GTTTTGAAAT CACGCTCTTG ATACAAAGGT      360
GGCTCGAG                                     368

```

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

```

GAATTCGGCC AAAGAGGCCT ATCCGGGGGG AGTAAGGTGA GGACAAGGAA CAGAAAGGCG      60
TGAGGTGATG GAAGGAAGTC CGGGAGAACC ATATGAAGGA GCAGGAGGAG AGGAAGAAAC      120
TTTTTTTCCT TCTTTTCCAG GAGTAGCTGG AAATTAAGAT CGGGTTCCTT TTCTGCCAGC      180
TTGGAAGGGC AACCCCATGA CTGATTGCCA TTCTGAGGAT GTCTATGCAA AGTTGGATTCT      240
TTGTTACAGT GTATCCAATC TGAAGTATTG CACATCTGAA CTGGGACTGT TAACACTGAT      300
GCCAATACAG TGTGGGGTGC CAGAAAGTGT CTGCTGATAT TTGTGGAAAA AAAATCTATT      360
TTGTTTACCT ACTGTATCAA AGGGGAGGAA CTCGAG                                     396

```

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

```

GAATTCGGCC AAAGAGGCNT AGATTGTTTT CATTAGCAAA CTCATAATTA TCCTTTTCCT      60
TAACACTTCC AGTTGAGAAA ACAAGTATTT GTTAATGACC AGTAATAATC TTGATCCAGG      120
GTAGGCAAAA TTTTCTTCC AGGGCCAGAT TGATACTTA GGCTTTGCAG GCCACGGGGT      180
CTCTGGCAAC CCCAGCTCT GCTGTTGTAG CACAAAAGCA GCCACAGGCA CAAGTAAACA      240
CATGGGTGTG TCTCTGTACC AATAAACTT TATTTACAGA AACACAGGGC AGATGACTGT      300
CTGGCCCCCTG GTCTTGTGAG CATTTTGTGG TGGTGAACAA AAGAACTGT TCAGATCATT      360
ACATTTACAG TCATTACCAA AAATAGAATC TTCACAGTAG TTGTACTGTT GATGAAGCAA      420
GCTCGAG                                           427

```

(2) INFORMATION FOR SEQ ID NO:1112: --

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

```

GAATTCGGCC AAAGAGGCCT AGGTTATAAT AGCAGCTTAC TTTTGATAAG CGTACTAACT      60
GGTACATAGT AAATACATAC TGTGCATGCA TTATGTCATT TATATCCACA CAGTCACCTT      120
CAAATTCAGT ACAATTGTGA TTCCCGTTTT ACAGATGAGA AAGCATATTT TGGTGAAGTC      180
AACCAAGGTT ACATGACTAG TAAATTTTAA ATGAGATTTA ATTCAGTAC TTACTAACCA      240
TTATGCATTG CTAAATTTGA ACATTACTTT AAAATATAAC TTCTAAAGTG TTCATATTAG      300
AAACCTATAA ATATACATAG ATTTGTCTCC TCTCTNACGA AGAACACATG AAGGAAAGAA      360
AGATATTAAT TTGGTGGCTT ATCATATGCC AGACATAGAT ATAGATGCTT GTATGTATGG      420
CATTTAATCC TTATCTGTGA GGTAGTCTT TTTATGCCTT TCTATAGATT TAAATTAAG      480
GTTCAAGTTA GTAACCTGCT CGAG                                           504

```

(2) INFORMATION FOR SEQ ID NO:1113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

```

GAATTCGGCC AAAGAGNNCT AGAGGGATAT AGAACTTAA CAGCAGTGGC TGACATTTTT      60
GCTTATTTGT TAGGTATTGG TGGTGGTGT AATCGGGTAC GCATATGCTT TCCTTAGGAT      120
TTGCATTGCG TGTTCCCTGT GTCTAGAACC CTATTCTTGA GATAAATCTT CATTCCTTAC      180
CTCCTTAAAA TGTTTTCTCA TCTATCACCT TCTTAAGTCT GTACTGATCA CCCTACTTAA      240
AATTATAACT GCCCCTCTTT GCTTGCACTT CTAAGCTTCC TTACCCTAGT CTGTTTAGCA      300
GTTACCTCCT TGAAACATGC TCTGTAGAAT TTAATTATTA TGACTATTGT CTCTCTTACT      360
ACCCTCGAG                                           369

```

(2) INFORMATION FOR SEQ ID NO:1114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GAATTCGGCC AAAGAGGCCT AGTTAAAAAT AGAATTTGAG ATATTTAATT TTCTGCTCTT 60
TTTAAGTTAT GAAAACGTAT TTAAGTCGAG 89

(2) INFORMATION FOR SEQ ID NO:1115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GAATTCGCCA AGAGCCTATT AATTTGTAAA CCTTAATATA GTGTAACTG AATAAAAGTA 60
AATAATTATT ATTAGAATGG TAACTAAGTC ATTAAATTTT TTNGCAGAAC TGAACTTGT 120
ATGTTATTAG TTTATTTTCT TAGACCAGTG TAATAATGGA CTGTAAATAG AAAAATAAAT 180
GTCACTTTAC AGTTAGATGT ATCACAGTCG TTTCAGGAGA ATTTTTCCTA TATTGTTACC 240
TTGATTCATT GTTTAAAATT GGTAGGATT GTATAGATAT AGGATAGTGT TTTATTTATA 300
CTTTATCATA AGCCATAATC ATTTTAAGAA TACTTTATTG GATAGATTTT AGTACTTTTT 360
AAATTCTAAA GTTCTATTTT TCTTTTCACT TCCCCTTCCT TCCCCTTATA AGATCATTTT 420
CATGCTTTTG TTGGTGATCT CAGCCCAGAA ATTACAACTG AAGATATAAA AGCTGCTTTT 480
GCACCAAGTC TCGAG 495

(2) INFORMATION FOR SEQ ID NO:1116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

GAATTCGGCC AAAGAGGCCT AGGGAAAAGA AGGGCTTTGG GGACCTGCCC ACTTCAAAAA 60
CAGTTTTTCT CATCCTTTCG CTTGGGCTCC AAACCCAGCT TGGTGTTCCT CTAAGGGAGC 120
TACAAATTCT GGAGCATCCC ATGAGGATGA TTTGCTGGCC TCGGTCATTA GGGGGAAAGG 180
ATGTTCTCAG AAAACAGCC CTGCACGCTG CTCAGCAGAG ATCTTGAGGT CGTGGCCACG 240
ACTGGACTTG GTGCAGAGCT GAACCCGAGA CTCCAGCTGC TCGCTGAGTT CGTCCAGAGC 300
CCCGGTGCAG GACTCCAGGC TCTCGGCCAG TTTCTGAATC TTGGCCTTCA GCACGGCCTG 360
GCTAACCTTG GTGTCCCCCT CCGCCCGCCT GGGGATGAGG AAGCCACGTG AGCCAAAGAA 420
GACGATGAAG TAGACAGAAT TGTACAGGGC GATGGAGGCG TTCCTCCCGC ACTGCAGCAG 480
CTGGCGGTCC CCGCAGCCCT GCCAGCGGCA GAAAACTCG AG 522

(2) INFORMATION FOR SEQ ID NO:1117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AAAAATATTT TACTTGTTC ATCCACAGTT CTCTACAGAA | 60 |
| AGAACCAATG AACCCAATAG GAACAAATTC TCTGTGGAAA ACAAAGCATA GCTGTAGTAG | 120 |
| ATACGAATCC AATCACAGAG GAAACAGGAA GAGAAAAACA TCCAAGACTA TAGTGAAAAAC | 180 |
| TGGAAATGGT CTGTTTTCTG GATATTCGTA TGATTAAGAT GCAAATTTTT TCTTAGGAAA | 240 |
| ATGTGATTGT TAACTAGCAT TCTGTTTAC ATGTTGACAT TTCTAACACA CACACCACTG | 300 |
| ATTTGAACTT CAAAATTTAT TTTCTGATTA TATATGCTAG GTCATGCTCG AG | 352 |

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGCCCACT CATTATGTA CTGTCTATAG CTATTTTCAT | 60 |
| GCTACAATGG CAAAGCTAAG TAACACTCAA GGCCTAAAAT ATTCACTATA TGCCCTTTGA | 120 |
| AGAAAAAGTT CACTCAACTC TGCCCTAAAC TACAGACCCT GGCCAAGGTG GGAGGATCAC | 180 |
| TTGAGGCTAG TAGTTCAAGA CCAACCTGAC TCTGTCTCTG ACTCTGTCTC TACCAAAAAA | 240 |
| AATTAGCTGG GCGTTGGGCT TATCCCTGTA ATCCAGCTA CTCAGGAGTC TGAGGCAAGA | 300 |
| GGATCACTTG AGCCCAGAAG TTCAAGGACA CAGTGAGCTA TGATTGCACC ACTATACCCC | 360 |
| AGCCTGGGCA ACAGACCAAG ACCCTGTCTC TAAAAACATA AAATAAAAAA TAAAAAATAA | 420 |
| AAATAAATAA TAAAGAAAAA AGAACAGAA TTAAAGAAAT TCTTTTGCTC AAAGTCTCGA | 480 |
| G | 481 |

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGTTGTGTC AGTGTCTCTC CTAAGGTAGT AAATATAATT | 60 |
| GACTTATTCT GAACCCATTC TATTTTGAAT CTCCCCTTTC CTCTCACAAT ACTTGAACAT | 120 |
| TTTAATCTTT TGGAATATTG TCTTCTTTG TTATAACTAT TCATTTTGTAG CTTTGTCTC | 180 |
| CAGTGCATGA TCTCATATTT TTGCTTTTAT TTTTAGTATA AGAACATTTA TAAATCATA | 240 |
| TTTTTGTTAC TGCAATTGTT TTATTGTGTT TGTGGCAAAT GAGAAATCCT TTATTTATTG | 300 |
| TGCTGTATCT CGAG | 314 |

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

```

GAATTCGGCC TTCATGGCCT ACCAGATACT GTTTTTTTAA TACATATTCA AAAGAAAGCT   60
ATTAACCCCTG ACAGACATTT CTCAGTCTGT GCTTTTTTCT ATTTTATCAT TTAAAGTAC   120
TTAAGATAGA AAGATGAAAA AGCATTGTGT GGCTACTTGG TTAGCTTCAC AAATTTTCCC   180
CCTTCCTACG CAGCTCGAG                                     199

```

(2) INFORMATION FOR SEQ ID NO:1121: ..

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

```

GAATTCGGCC TTCATGGCCT AGTAGCATAT TAACAGTGTA ATAAAAAATA AAAACAAACT   60
CTAGTATCCA GAGGATCACA TGCTGACCAG ACCCTGTGTA GAAAGTGCCG AAGAGCATCA   120
AGGAAATGGA AACGTTGGAA TTCCATCCGT GCTTGTGGCT TTCCTTAAAC TTTTGTATG   180
GAAAATTTCA AATATACCCC GAAGTGGAGA TTGGCTTAAA TCAGCCCCAC GTGCCCATCA   240
CTCGGCTCCA GTCATTATCC AGTGTGGTTC CTCTGATCTT CACCACCCCC TCGAG       295

```

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

```

GAATTCGGCC TTCATGGCCT AACGGAAGCG TCTCCTCATT GATGGAGATG GTGCTGGAGA   60
TGATCGGAGA ATTAATCTGC TAGTGAAGAG TTTCATTAAA TGGTGCAACT CTGGGTCCCA   120
GGAAGAGGGA TATAGCCAGT ACCAACGTAT GCTGAGCAGC CTGTCTCAAT GTGAATTTTC   180
AATGGGCAAA ACTTTACTAG TATATGATAT GAATCTCAGA GAAATGGAAA ATTATGAAAA   240
AATTTACAAG GAAATAGAAT GTAGCATAGC TGGAGCACAT GAAAAAATTG CTGAGTGCAA   300
AAAGCAAATT CTTCAAGCAA AACGAATACG AAAAAATCGC CAAGAATATG ATGCTTTGGC   360
AAAAGTGATT CAGCACCATC CAGACAGGCA TGAGACACAG GGAAGTCTGAG       410

```

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

```

GAATTCGGCC AAAGAGGCCT ACCTTTCTTT CCTCCCTTCC TCCTCCCATG TCCCTCTCTC   60

```

| | |
|---|-----|
| CTCCCTCCCA CCTCTCAGCC TTCTCCATCC CTCCTCCCTC TTTTCTTTTG TACTTTCCAG | 120 |
| CTGGAGCAGC AGCAGCAGCT GGGCCTGAAT CAATGATTGA CTTCCCCCAG ACCTCCCCTT | 180 |
| CTCTTTTGCC AATGATATCT CTTTGCCCTT CCACTCATCT TTTAATTTA TCGTGTATGG | 240 |
| TTTTGCTTCT CTTTCTCTCT CCTCTCTCT TCCCTCTTTC TCCCCCTCT CCCCCACCGA | 300 |
| CAGTCGAG | 308 |

(2) INFORMATION FOR SEQ ID NO:1124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs-
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAATTTTGC CATGGTTCTG CTCATTTTTC CTGCAATTCT | 60 |
| CAGCATGGAT TTATATCGAC GCGAGGACAG GAGACTGGAT ATTTTCTGCT GTTTTACAAG | 120 |
| CCCCTGCGTC AGCAGAGTGA TTCAGGTTGA ACCTCAGGCC TACACCGACA CACACGACAA | 180 |
| TACCCGTAC AGCCCCCAC CTCCCTACAG CAGCCACAGC TTTGCCCCATG AAACGCAGAT | 240 |
| TACCATGCAG TCCACTGTCC AGCTCCGCAC GGAGTACGAC CCCCACACGC ACGTGTACTA | 300 |
| CACCACCGCT GAGCCGCGCT CCGAGATCTC TGTGCAGCCC GTCACCGTGA CACAGGACAC | 360 |
| CCTCAGCTGC CAGAGCCCAG AGAGCACCAG CTCCACAAGG GACCTGCTCT CCCAGTTCTC | 420 |
| CGACTCCAGC CTCCACTGCC TCGAG | 445 |

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

| | |
|---|-----|
| GAATTGCCTT CATGGCCTAC ACCAGCCTAT TCTCTGCTTC TGTGAGTTTG ACTCTTTTTT | 60 |
| TTTTTATGAG ACAGAGTCTC ACTCTATCTC CCAGGCTGGA GTGCAGTGGC ACAATCTCGG | 120 |
| CTCACTGCAA CCACCACCTC CCAGGTTCAA GCAGTTCTCC TGCCTCAGCC TCCCAAGTAG | 180 |
| CTGGAAATAT AGGTGTGCCC CACCACGACT GGCTAATTTT TGTATTTTGA GTAGAGACAG | 240 |
| GGTTTCACCA TGTTGGCCAG GCTGGTCTCG AACTCCAGGC CTCATGTAAT CCGCCCACCT | 300 |
| TGGCCACACT CGAG | 314 |

(2) INFORMATION FOR SEQ ID NO:1126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

| | |
|---|----|
| GAATTCGGCC TTCATGGCCT ACACGCCCCC GCCCCGCTG CTGCCAGGA ATACTTTCTC | 60 |
|---|----|

CAGGAAGGCT TTCAAGCTGA AGAAGCCCTC CAAATACTGC AGCTGGAAAT GTGCTGCCCT 120
 CTCGCCATT GCCGCGGCC TCCTCTTGGC TATTTTGCTG GCGTATTTCA TAGCAATGCA 180
 TCTGCTCGGA CTCAATTGGC AACTCCAGCC TGCAGATGGG CACACCTTTA ACAATGGGAT 240
 AAGGACCGGC TTACCAGGAA ACGATGATGT GGCAACAATG CCATCTGGAG GCAAAGTGCC 300
 CTGGTCGTTG AAAACAGGC AACTCGAG 328

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC TTCATGGCCT AGTGAGGCTC CATTATTTTC ATTTTAAACA AGTTTCAAAA 60
 TGTGGCTGCT GCTGTTGCTG GTGGTCCGGA GCCTGCAGAC AGGGGGATTG GCCTGGGAAG 120
 GAGAAGTAGA AAACAACGTG TACAGCCAGG CTACAGGGGT GGTCCCCCAG CACAAGTATC 180
 ACCCCACAGC AGGCAGCTAT CAGCTTCAAT TTGCCCTGCA GCAACTTGAA CAACAAAAAC 240
 TTCAGTCCCG GCAGCTCCTG GACCAGAGTC GAGCCCGGCA CCAGGCAATC TTTGGCAGCC 300
 AGACACTACC TAACTCCAAT TTATGGACAA TGAATAATGG TGCAGGTTGT AGAATTTCCA 360
 GTGCCACAGC TAGTGGCCAG AAGCCAACCA CTCTGCCACA AAAAGTGGTA CCACCTCCAA 420
 GTTCTTGCGC CTCCTTGTT CCAAACCCC CACCGCTCGA G 461

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

GAATTCGGCC TTCATGGCCT AGAATTATCA TGGCATCTGT AACACACATG CCTGTGCTAT 60
 ATTCTCACAA TTTTGTTCAG GTTGTGCATA TAAAATATG GAGCTCCATA TTTTTCCT 120
 TCCTAGTTGA TCACAGTTGA CTGGGTTGTC TTTTCTGTCA CCTGTAGTT TTGAAGAGAT 180
 GTCTCATATG TAGTGATGTT AGGTATGATG CATTACAGCA TAGTAAATAC CTGGTACTGT 240
 CTCTCAAAAA AAGCCTTTAG CTTTTTTGTA AAGAGGACAA CAGAAAACAC ACCAAAAAAG 300
 CAGAAAAATA TGTGTCGGTG ATAGTGGGAG AAACCTTATA ATCATGGTCA TATGTTACCC 360
 CAGAGAAGGC TTACACAAGG TCAGCTACAG TTTACCCAAT AACGCTGTGA TTGTCTGGTT 420
 CCTTGGCTTA GAAAGCTTAG TCTCTGCCAA GCGGCCTCGA G 461

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

```

GAATTCGGCC TTCATGGCCT ACAAGAATGA AGCACTGAAA AGCGAAGAAG GCTGCATTCC      60
GAATATCGCC CCAGACATCT GCATAGCATA CAAACTGCAC CTAGAGTGTA GCAGGCTCAT      120
CAACCTCGTG GACTGGTCAG AGGCTTTTGC AACAGTTGTG ACAGCTGCTG AAAAAATGGA      180
TGCAAATTCT GCAACCTCAG AAGAAATGAA TGAAATTATC CATGCTCGGT TTATTAGAGC      240
TGTTTCTGAA CTAGAACTTT TAGGATTTAT AAAACCTACC AAACAGAAGA CTGACCATGT      300
GGCAAGACTA ACATGGGGAG GCTGCTAGAA AGCAAATAAG CAAAGCCAGA ACTATCACAT      360
TTAGCTTAAG AGAAAAAGGT GACCAGTCAT ATTTACATAT ATTAGAGGAG CCTGTTTGT      420
TGAGAAGATA AATGTGTAAC CCCCATTGAT GTTTAACCAG AAAAGTACAT TGCTAACCCC      480
AAGAGCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

```

GAATTCGGCC TTCATGGCCT AGGGCAACAG GAAACTCTTT ATTATGGTGA TGAGATCGAC      60
AATCTCCCCT ACTGTTAACC TTCGCTCCTG CACACTTCAG TGTCTCACT CTGTAGGGCT      120
CGCTGGCCTG GGCTTCTGCG ACCCGCGATC GTCCAGGAGA GGGCACTCGG CGCCCTTCCT      180
GGGGCGCTTC TGGGGCGGAA TTTGCTAGGC CGCCGTAGCA GCGGTGCCAG GTCAGAAGCC      240
GAGCCGGCCC GCTTTTCGTT CTTTAATTGG ACTCTGGCT AAGACGCTAC CGACACCCCG      300
TCAGGTGGTG GAGGAAGAAG GACAACAGGG AGAGGTCGAG GGCCGAGACG GCCTCGAG      358

```

(2) INFORMATION FOR SEQ ID NO:1131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

```

GAATTCGGCC TTCATGGCCT AAACATCCTC CTGCCACTTA GGAGGAAACA CCTCCCTATG      60
GTACCATTTA TGTTTCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC CAGCAAATAG      120
TTGGCACTCA ATAAAGATTT GCAGAATTTA ATACAGATCT TTTCAGCTGT TCTTAGGGCA      180
TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA TGTGGAGCTA      240
GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGACC TCGAG      295

```

(2) INFORMATION FOR SEQ ID NO:1132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATGAAAAAC | AAAACAAAGA | TGATGAAGCA | GAGTGGCAAG | 60 |
| AATTACAACA | AAGCATACAG | CGAAAAGAGA | GAGCTCTATT | GGAAACCAAA | TCAAAAATAA | 120 |
| CACATCCTGT | GTATAGCCTT | TACTTTCCTG | AGGTAGAGCT | GAAGTTTCCT | GCACCAGGCA | 180 |
| AGCCTGGAAA | TTATCAGTAT | ACTGTGTTTC | TGAGATCAGA | CTCCTATATG | GGTTTGGATC | 240 |
| AGATTAAACC | ATTGAAGTTG | GAAGTTCATG | AGGCTAAGCC | TGTGCCAGAA | AATCACCCAC | 300 |
| AGTGGGATAC | AGCAATAGAG | GGGGATGAAG | ACCAGGAGGA | CAGTGAGGGC | TTTGAAGATA | 360 |
| GCTTTGAGGA | AGAAGAGGAG | GAAGAAGAAG | ATGATGACTA | AGCAGTACTC | TGAATGGACC | 420 |
| ACAGTGTGTTG | CACATATTTG | CAATTTTTTG | CTGTTTGA | AGTGATCAT | AAACCAGAAA | 480 |
| CAGTACATAA | CAATCTCGAG | | | | | 500 |

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGATTATATT | GCATATATTT | TATAGAACAA | GGCAAGCAAA | 60 |
| ATATTTTAGT | ATTTGCAAA | CATGTTACTA | TAATTATTAG | ATCATAGTAC | CATTTATATA | 120 |
| AAGTATTAGG | TTGGTGCAAA | AGTAATTGCG | GTTTTGGACC | GTGAATTTTA | AATCATTATA | 180 |
| AGTCGGCTCA | GACACGTCTT | TATTAATCAG | AGCAGGAAGC | ATTATAATCA | ACACATTTTT | 240 |
| GCCAAATGAGA | AATAAGTTTG | TTCATTCCTG | TAGCTTAAAA | ATTCATGCTT | TGGGATTG | 300 |
| AAAGCATTTT | CTGCTTTCCA | AAAACCTGCT | GGTTTTGGAA | GCATTTTCCT | TTCAAATAGT | 360 |
| TGTCGAGATG | CTTGAAGAAG | TGGTGTTGA | CAAGAGGTCA | GGTGAATACG | GCGGCTCGAG | 420 |

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

| | | | | | | |
|------------|-------------|-------------|------------|------------|-------------|-----|
| GAATTCGGCC | TTCATGGCCT | AACTAGTCCT | GACTGCTTAG | ACAAAGTCAT | AGATTATGTT | 60 |
| CCAGGCATTT | TCNAGAAAA | CAGTTTTACA | ATCCAATACA | TTCTGGACAC | CAGTGATAAG | 120 |
| CTGAGTACTG | AGCTCTTTCA | GGACAAAAGT | GAAGAGGCTT | CCCTTGACCT | CGTGTGTTGAG | 180 |
| CTGGTGAACC | AGTTGCAGTA | CCACACTCAC | CAAGAGAACG | GAATTGAAAT | TTGCATGGAC | 240 |
| TTTCTGCAAG | GCACTTGTAT | TTATGGCAGG | GATTGTTTGA | AGCACCACAC | TGTCTTGCCA | 300 |
| TATCATTGGC | AGATCAAAAAG | AACAACCTAGC | TCGAG | | | 335 |

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGCAATTTT CCCTCAGGGG GGCTCCCATC TTCTTACACA | 60 |
| GAGAGGCAGC TGAGGCAGGA CAGTGGGGCT AACTGTAGAC CAGGCGAGGG CACGGGCTGC | 120 |
| TGGGGTGGCC CTGCTTCCCC AGTGATACATA TTGTATCTGT GTAACATTTT GTATATTCCA | 180 |
| GGGGTAGGGC CGCCCCCTGT ATCATACCTA GCAGAGGTTG GAGCTGGCAC ATGGGGAGGA | 240 |
| GGTTCTAATA ATTATTTGGG GCTGGGAAAC TTATTTATTG ATAGCATAGG ACAGAGCCCA | 300 |
| CTCTCGAG | 308 |

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCGAGGCTT CAGCGGGTGC CGCCCGCCTA GAGGGAGTGG | 60 |
| AGCGGCTAGA CAGCTTTAGG AACTGAAAGG TTCACGAGGC TGTAACGAAG AGTCGAGTTG | 120 |
| CTCCAGAGAG CCTACGACTA GATTTGCATC TTTACGTCCT GCGCGGAGGC TGCTACACAC | 180 |
| ATGCAGAAGT CATGCTGGTG GCCTGGACAG TGAAGGGAGA GAAGTGGATT TGGGAGACAT | 240 |
| TTAGGAGGAA CAGTAAGAGG ACCTTGTGCA TGAATAATTT GTTCCACAC TACAGAGTGG | 300 |
| GTAATAAGCA GATTAGTAAA AACAAATCTG CTTCACTTCA ATAACAGCCT CCTCCAATC | 360 |
| ATTTTTTCTC AACAACTTA TTTTCCAGCA GAAGAATCCC AGACTTCTTA GAGAACCAG | 420 |
| TGACTTTTGG CACCTTAAAT CTGTGAAATC CTCATGTTTT CTTCTGCCGT ATCCATAGTT | 480 |
| CAAACAAGAA CCTCGAG | 497 |

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAATTGTAT GCTGAAAAAT GGGAGTAACT ACATGAAATG | 60 |
| AGCAAATGCC TAGAAACAAA AAACCTACGA AGATTGTATC ATGAAGAAAT AGAAAATATG | 120 |
| AATAGACGTG TGTATTAGTC TGTCTCACA CTGCTAATAA AGACGTACCC AAGACTGGGT | 180 |
| AATTTTTTTG TTTTAAGAA AAAAGAGGTT TAATGGACTC ACAGTTCCAC GTGGATGGGG | 240 |
| AGGCCTTATA ATCATGGCAG AAGGCAACA GCACGTCTTA CATGGCAGCA GGCAAGAGAG | 300 |
| AATACTCGAG | 310 |

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGCAAATCA | CTTTTCCCGA | TTGAAAATAC | ACTTTACAAA | 60 |
| AGTGTTTTCA | GCTTTTGCAT | TGGTTAGGAC | TATACGGTAT | CTTTACAGAC | GGCTACAGCG | 120 |
| GATGTTAGGT | TTAAGAAGAG | GCTCTGAGAA | TGAAGACCTC | TGGGCAGAGA | GTGAAGGAAC | 180 |
| TGTGGCATGC | CTTGGTGCTG | AGGACCGAGC | AGCTACCTCA | GCAAAATCTT | GGCCAATATT | 240 |
| CTTGTTCCTG | GCTGTTATCC | TTGGTGGTCC | TTACCTCATT | TGGAACTAT | TGTCTACTCA | 300 |
| CAGTGATGAA | GTAACAGACA | GCATCAACTG | GGCAAGTGGT | GAGGATGACC | ATGTAGTTGC | 360 |
| CAGAGCAGAA | TATGATTTTG | CTGCCGTATC | TGAAGAAGAA | ATTCTTTTCC | GGGCTGGTGA | 420 |
| TATGCTGAAC | TTAGCTCTCA | AAGAACAACA | ACCCAAAGCA | CTCGAG | | 466 |

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATTTTTTTT | AATAGAGACG | AGGTCTTGCT | ATGTTGCCCA | 60 |
| GGCTGGTCCC | AAACTCCTGG | CCTCAAGCAG | TCCTTCCACC | TTGGCCTCCC | AAAGTGCTGG | 120 |
| GATTATCAAT | ATGAGCCACC | ATGCCAGATT | TGTCATTTT | TAAATATTTT | TATCTCTTCA | 180 |
| AGTCATCTTT | TGATCTTTTA | AAAAGCACCT | TCAAACAGCT | GCACCTTCCA | TTTGCACTAG | 240 |
| GAAATGAAGG | TAGTGATGGG | ATTGGCAATG | TTCCTGGCAG | ATGTTTCAGC | CCAAAAGCTC | 300 |
| TTCTACAGAC | CGGTTTAGAG | CTGGTGCCCT | ATGAGAATAT | TAGGGAGCTT | TTATTTTAAA | 360 |
| TTGAACTTTA | CCCTTGTCCT | TGCAAGGCAT | TCCTCCTGAA | TGCATCCATG | AATTTGTTTA | 420 |
| CTTTTGGCTC | AAACATATGA | GCCATTGTCA | TGCTCAGCAT | GTGCCACCTC | GAG | 473 |

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAATGAAGAT | CAGCTTCGTG | CAAAGGGTTA | TGACAAAACA | 60 |
| CCAGACTTCA | TTTTACAAGT | ACCAGTTGCT | GTAGAAGGGC | ACATAATTCA | CTGGATTGAA | 120 |
| AGCAAAGCCT | CATTTGGTGA | TGAATGTAGC | CACCACGCCT | ACCTGCATGA | CCAGTTCTGG | 180 |
| AGCTACTGGA | ATAGGGTCCC | AATATAACAG | ACAAATGGTG | AAACAGAGGG | ATACTCACTA | 240 |
| GGAAACAGAT | TTGGGCCAGG | CTTAGTCATC | TATTGGTATG | GATTTATCCA | GGAGCTGGAC | 300 |
| TGCAACCGGG | AAAGGGGCAT | CCTGCTCAAA | GCCTGTTTCC | CCACGTCCTC | GAG | 353 |

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGNCT | ACCAATTTCT | CATGGTTCCC | TAGGACCTTC | CTAGCTCCCC | 60 |
| AGGGAAAGCC | TNTGCTGTTT | CCCTTGNITT | CTTTTCACTT | GACAAACTCC | TACTCAAAC | 120 |
| TCAAAACCCA | ACTCAGGAAA | CATCTCCCTT | AGGAAGCTCT | CCTTAACCTT | TTCTGCTGGG | 180 |
| TCCCGCTGCC | TCTGCTAAAG | TCCACGTGAG | GGACTGCCAA | GANGTTTGCT | CTGTCTCACA | 240 |
| GATTGAGTGC | CAAGAGGGCA | GGGACNTCTC | TTTGAGAGAG | TTTAACCTCT | GTAACATAAG | 300 |
| CAAGTTTACT | TAATCACTGA | TAAACCACT | TTGTGCCTCA | GTTTCCCCAT | TTGTTAAGCA | 360 |
| TGAATTATCA | CTGTCACTAT | CTGCCAGGAC | TGTGAAGGGG | GTGTAAATGC | ATGAACATCA | 420 |
| TAAAGTGCTT | AGAAGCATGC | CTGGTACAAA | GAAAGTTCTC | TAGGNAAACA | ANAAACAAAC | 480 |
| AAAAAAAAC | AAAACAGAAA | TGTATCTAGA | GGTCAGATAC | CAGTCCCACA | TCGAGTGCAG | 540 |
| ATAATGGGCT | AAGTAACCAA | TGAGTCTCGA | G | | | 571 |

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTAAGGAGA | GCCTCTATCA | AAGGGTGGCC | TGGAGCAGAA | 60 |
| TATCAGGCTA | TGTGTATTAG | TTGTTTTCA | CACGCTATGA | AGAACTACCT | GAGACTGGGT | 120 |
| AATTTATAAA | GAAAAGAGGT | TTGATTAACT | CAGAGTTCCC | ATGACTGGGG | AGGCCTCAGG | 180 |
| AAACTTACAA | TCATGGTGGA | AGGCATGATA | GCAGGAGGGG | TGGAAAGAGG | GGAGTGTAC | 240 |
| ACTTTAAAC | CATCAGATCT | TGTGAGAACT | CACTCACTAT | CATGAGAATA | GCAAGGGAGA | 300 |
| AATCCACCAA | CTCGAG | | | | | 316 |

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTCAAGCGT | TTCACTGTGC | GATATCTGCG | ACTGCTCGCA | 60 |
| GTCTTGCTTT | CCTTGTTCT | CCCCTGGGGG | CTCAGGATTA | CGAGGCCTGA | AGTCTCTAGA | 120 |
| GGCTAAATGC | CAGGGGGATG | GAGTGAGCTA | CGAGGAAACC | ACTATTCCCC | GACCCAGCGC | 180 |
| CTACCACAAT | CTGTTTGAT | TACCACTGAT | TAATCGTCNA | GATGCTGAGG | TGGTACTGAC | 240 |
| GAGTCGTGAG | CTTGACAGCC | TGGCCTTGAA | CCAGTCCACG | GGGCTGCCTA | CCCTTACTCT | 300 |
| ACCCCGAGGA | ACGACCTGCT | TACCCCTGCT | CTTACTCCCT | TACCTGGAAC | AGTCCGGCG | 360 |
| GATTGTATT | TGTTGGGGG | ATGACCTTCG | GTCCTGGGAA | GCCGCCAAGT | TGTTTGACG | 420 |
| AAAAGTGAGC | CCCAAACG | AG | | | | 442 |

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCATCTACA GCTGTATTCT TGTTCCCTTG ATGGCACAAT | 60 |
| TAAACTGTGG GACTATATAG ATGGCATCTT AATAAAGACT TTCATAGTTG GATGTAAACT | 120 |
| TCATGCCCTC TTTACTCTTG CCAAGCTGA GGATTCTGTC TTTGTTATAG TGAATAAAGA | 180 |
| AAAACCAGAT ATATTCAGC TGTTTTCAGT GAAACTGCCA AAATCCTCAA GCCAGGAAGT | 240 |
| AGAAGCCAAG GAGCTGTCCT TTGTTTGGGA TTACATAAAC CAGTCACCA AGTGCATTGC | 300 |
| CTTTGAAAC GAGGGAGTAT ATGTTGCGCA GTACTCGAG | 339 |

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGCCAGGGG ACCCGGCCTC AGGTCTGTGG AGGTGCTTCA | 60 |
| ACAGCACGAT GCTCATTCTC TGTCCTAGT GTCTCCATAT ACTTCTCAT CTCTCCACC | 120 |
| ATCCAGGAGG GTAGGACAAA GGATTTCAT TCCTCTAGCT TCAGATCCAG GCATCCTCTG | 180 |
| TAATCATCAC TGGCCGCAAG GTCCCGGATG TCCTCCTCGA TGAGGAGGTA GGCCATCTTG | 240 |
| CCCCCTGTTG CCCGCATGTG ATGCTGCTCA GCCAGCCAGT GCTTATCCTG GGGGTCAGCT | 300 |
| GCATACTTAA AGAGGTGTGG GTGCTTGATG TAGATTCTTC CTCTGGTGCC CCCCATCCCC | 360 |
| AGGGCTTTGT TGGCTCGAG | 379 |

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGGAAAGCTG GGGGCAAGGA AGAGCCTTGA ATCTTGAGGT | 60 |
| GGGACGTTGA CTCTAAGATG TCCTTGAGCA GTGGAGCCTC CGGAGGGAAA GGAGTGGATG | 120 |
| CAAACCCGGT TGAGACATAC GACAGTGGGG ATGAATGGGA CATTGGAGTA GGGAAATCTCA | 180 |
| TCATTGACCT GGACGCCGAT CTGGAAAAGG ACCAGCAGAA ACTGGAAATG TCAGGCTCAA | 240 |
| AGGAGGTGGG GATACCGGCT CCAATGCTG TGCCCACT ACCAGACAAC ATCAAGTTTG | 300 |
| TGACCCCACT GCCAGGTCCT CAAGGAAAGG AAGGGCTCGA G | 341 |

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGGGGGGCC ATCTTTAATT CTGTAAGTTC ATGGTAAAGG | 60 |
| TATCTCCCCC CACACTGGGG CAGGCGCGG AATAAGCTCC AGCGTTCATG CGCCACTCAC | 120 |
| AGGACTGCTT ACCCCCACTG CACTTACAAT GCAGTCACAG AGTTACGGCA TGTCACCCG | 180 |
| TGTCCATGAC AAGCAACACC AAGTATAAAT AACAGAACTA CAGCAGAGCA AACTAAGATA | 240 |
| AATATGTTTT TGCATCGTCC TCCACATAGT TTCCTTTTAA AAAGAAGAGT CACATCCAGG | 300 |
| GGTCTATCCC TCGAG | 315 |

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGCTCTTTGG GGAGCTGTTT CAGAGGGAAA GTGGATGAAG | 60 |
| GCTGAAGTGG AGGCCAAATT AGGTGCTCTA GTACCTCTCT TTGGATCTCT TTCAGCTTTT | 120 |
| ACCTGTTTTA TATGCTGGGA TTTTATATAC AACTATTTGC AGAACTCAAC TGCTAAAGTA | 180 |
| AAACGGTGGG GAGGACTATT GGATTGGGAG ATCTCTAAAA TCCCATTTGGG ATTGATGAAA | 240 |
| AAGAGAACTA TCAGCAGAAA AGAGGAAGGG AACAAATGAG TTGTTAGTAC CTTAGTTCCT | 300 |
| AATTTATGTT CCTTTATTGT AGATTCTTTT CTGGCCACT ACACCTCCTTA GAAATATAAT | 360 |
| TCAACACTGT TTCTTTTACC ATTTTGTATG ATATGCAAAG TCCAGCTTTA CTCAGCCACA | 420 |
| TTTTGTCCAC TGGCTTATAT TTAATTATA TTTTAGGATA CAGATAACTC GAG | 473 |

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

| | |
|---|-----|
| GAATTCGGTC TTCATGGCCT ACTCTGGGTT GCCTGTGGTC ACTTCTGGTT GCCTAGGACT | 60 |
| AGAAGGCTCA GATTTTCAGT GTCGGGACAC TCCCATTCCT CATCAAAGAA GATCAATTGA | 120 |
| ATGCTGCACA GAAAGGAACG AATGTAATAA AGACCTACAC CCTACACTGC CTCCATTGAA | 180 |
| AAACAGAGAT TTTGTTGATG GACCTATACA CCACAGGGCT TTAATTATAT CTGTGACTGT | 240 |
| CTGTAGTTTG CTCTTGGTCC TTATCATATT ATTTTGTTAC TTCCGGTATA AAAGACAAGA | 300 |
| AACCAGACAA CTCGAG | 316 |

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

| | |
|--|-----|
| GCCACGAAAG GTACCCCTGA ATTCTGGACT CATAAAATCT CTTAGATAAT ACATATTTGT | 60 |
| TGTTTTTAACC CACTCAGTTT TGCATTGGTT ACACAGCAAT AGAAAATAAA GGAGGCAGAT | 120 |
| GAAATTGATG GAGAACAATT GCAACGAAAA CAGAATACAC AATGCACGAG CCTGTGTCAG | 180 |
| GAATGACAGT GCATTCCACG GAAGAGTTGC ACAGAGAGAG ACGCCGCTCG AG | 232 |

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGCCTTTAAC ACTTGATATA AAATCCAAGC ATTTTTCAGA | 60 |
| CCTCAACCCA GAATAGTAGA TACCTGAAAT TAAGATTCTT ATTGGTGAGA AACAAAGATCT | 120 |
| GTATATTTCC CTATCCCTAT CCCCAAATGC CAGTGGGTCA TTTTCCCAT GCCTAGCTCC | 180 |
| ATTCACAGCT AATATGTGGA TTGAGGCTTT ATTCCAAAAC ATTTAGGTTT TATATTCTTC | 240 |
| CCTAGCCCTG ATTAGCAGTG CTCATCTTTG AAGATCATTG TGACTTTTCA GACTATTGTA | 300 |
| GTGATGGCTC AACCTGACCC CTTCTCCTCC TTTCAGGATT TGGCAGAGAG AACGGCCGCT | 360 |
| TCTCGAG | 367 |

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

| | |
|---|-----|
| GAATTCGGCC TTCATGGACA GCACAGTGGC CAAAGAAGGC ACTAATGTAC CATTAGTTGC | 60 |
| TGCTGGTCTT TGTGATGATG AAGGCATTGT GACTAGCACA GGCGCNAAAG AGGAAGACGA | 120 |
| GGAAGGGGAG GATGTTGTGA CTAGTACTGG AAGAGGAAAT GAAATTGGGC ATGCTTCAAC | 180 |
| TTGTACAGGG TTAGGAGAAG AAAGTGAAGG GGTCTTGATT TGTGAAAGTG CAGAAGGGGA | 240 |
| CAGTCAGATT GGTACTGTGG TAGAGCATGT GGAAGCTGAG GCTGGAGCTG CCATCATGAA | 300 |
| TGCAAATGAA AATAATGTTG ACAGCATGAG TGGCACAGAG AAAGGAAGTA AAGACACAGA | 360 |
| TATCTGCTCC AGTGCNAAAG GGAGTCTCGA G | 391 |

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGCACTTGTC | TCATTTTAAT | GTAAAGATT | GCTTCCATT | 60 |
| TCCTACAGGC | AGTCTCTCTC | TTCCTCACAG | TCCCCTGTG | CAGGTGCTAT | TGTTACTCTT | 120 |
| ACGAATATTT | TCAGTAATGT | TATTTTCTTC | TAAGTGAAAT | TTCTAGCCTG | CACTTTGATG | 180 |
| TCATGTGTTC | CCTTTGTCTT | TCAAACTCCA | AGGTTCCCCT | GTGGNCCTCT | CCCTTACCCT | 240 |
| GGGAAGGCCT | CTTGGAGACC | TTACCCCTTG | CTGTTTGGAC | TTTGTATACT | TTAAATAATT | 300 |
| TAATAACCT | TAATTACTTA | AAAAAAAAAA | AAAAAAGCTT | TATGATTTTC | ATAACTTATT | 360 |
| GCTGATTTTA | ATGGATTGTT | AATTTAGTC | CTGTAGTTT | ATTTTATGTT | TAGATAGGGC | 420 |
| TGGGCAAGGA | AAAAGAAAAT | AAAGACAACC | ATACTCGAG | | | 459 |

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACTCCTTCAG | ACTACAAGCT | CCACAGAGCC | GCGGGAGGAC | 60 |
| GGTTGCCTGG | TATTATTAGC | AAGCAGCAA | TATGGCGGTG | GCGCGCGTGG | ACGCGGCTTT | 120 |
| GCCTCCCGGA | GAAGGATCAG | TGGTCAATTG | GTCAGGACAG | GGACTACAGA | AATTAGGTCC | 180 |
| AAATTTACCC | TGTGAAGCTG | ATATTCACAC | TTTGATTCTG | GATAAAAATC | AGATTATTAA | 240 |
| ATTGGAATA | CTGGAGAAAT | GCAACGATT | AATACAGTTA | TCAGTAGCTA | ATAATCGGCT | 300 |
| GGTTCGGATG | ATGGGTGTGG | CCAAGCTGAC | GTGCTTCGT | GTATTAAATT | TGCCTCATAA | 360 |
| TAGCATTGGC | TGTGTGGAAG | GGCTCTCGAG | | | | 390 |

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACGAATGTGG | CCGGGTGGGA | CCCGGACATA | CGAGAGATTG | 60 |
| TCCTCATCGT | GGCCATGATG | ACATTGTCAA | CTTCGAGAGG | CAGGAGCAGG | AGGGAGAGCA | 120 |
| GTACCGTTCC | CAGAGGGACC | CACTGGAGGG | CAAGCGGGAC | CGGAGCAAGG | CCAGGTCTCC | 180 |
| GTACTCGCCA | GCCGAGGAGG | ATGCCTTGTT | TATGGATTTA | CCCACTGGCC | CAAGAGGCCA | 240 |
| GCAGGCACAG | CCCCAACGGG | CAGAGAAGAA | TGGAATGCTG | CCTGCCTCAT | ATGGCCCAGG | 300 |
| AGAACAGAA | GGGACTGGTG | GGTACCAGCG | GGCCTTCCCT | CCCAGGACCA | ACCTGAAAAA | 360 |
| ACACAGCCAA | AGGAAGAGCA | ATCTGGCCCA | GGTGGAGCAC | TGGGCAAGGG | CCCAGAAAGG | 420 |
| GGATAGCAGG | AGTCTTCCCT | TGGACCAGAC | GCTTCCTCGC | CAGGGTCCTG | GCCAATCCCT | 480 |
| GTCCTTCCCA | GAAACTACC | AGACTCTTCC | CAAGAGCACC | CGAAACGCCT | CGAG | 534 |

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AATGGATCTA GTCACCTTTCA GATTTCAATT TGAGGTAAAG | 60 |
| TATATAAAGC ACATCCCAAT TTTATATGCT GCCTTGAGAA AATTACAGGA TGCACGGCAA | 120 |
| TTTGTAGGAA TTTCAAATGG GATCATTTAA ACATTTGAAA AATTATTTTA AAAACCATCT | 180 |
| AGTTTGCTTT TGGATTTTAG ACATTAAAGC CTATGTTGTC TTGTTAACAG GGGTGAATG | 240 |
| TATAACCATC AGATTCAGCA TGTGATTTC CTTTGAATC TGAGTATTC TCCCTATCT | 300 |
| TCTTTGAGTC ATTTTGGAG CAGACTGTCA CCAGTATTGA TAACTAAGCA TTAAAGGGAA | 360 |
| AAGTTCATT GCAACTATGC ATTGGTTTCC TGGAAGAACT TTTCTTTGT TTTAGTGAAT | 420 |
| GAAGAGGCTT GATGGGATCA CTTACTGTAA CTCCTTCTAC ATAAGGACCC CTTCTGCAAG | 480 |
| CAGAACACAA AAGAACACGC TCGAG | 505 |

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATGTTATTGG GAAGGACCCA GAGAACAAAA AGTTGAATAC | 60 |
| GGAAAAGAAA ATAGGATTTG CAAGAAGCAC NTTTTTTTTT TTTTTTTTTT TTTNGAGACA | 120 |
| AANTCTCGNT TTGCANTCCA GCCTGGGTGA CAAGAGCAAA ACCTNGTNTC CAAGNAAAAA | 180 |
| AAAATACAGT TTTGGTGATA ATACAGTTTG AAAGTAATTA GCATGTGGAT AGTCATAGAA | 240 |
| ACCACAGGCA TCAATGAAAC TGGCTAGGAG AAAGGACACC AAGAGGAAAT GGCCAGAGGT | 300 |
| AACAGGAAAA TCAGGGGAGT GTGGTTTACA GAAGCCTGGG AAGTGCTATT TCAAGAAGAG | 360 |
| AGTGGGTGGA AATTGTTAAG TGTCTAATGC TGCTCAGAAG CCAAGCAAGA TAAAGACAGA | 420 |
| AGAATCTAGT GGGAACTCGA G | 441 |

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGCAGAACCC GACCAGGGGA GCCTTGCCCTG TGTGTTTCAG | 60 |
| GTGCTCTGCG ACCACTTCTA TAAAACCTAA AAAAGGAGAT TGCTCTGATT GCAACAGGTG | 120 |
| TGGGGGACCA GTATCCCATC CCATTGGCCC TGCCCTCCCA CCTGTAAGGC AGAATATGGT | 180 |
| TGGGAAATCA TTGCCATATG CAGAAGGGGT CACTGAGGGG TTTTAAACAA CAGTGACATG | 240 |
| CTCAGTTCTC TGGGTTGAGG CATCATCACC CTGGTGGCCA TGTGGAGGAT GGAAGGAAA | 300 |
| AGGCATTTCAG TTAGAAGACC TCTGCAGGAG TCCAAGGAAG AAACAGGCAA ATCTGCAGGA | 360 |
| GGCAGGCATA TCCAAGCTCG AG | 382 |

(2) INFORMATION FOR SEQ ID NO:1159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

```

GAATTCGGCC AAAGAGGCCT AGCCTCGGTG ATTTCCAGTG GAAGAATGTA GGTCCCAATA      60
CCACAAGCAC AGTCATTAGC ACAGATGCTT TTAGGCCAGG AGTTCGATAT GACTTCAGAA      120
TTTATGGGTT ATCTACAAA AGGATTGCTT GTTTATTAGA GAAAAAAAC AGGATACTCT      180
CAGGAACCTG CTCCTTCAGA CAACCCTCAC GTGCTGGTGG ATACATTGAC ATCCCACTCC      240
TTCCTCTGA GTTGGAAAGA TTACTCTACT GAATCTCAAC CTGGTTTAT ACAAGGGTAC      300
CATGTCTATC TGAAATCCAA GCGAGGCAG TGCCACACCG ATCTCGAG      348
  
```

(2) INFORMATION FOR SEQ ID NO:1160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

```

GAATTCGGCC AAAGAGGCCT AGAAAACTG AAAAAATAAG AAACCTTAGA GAAAAAGAGG      60
AATCAGTGCA GGCTAGGGGA ATGAACCTGG TAATCCAGTA GTCTTTCCTT GCCAGCATT      120
TGATTGATAA GCTAAGTGTC TGCTTTTCT CATCCCTTAT TTTTGGCAG GAAACCAGTA      180
TTTGATACT TGAATGCCTT CTTTCTATCT TAAGGGAGAA GCCTTCTTAA ACTTCAAGTG      240
TGAAGTAGAT CCTTTAGGTA TAGGATGAAA AATTAAGTGG GACTATTGT GAATTACTAA      300
ATCGCAACTC GAG      313
  
```

(2) INFORMATION FOR SEQ ID NO:1161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

```

GAATTCGGCC AAAGAGGCCT AGGAGCCTAG AAAAGAAGAA AGGTCTATTT TTATAAAAC      60
TGATGAAATA CTTGTGGCAG GGAGTCCTCG AG      92
  
```

(2) INFORMATION FOR SEQ ID NO:1162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

| | |
|---|-----|
| GAATTCGGCA AAAGAGGCCT AGTGCATAAG GAATCACTGT GTACAAACTG GCCAAGTGCT | 60 |
| TCTGTAGATA ACGTCAGTGG ACTAAATATT CGACAGGCCA TAACTTGAGT CTATTGCCTT | 120 |
| GCCTTTATTA CATGTACATT TTGAATTCTG TGACCAGTGA TTTGGGTTT ATTTGTATT | 180 |
| TGCAGGGTTT GTCATTAATA ATTAATGCCC CTCTCTTACA GAACACTCCT ATTTGTACCT | 240 |
| CAACAAATGC AAATTTTCCC CGTTTGCCCT ACGCCCTTT TGATACACCA CTCGAG | 296 |

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTAAAAATA AGTGTCTAAT ACTGTGTATT CATATAGCCT | 60 |
| TTATATCTCA ATACGTGCTT ATCTGTTGGT ATACCTTAGA GAAATAACCC ACCATCAATG | 120 |
| AGAAGAAGGA AAGGCAGGAG GAAAAAAGTT TATATAACAC TTAAAAATGG TAGATTATTT | 180 |
| GTGGCCATTT GAATTACTG ATTTGAAGTT CTAAAGATG CTGAGCCATG CCTTACATAG | 240 |
| TTATTTTAGA ATCTAAAGTT GTTCTGTATT TGCATAACGT TTCTGTTCTT TTTCTTCTTT | 300 |
| AAACCCTGAA AGTGATAGAT GGAAGGAGG AACCAGATAT TTGGCATGGT CTGACAAAAA | 360 |
| TTAACTTGTC AACTCGAG | 378 |

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTCCAGGGT ACTTTTCCCC TAGGCCTGAC CTTTATGTGT | 60 |
| CTTTTGTGCC ANACATATTT AAGACCAGAG GAAAAAAGCA ATTGCTTTAG TTTCTATGTT | 120 |
| TGGGTAACAA AATCTACCCA CAGACAAGAG AATAACAAAA ACCAAACAGT ACAGTGGGAA | 180 |
| ATATACCAGA AAGGAAAAAA AAGATCATCA CATTAAATGT AAATGAGGTA AATTTTATA | 240 |
| ATAAAGAATC TTTTATGAAG AATGTCTCAA ACCAAATATT GTACTTTCCA ATTTCTTGGG | 300 |
| CACTGGGGAT GCTGAAGTGT AGTTAGATGA GTATATAACC CTATAGGGCT CTCGAG | 356 |

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTCTTCTGC CCCCCTATGA AGTTTGAGTT TCAGCCCCAC | 60 |
| ATGGGGGATA TGGCTTCCCA GCTCTGTGCC CAGCAGCCTG TCCAGAGTGA GCTGGTACAG | 120 |
| AGATGCCAAC AACTGCAGTC TCGCTTATCC ACTCTAAAGA TTGAAAACGA AGAGGTAAAG | 180 |
| AAGACAATGG AGGCCACCCT GCAAACCATC CAGGACATTG TGAAGTCCGA GGACTTTGAT | 240 |
| GTGTCTGACT GCTTCCAGTA CAGCAACTCC ATGGAGTCCG TCAAGTCCAC GGTCTCTGAA | 300 |
| ACCTTCATGA GCAAGCCCAG CATTGCTAAG AGGAGAGCCA ACCAGCAAAT CCTCGAG | 357 |

(2) INFORMATION FOR SEQ ID NO:1166: "

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGACAGGCGG ACCCAGAGAG ACTTGCACTA CGTGGAGAAG | 60 |
| ATGGAGAACC AAATGAAAGG ACTGGAGTCC AAGTTCAAAC AGGTGGAGGA GAGTCATAAG | 120 |
| CAACACCTGG CCAGGCAGTT TAAGGGCTAA CTTAAAAGAG TTTTTCAT GCTGCAGTGA | 180 |
| CTGAAGAAGC AGTCCACTCC CATGTAACCA TGAAAGAGAG CCAGAGAGCT TTTGCACTA | 240 |
| TGCATTTTTA CTATTATTTT CCAATACTTA GCACCATTTT ACTAAGGAAC CTTGAATACA | 300 |
| ACGAGGATCC TCCTTTGCAT GCGACTGTAG CTGCATTTCA TGAATAGTTT GAACCCTTGT | 360 |
| CAATGCAATC TCGAG | 375 |

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

| | |
|---|-----|
| GGCTTATTGA TGACTCTTAT TTAAATTATG TTTTAGCAA TGATAAGTTA CAATATAATA | 60 |
| GCTGGAGATA CTTTGAGCAA AGTTTTTCAA AGAATCCCAG GAGTTGATCC TGAAAACGTG | 120 |
| TTTATTGGTC GCCACTTCAT TATTGGACTT TCCACAGTTA CCTTTACTCT GCCTTTATCC | 180 |
| TTGTACCGAA ATATAGCAAA GCTTGGAAG GTCTCCCTCA TCTCTACAGG TTAAACAACT | 240 |
| CTGATTCTTG GAATTGTAAT GGCAAGGGCA ATTTCAGTGG GTCCACACAT ACCAAAAACA | 300 |
| GAAGACGCTT GGGTATTTGC AAAGCCCAAT GCCATTCAAG CGGTGCGGGT TATGTCTTTT | 360 |
| GGGGACGTTT TCGAG | 375 |

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

```

GAATTCGGCC TTCATGTCTC TGCAATCTGA AAATAGTGCC TTTTACCAAG AAGAGGACAG      60
AATTGGCGTT TGGAAGGCTG AGGGTCATGG TGTAAGGGCT TTTGAGTCAA AATCTTGGTG      120
TCAAGCAGAT GAGGCTGCAA CACAGACCTG TGACCAAAC TGTGTGGAGC GTGTGGTGGA      180
CACGCAGGGG ACTGTGCAGA GGACAGATGG CCTAAAGCTT AGCATGGCAC AAGGAGTGCC      240
CCCCGATGGC AAGTCTCCCA GTCAACTCCA GATCTCTTCA CAGTAACTGT GTTTCCTCCG      300
CATTTATTTT CAACCTGCAC AGAGGAAGAA GAGAGGGAAA CAAGCCCAGG TGACAAAACA      360
GAGGGTGAAA TATGTGTGAA GAGTTCAGTC AGTGTGTAC GAGACCAGCT GAGTGACCCT      420
CAAAGGTTAG AAGGTAGTGA AAAAGAATCA CTGCAAGCAA AGTATAGTGA GACAAGTGAA      480
GATGACATAG AGACTGTCAA GTCAGATTCT AAAACAACCT ATGAGTGGA AACAGGNACA      540
CAAAAACCTCG AG

```

(2) INFORMATION FOR SEQ ID NO:1169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

```

GAATTCGGCC TTCATGGCCT AGAGCGGAGT AAATTCTCCA CAAGCTGGGA ACAAACTCG      60
TCCCAACTCC CACCCACCGG CGTTTCTCCA GCTCGATCTG GAGGCTGCTT CGCCAGTGTG      120
GGACGCAGCT GACGCCCCGT TATTAGCTCT CGCTGCGTCG CCCCGGCTCA GAAGCTCCGT      180
GGCGGCGGCG ACCGTGACGA GAAGCCCACG GCCAGCTCAG TTTTCTTCTA CTTTGGGAGA      240
GAGAGAAAGT CAGATGCCCC TTTTAAACTC CCTCTTCAAA ACTCATCTCC TGGGTGACTG      300
AGTTAATAGA GTGGATACAA CCTTGCTGAA GATGAAGAAT ATACCATATT GAGGATATTT      360
TTTTTCTTTT TTTTTCAGG TCTTGATTG TGGCTTACCT CAAGTTACCA TTTTTCAGTC      420
AAGTCTGTTT GTTTGCTTCT TCAGAAATGT TTTTACAAT CTCAAGAAAA AATATGTCCC      480
AGAAATTGAG TTTACTGTTG CTGTATTG GACTCATTG GGGATTGATG TTACTGCACT      540
ATACTTTTCA ACAACCAGAA CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

```

GAATTCGGCC AAAGAGGCCT AGGGAGTCAA TCATGATCNT TTCATATATG CTGGCNATAG      60
AAAATGGTCT CGGTGAAGTA ATGGTCTGTC TGCAAGCAT GACATCCTTG CCTGTGTTAA      120
GTTTTTGTG CTCTTCTGGG ATGTTGATCG TGACGTCTTG TCCGGGATTG AGAAGCTTCT      180
GTTGCTCTTC TGGGATGTCA TTCATGATCT CTTATATAT GCTGGCTATA GAAATTGGGC      240
TCTGTGAAGA AATAGTGTGT CCAAAACCTT GGTACAGGCC CCCTGGGGAG GGTACCTTGT      300
AAGAACCAGA AGTTAGATCT TGTGAAGAAG AAGAAAGTAG GCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

```
GAATTCGGCC TTCATGGCCT ACTTTTGGG GACTGGTACT GGAGAAAAAT CTGAGAGCAA      60
AAGTGCTTGG CTAAATTCCT TTTTCTTCT TTTAGTTTTT GAAATCATGA ATCCTGTTTA      120
TAGTCCTGGA TCTTCTGGGG TTCCCTATGC AAATGCCAAA GGAATTGGTT ATCCAGCTGG      180
TTTTCCCATG GGCTATGCAG CAGCAGCTCC CTGCCTATTC TCCTAACATG TATCCTGGAG      240
CGAATCCTAC CTTCCAAACA GGTTACACTC CTGGCACACC TTACAAAGTG TCCTGTTCCC      300
CCACCAGCGG GGCTGTGCCA CCGTACGTCC CCGTCGAG      338
```

(2) INFORMATION FOR SEQ ID NO:1172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

```
GAATTCGGCC TTCATAATCT CCTGCTCTTG AGAATGTGCC GATATGTCAA AATATCTACT      60
GAAACTGAAG AAAGTGAAGG ATCCCTACAC TGCTGTAAGG ACCAAAATAT TAATGGGAAT      120
GGCCCAAATG GCATACATGA AGAAGGCTCA CCAAGTGAAA TGGAAACAGA TGAGCCAGAT      180
GATGAATCCA GCCAGGATCA AGAACTTCCC TCAGAGAATG AAAACAGTCA GTCTGAAGAT      240
TCAGTTGGAG GAGATAATGA TTCTGAAAT GGATTATGTA CCGGGATACT CGAG      294
```

(2) INFORMATION FOR SEQ ID NO:1173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

```
GAATTCGGCC TTCATGGCCT ACATAAAGA ACGAAAAGGA AGGAACTTCA GTCAACATAT      60
TTTCATTGAC TCCTTAGTAC AAGGGAACCT TAATGACCAA CAGATCCTAG AAGACAGTAT      120
GATATTTTCT CTGGCCAGTT GCATAATAAC TGCAAAATTG TGTACCTGGG CAATCTGTTT      180
TTTAACCACC TCTGAAGAAG TTCAAAAAAA ATTATATGAA GAGATAAACC AAGTTTTTGG      240
AAATGGTCCT GTTACTCCAG AGAAAATTGA GCAGCTCAGA CTCGAG      286
```

(2) INFORMATION FOR SEQ ID NO:1174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAATATGAAA | AGACTAGACA | TACAGAGATA | TTTATCATAG | 60 |
| CAAAAAGTTG | CAAGTACTGG | GGATTGACAA | AATTATCACA | ATGGTTATAT | TATTATTATT | 120 |
| ATTATTATTA | TTATTTAATC | AATCAGTGTC | TTGCTTTGTT | GCCCAGACTG | GTTTCAAATC | 180 |
| CCTGGCCTCA | CGTGATCCTC | CCGCCTCAGC | TTCCCAAATT | GCTGGGATTA | CAGGCATGAA | 240 |
| CCACCGCGCC | TGGCCTATTG | TTCTGCCACA | TCTTTCTTTT | ATTTTGTAGA | GAGAGTCTTG | 300 |
| CTTAGTCCAG | GCTGGAGTAG | AGTTGTGCCG | TCATAGCTCA | CTGCAGTCTC | AATTCTTGG | 360 |
| GCTCAAGCAA | TCCTCCTGCC | TCAGCCTCTT | GAGTAGCTGG | GAATACAGGC | ACACTCTCGA | 420 |
| G | | | | | | 421 |

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TCATGGCCTA | GTGCTTAAAA | GCTGTTCTCA | TAAGAATTCT | ACTGGCCTGT | 60 |
| ATCTACCCAA | CCACTTTCTA | TACCTCTCTT | CCAACCAAAA | GTCTTAATAT | GGGAATATCC | 120 |
| CTCACCACGA | TCCTAATACT | GTCAGTAGCT | GTCTGCTGT | CCACAGCAGC | CCCTCCGAGC | 180 |
| TGCCGTGAGT | GTTATCAGTC | TTGCACTAC | AGAGGGGAGA | TGCAACAATA | CTTTACTTAC | 240 |
| CATACTCATA | TAGAAAGATC | CTGTTATGGA | AACCTAATCG | AGGAATGTGT | TGAATCAGGA | 300 |
| AAGAGTTATT | ATAAAGTAAA | GAATCCAGGT | GCACTCGAG | | | 339 |

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGGGTCACCG | GGTTCGGGGC | TAAAGAAGCC | CCCGCGCTCC | 60 |
| CTAGAATCCA | GGAACGGGGA | CTGGCAGAGG | CCTGGGTAGG | AGTCCATTGG | GCTGCTGGAG | 120 |
| GGCAGATTGC | CAAAGGGGAG | TCCACCTTGA | AGAAAGGGCC | TCTGCAGTGG | CGTACGGCTG | 180 |
| CCTTNTAGGC | CAGGGGTTCC | ACAACCCAGA | TGCTGTTCTC | GTTCAGAGCC | CAGAACATCC | 240 |
| TTGAAGAGCT | GCTGCAGGTC | CTTGGATTCC | ATCTTGGGCA | GTTCTCTGTG | GAAATCCTGT | 300 |
| CTAAGTCAGA | GCTAAGCATC | CCTTCACCTG | GGGTGCCTGG | CTTCTCAGGG | TCACTGGGCA | 360 |
| CTGGGGATGC | CTTCACGCCC | CCATCCTCAG | GTCCTGGTGT | ATCGGCTTTG | CCCTCGAG | 418 |

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

```

GAATTCGGCC TTCATGGCCT AAAGAACCCC GTGGTGATGG TGGACGAGAT TATGAGCTCC      60
AGCCCTCCCA AGTTCACCTT CCCTGAAGCA GGCTTACGAA TCATGATCAC CAATAAGTTT      120
GGACCTAGGA CCCGACTACG GATGGCCAGC AGGATCATCA TTAATGAGCG GCAGAGACTG      180
ATCAACTCGG CCAATGGTGT GAGCAGTAAG CCGCTTCAAA ACGGGAGGCA CGAGAACATT      240
GAGAACGGGA ATGTTCTGT GGAACACCCC GAAGACCCTC AGCAGAATCA GGAGCAGCAG      300
CCGCCGCCAC AGCCACCACC GCCAGAGCCA GAGCCTGGTG AGGCTGACTT CCTGTCCCCC      360
TTCTCCGTGC CGGGCTGGAG TGTAGTGGCA TGATCTCCGC TGAAGTCAAC CTCCGCTTCC      420
CGGGACTCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

```

GAATTCGGCC TTCATGGCCT AGTTGTTGTA AGCATATTTA TGGTAATTTG TTAGTGCACC      60
CTTGGGAAAC TAACACACCA AGGTTTCATGG ACAGCATGAA AAAGAAAAAC CATAGGCCAA      120
TATTTGTTAG GAAAAGACAC AAAAGATCTA AACAAATATT AGCTCCTACC CCTCCAAAAA      180
AGCAAATTCA ATCCAGTAAG GCATTTGAAA AATATGTCAT GACTAATGAA CTTATTTAAG      240
TTTACCCAC AATACAAGGA TGGTTTAAAT TTTACAAAAA GTATTCATTT AATTCATCAT      300
ATTGATAAAG GAGGAAATTT AATTAAGATA ATCTCTTGAT TGTCTCTTCA TATCTTTTGA      360
TTATCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

```

GAATTCGGCC TTCATGGCCT AAAAAATACA AAAAAAAAC NNNANNGAAG AAAAAAGAAA      60
AACTACCAG CCTGAAAATG CATAGTGTTC GCTACCTTAT TGCTTTTAGC ACATCTAGAA      120
AGACACTAAA CCCAGTGAGA TTGCAAGTTT CAAAATATTG TGTGTATAT GGCTTTGCTT      180
AAACGGATAT ATTTGTTTCT GAGTGAAAAC TTTTACGTA GAGGTTTATT TGTAGAGGCT      240
TGTAAGTTA AGTGTAAGTT TTAGTGTGTG TGTTAAGTTG TTCTTACCCC GCATTAGCAC      300
TCGAG

```

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

```

GAATTCGGCC TTCATGGCCT AGCTGGGAGG TGTAGGTTGT AGCGAGCCGA GATCACGCCA      60
CTGCACTCCA GCCTGGGCAC TATTGAGCAC TGAGTGAACG AGACTCCGTC TGCAATCCTG      120
GCACCTCGGG AGGCTGAGGC TGGCGGATCA CTCGCGGTTA AGGGCTGGAG ACCGGCCCGG      180
CCAACACAGC GAAACCCCGT CTCCACCAA ACCAGTCAGG CGTGGTGGCG CGTGCCTGCA      240
ATCGCAGGCA CTCGCAGGC TGAGGCAGGA GAATCAGGCA GGGAGGTTGC AGTGAGCCGA      300
GATGGCAGCA GTACAGTCCA GCTTCGGGCT CCGCATGAGA GGGAGACCGT GGAAAGAGAG      360
GGAAACCGTG GGGAGAGGGA GAGGGAGAGG GAGAGGGGAG CGATTCTGGT GTATCTTAAC      420
TTGGATTCT ATCCTGTTTG GGTTCGCTCA GCTGAATCTA TAGGTTGTG TATAATACCA      480
AAGTATTTTG TATTAGTGGT TACAACGCAA AGTTGGATCG TGAAGTCAAT TTTGTGGCTT      540
ATGACTAGTA TTATGATTGG TTTTAATAG AATAGAAAAT GAAAATATAT CCCAGGTATC      600
TCGAG                                     605

```

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

```

GAATTCGGCC TTCATGGCCT AGGAGAGTGG TGATGGTGGC ACAACAATGT GAATGTAATT      60
AATGCTACTG AGTTGTATGC TTAAAAATGA AAAATTTTAT GTTATACACA TTTTATGACA      120
AAAATTAATA GATGTATTAA TAAGATTAAA TGGGTTGTTT TAATGTTCTG TTAAATCAA      180
ACGCTGAGGG CATTAATAGA GATTCTTATT TACCCACATG TCCTTTTAAA ACAAGAACCC      240
TCTTTAATAT GTGTTTCTT CTGGTTTATA GAACATATTT TAAAACGGGC TTAATATTCA      300
ATAATATCAA TTGATTATTG AGGAATACAA GTTAATTAAA TTGTGCAAGT CAGTTGTTTG      360
GCCTTACTTC ATGCTTTTGG TGAACACTGA TGCAGTACTA GAATTACTCT TTTTGATAAA      420
TTGCCAAAAG CAGGCCACCT CGAG                                     444

```

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

```

GAATTCGGCC TTCATGGCCT ACTGTTTCAA AAAAAAAAAA AGGAATCCAA AGAAAAAAAAAT      60
ACATCACCTG CAAAAGGTGA AGAGAGAAAG GAAGCTTTTT CTCTAAAAAT GGTGCAGCTA      120
TCCTCTGAAC CAATTCCTT CGGTTTAATG TACCTGTATC TTGGGGTTTT TTCCACTTA      180
ATTTATCCTG GAGCTCTTTC CATAACAACA CTGGAAAGC ACTCTCATCC TTTTTCCT      240
GCTGAACAGA ATTCCACTGT GCGGATGGAA CTCGAG                                     276

```

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGCATGTTGA GATAACTTCT GGGATTAAAA TAGTCTTTTG | 60 |
| CTTTACTTTT TTGGTTTCCT AAAACAACCTT TATTGACTTT TAGTCCATAC TGTTATATTT | 120 |
| TTGTCTTAAA GAAAATTAA ACTACAAATA CCAAAAGAAA ACATTTTAAA TTTAGGGATG | 180 |
| AGACTTTGGT GTATCGTGGG TCTAGGTTTA ATGAACACAT CTGGGGTTAA GTTGGCATT | 240 |
| CTTCACATCT CCACACCCAC ACCAACCATC ACAGCCCCC AAAATCTCGA G | 291 |

(2) INFORMATION FOR SEQ ID NO:1184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGGGGAGGC AGAGGCTGTA GTGAGCCGAG ATCGCGCCAC | 60 |
| TGTACTCCAG CCTGGGCAAC AACAGTGAAA CTCCGTCTCC AAAAAAAAAA AAAAAAAAAA | 120 |
| AAACTTGTT TTCCCTTGT AATTGGTTT TCCTAAAAAT TTAGTATTT CTAGAGAACA | 180 |
| TTTTTTCCC AGGCTGTAA CTGGTCTGA AAACAATCTT ACAGTAAGTA TAATTTAAAA | 240 |
| CATACCTCCT TTTCCAAAAG CTCATTGTGT ACCAAGCAAG CACGTCTGTA GTTAAAATTT | 300 |
| GTTACTGAGG TTGGTTCAAG GTAAGAAGAA TGGAGAATAT TTACAACATC TTCAAATTCT | 360 |
| CGAG | 364 |

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAGTAAAGG TGGGATTACA GGTGTGTGCC ACCACGCCTG | 60 |
| GCTAATTTT TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT | 120 |
| AAACTCCCGA CTTCAAGTGA TCTGTCCACC TTGGCCTCCC CAAGTGTGGG ATTACACGTA | 180 |
| TGAGTCACCA AGCCCGGCCT GTATCCTTTA TAAAAGAAA CAAACAAACA AACAAAAAAC | 240 |
| CCTTTCTTG ACTGACATCC CTTTCAGCT GCAGCCCTGT TTCTTTGCTA CCTTTGTAGC | 300 |
| AAAATTCAC AGGTTGTTC TACTTGCTGT TTCCAGTTT TTGGTTTTT TCCTTCCTA | 360 |
| GGAAATGAGA GGCCCATGCT CGAG | 384 |

(2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCGAGGGGG | TCAATTCCTG | GGGGCTCTTG | ATATTGCTCA | GAGCTCTGGA | GAAGTGTTCA | 60 |
| TCCACTACGC | TGCTGATGTC | CCCTTGGAAG | TAGGTGAAAA | GGACACACCG | GGAATTCCAT | 120 |
| TCCGTCTTTA | TAGGCTTCTG | TTTGCCTTTG | GGCAGCCGGA | TGGCAGTCTT | CTTCATTCTT | 180 |
| TCCATTGTGA | GTGAATGACA | CAGGTGACAG | CTCTTAATTC | TGGACCATCA | CCTGATTCTG | 240 |
| TGGCTGGGAA | AAGATGGCCA | GAGCTGCCTG | GCTCACTTCA | GAGCAGGTTA | GTGCTTGCGG | 300 |
| AAGCAGGAGC | TGAGGATTTG | TACTAGGCCA | TGAAGGCCGA | ATTTC | | 344 |

(2) INFORMATION FOR SEQ ID NO:1187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 0 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

(2) INFORMATION FOR SEQ ID NO:1188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGCGATGGCT | CACATCAGCA | CTTTGGGAGG | CTGGGGCAAG | 60 |
| AGCATCACCT | GAAGCCAGGA | GTTCAAGCCC | AGCCTCGGCA | ACACAGTGAG | ATCTCATCTC | 120 |
| TACAAAAAAT | TTAAAAATGA | GTTTGGCGTG | GTGTACATA | ATCGTGTAGT | CCCTGCTACT | 180 |
| TGGGAAGCTG | AGGCGGAAGG | ATCACCTGGG | CTCAGAAGTT | CAAGGCTGCA | GTGAGCTATG | 240 |
| ACTGCACCAC | TGCACACCAG | CGTGGGTGAC | ACAGTGAGAG | CCTATTAAAA | AAAAAAACAA | 300 |
| AACCAATAAA | CCAAACAAAC | AAAACCTAAA | ATACAAAAAA | TTAGCTGGGC | GCAGAGGCAC | 360 |
| GGGCCTGTAG | TCCAGCTAC | AAAGAAACCT | CGAG | | | 394 |

(2) INFORMATION FOR SEQ ID NO:1189:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGAGATGTA CCTGATAGCA ANTTACTGCN TCTCAGCTCA | 60 |
| AAATTCACCC TTCAAAACCT TTTCTACACC AATGGATAGA ATTCCTGTCA GCATTCTCT | 120 |
| TNNAACGTTG AACACAATGT TAAGCTTCCT CAGTGAAGGA CCCTAGATGG ACATTGCAGG | 180 |
| AAGAAGGGAC TTCCCTGTT GGACCTAGAG GTTGTACCAG CATTGTAGGT GGGAGGACAT | 240 |
| CCACTGGCTC TTTGCAATAG CCATGTGTCC ATAAAGTATA GTTTCTCAGC AATCTCATTG | 300 |
| CCCAGTCTAG GCNTGGCAAT CACCCTCCTG CAGCCTTATC AACACATTGC TCGAG | 355 |

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTTGGAGAG CCTCATGCCG TCTCTACCTT CGCACACTGG | 60 |
| TCAAGTATCT GCTGAGCTTC TTGGCCGCAA GGATGCAGAA ATAGGCTGAG GGTCCATGGG | 120 |
| AAGAAAGACA CAATGAGGCA GTAGGAGGTG GGAAGAAAAG AAGACAGACT TTCAAATGG | 180 |
| AATTAGGCAC TGGGGAGAGA TCAGTTTCCC CACATCAGGG AGAAGAAGGT ATAGGTGGGG | 240 |
| AAGGGGGTGG CCAGGAGCAG AAGGAAGAAG ACTCAAGATG GAAAGGGAGC CGCTGTGCCT | 300 |
| GTGGCAATAC CACTTGGAGA GGTCGACTTC ATACCTTCAA GCCTTTTCCC CTGGGCTTTT | 360 |
| GATTGTGTCT GTGCCCCCTT TCTTGTCTC TCTGCAGATG CCCAGTAGGG GCTACCTCAT | 420 |
| CCTCGTGCTG TTCTTGTGTA GCATTCTCGA G | 451 |

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AACAGAGATG GCTTAGACTT CAAGACTTGA TTTGTAGCTA | 60 |
| TGTTCTACCA GCCTCCAGCT GTCTATGCGT TGGCCTCACG CATGTCCCAA ACGTGGTCCC | 120 |
| ACACATGTTT ACACATTGGT CCCACATATG CTGAGAGTAA TTAATTTCTA TTCATCAGAG | 180 |
| GTCAGAATAG AATAAAGAAT GTTTATGTCA TAGTATGACT TTTTAGGTGA TTTTGAAAAG | 240 |
| CAAGAATATG AATTCTATGA AAAAAATCTA TTAGGAAATT ATGGAATGA CAGAATGCAG | 300 |
| AGGTATTTGG AATAGAAAA AAAACGGGTG ATCTCGAG | 338 |

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACCGACCACA | TTTCACTCTC | ACCGCTGTAG | GAATCCAGAT | 60 |
| GCAGGCCAAG | TACAGCAGCA | CGAGGGACAT | GCTGGATGAT | GATGGGGACA | CCACCATGAG | 120 |
| CCTGCATTCT | CAAGCCTCTG | CCACAACCTG | GCATCCAGAG | CCCCGGCGCA | CAGAGCACAG | 180 |
| GGCTCCCTCT | TCAACGTGGC | GACCAAGTGGC | CCTGACCCTG | CTGACTTTGT | GCTTGGTGCT | 240 |
| GCTGATAGGG | CTGGCAGCCC | TGGGGCTTTT | GTTTTTTCAG | TACTACCAGC | TCTCCAATAC | 300 |
| TGGTCAAGAC | ACCGCACTCG | AG | | | | 322 |

(2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTCGAGGGGT | GCTGAGCATT | TTTTTCATGA | ACCTGTGGTC | ATTCATATGT | CTTCTTTTGA | 60 |
| GATGTGTCTA | TTCAGGTCCT | TTGCTTATAT | TTTAATCAAG | TTATTTGTTT | ACTATTGAGT | 120 |
| GAAAGAGTTC | TTTATGTATT | TTGGTTATTA | GCCCCCTAAC | AGATATATGT | ATAGCTTGCA | 180 |
| AAATATTTTT | CCCAGTCTGT | GGGTTGTCTC | TTCAATTGT | TAATCTTTT | TTTTTTTTTT | 240 |
| GTTGCTGGGC | AGAACGTTT | TAGTTTGATG | CAATCCCATC | TGTCTATTTT | TGCTTTTGTT | 300 |
| GCCTGAGCTT | TTGGGGTCAT | AGCCAAAAAA | TCCTTGCCCA | AACAGCAGTG | TTATGGAGCT | 360 |
| TTTCCCTAA | GTTTTTAGGC | CATGAAGGCC | GAATTC | | | 396 |

(2) INFORMATION FOR SEQ ID NO:1194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | AGGTAGGGAA | TGCAAGCAGG | CACTGGGGAG | AAATNGGGCN | 60 |
| GGAAAGTAGT | CTCATGGAAT | AAGCCTTTTT | TACTTTAATT | CAGCATTTAT | TGCTTTGATT | 120 |
| AAAAAATAAT | TTCAAAAATC | TTTCTGCTTA | CTGAATAAAG | AATGCNTTGG | AAAGAACAAG | 180 |
| AATGGATAAA | GGAGAGTGCT | TAGGAGGCTC | CTGGAGCAGG | AAGAGGTGGT | GGCGAATAGA | 240 |
| CTACCGGAGC | AGTGGAGGGT | GGAGATGGAG | AGACGTGGAA | AGACTGAAGA | CATATCCTCG | 300 |
| AG | | | | | | 302 |

(2) INFORMATION FOR SEQ ID NO:1195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| GAATTCGGCC | AAAGAGGCCT | ACTCAGAAAC | ACAAGGGAAA | GGACAGAAGA | GGGACCGGGG | 60 |
|------------|------------|------------|------------|------------|------------|----|

| | |
|--|-----|
| AGGAAGAGAG TGAGGAGAGA GGTATGTAAG GTGTTTAGTA CACAGTAAGT GCTCAAAATG | 120 |
| TGTCCACTCC CTCTGCCAGG AGAGAGCAGA AAGTCAGAAA GGAGAGGACA CCAATAGAGA | 190 |
| GGAAAGAAAG GGGCCAGGCG CCGTGGCTCA TGTCTGTAAT CCTAGCACTT TGAGAGGCAG | 240 |
| AGGTGGGAGG ATCGCTTGAG CCCGAGAGTT CGAGACCAGC CTGGCCAACG TAGAGAGACC | 300 |
| CTGTCTCTAC AAAAAATACA AAAATTAGGC TGGGTGCGGT GGCTCATTCC TGTAAATTCCA | 360 |
| GCACTAGGGA GCTCGAG | 377 |

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGTACAC AGCACTCACA CTAAAGATGA AAAATTCCAT | 60 |
| TAGCTCATCC TGGTTCTTCT GCTTACTTAC CTAATCATCT GTTTATGATT TAAAAAATA | 120 |
| GGGTTACTGT GAAGAGAGTG CTTGTGTGTG AGACAGAGAG GGAGGGTTGT TTTTCAAATG | 180 |
| TATAGAATAT ACCAATGTAG TTTTGGTTG GGTATTTTTT TAAATCATGA CTTTATTAAA | 240 |
| TTTACTTAAT TAATATTCAT TTTTATCCTT TTTTATGTT TTTAAAGTTT TTATTATTTA | 300 |
| TTAATTTATT TGAGATAAGG TCTTGCTCTG TCACCCCTCGA G | 341 |

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACAGAAATTT AAATTAATCT CTCATCCATT GGCTTTTGCT | 60 |
| ACTTTAGGTT AATATTAAAA TATAACATAC ATTTTGGGG TTTATGCTGT TAGCTCCAAA | 120 |
| CCAAAAGATT TTGGAAATTT ATTTTGGAAA TTTTGTGTTT AGAATATGAA TAAATCTGCT | 180 |
| TATTCAGAAA AATTAAACCT TGATAACTTG GGACCTCCTA TTCCTGTATG TTCTCTGACA | 240 |
| TACATTGAGG GATTTGCTC TCTTTTGTTC ATTTGTTTTA CTAGTCAGAC ATTCCTTTGG | 300 |
| CTGCCCATAC TTAATCTGT TGGGTGTTTC CGCCCCGCC CTCAGCTTCT GAAGCTACTC | 360 |
| GAG | 363 |

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

| | |
|---|----|
| GAATTCGGCC AAAGAGGCCT ACCTGACAAG TGTTAAGCAG ACACATAGAG AAAGTTAAAA | 60 |
|---|----|

TTTGTTTTGA GTCCTTAAGA GTGAAGTTAA GGAATAAGAC CTATAAATGG ACACCATGTG 120
 ATGAGTGCTG TCATCAAAGC ATGGACAATG GCCTTTGAGA GTACTCGAG 169

(2) INFORMATION FOR SEQ ID NO:1199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

GAATTCGGCC AAAGAGGCCT ATAAAAACCT TATGTTATTT TTGGAAGTTT TTCTCATATC 60
 TCTGTTGCCA GGGTCACTCG AG 82

(2) INFORMATION FOR SEQ ID NO:1200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

GAATTCGGCC AAAGAGGCCT AAGGTGGTGC AGTGGGGACA GCACCTCCGA CCCTATGGGG 60
 TGTACCTTCA AGTAGCAAGG CTGACAATGA TGTCTAGPAA GGTCTCCACT TCTGCCTGAG 120
 TTTTGCCAAA CCCAGTGGTC TATAGGGATG TGGCAAAAGA ATGACCTACC GCAGTGTGAT 180
 TATCAGTGTT TTTTAAAATA AAGAGCACAG TTTTGCCTTT AAAATAATTC ACATCAACGG 240
 TATTGGGGAG AACATGGAGC TGGCATAACA TTGGCGTAGA AAGCAGGGCC AGGCCCAACC 300
 ACGGGGCCCT CGTGTGGGGA CGGGTGCCTG AGCCCCTGAG CCCCTCGAG 349

(2) INFORMATION FOR SEQ ID NO:1201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

GAATTCGGCC AAAGAGGCCT AGGGGAAGAG GTTCAAATGT GGGGCTGGAC GTGGCCTTGG 60
 GGTGCGGATC CTCACAAAN ANTTCGTCTT CATAATCCTN ATGAGGTNGC GGGGAGTCCC 120
 GCAGGACAGA CTCAGATATT CGGAGGGAGA TCCTCCCTGG AGTGCTCGGG GCCCAAGAG 180
 GTGTGTCTGG GTCAGAAGTG CTGCATAAAC TTGGAAGACT CTGCTGTTTT TGATAGTGCT 240
 TCAGGTTTGC AAAATCAGGG GCTGAGGATT CCTCAGGAAG GNTGTCCTCT CTGGCTGCGT 300
 GGGCCCACTT TGCTCGAG 318

(2) INFORMATION FOR SEQ ID NO:1202:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTACAAGAT AACTTCCCAG TACTTTAAAA AAGTCTCAAA | 60 |
| GTCATAAACA AGAAAGAACT GAGGGACTAT TGCATATTGG AGCGATCTAA AGAAGTATTA | 120 |
| CAATTGTGG AATTCTTGAT TAAATCCTGG ACCAGCAAAA GGACATTAGT GGGAAAATTG | 180 |
| ATGAAATTCA AATGAGATCT TATATTGAAG TTAATTGTGT CAGTGTACAT TTCCTGGTTT | 240 |
| TCATAATTGC AAGTGATTAT GTAAGGTTTG TTAATATTGG GAGCAACCTC GAG | 293 |

(2) INFORMATION FOR SEQ ID NO:1203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGTTTTGAGA AATAAATGGG ATAGCACGTG TAAATCACAT | 60 |
| AGAACAGTGC CTGGCACATA AACACTCAAT AAATGTTAAT TGATACTATA ATTTATCTAA | 120 |
| TTTATCTTTA TTCCTCCTGC AAAGATTCCT TGGACTATTT AGAATCTCTG GTCACCTCTAA | 180 |
| TGAGATGGTG GTGTTTTTTT TTGGTTTTTT TTTTTTTTGC TTAAAGAAC TTCTGTAGAT | 240 |
| CAGCTGTAAT TTAAGTCTAA ATAATCTCTT GTAGTTATTA TTTTCAGTCT ACTTGGGATC | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:1204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACGAGATAAT ACTGGAGTCA ACTGTACATT AACTTGCTTG | 60 |
| GAGGGCTATG ATTTACAGA AGGGTCTACT GACAAGTATT ATTGTGCTTA TGAAGATGGC | 120 |
| GTCTGGAAC CAACATATAC CACTGAATGG CCAGACTGTG CCATTTCTAG AAAAACGTTT | 180 |
| TGCAAACCAC GGGTTCAAGT CCTTTGAGAT GTTCTACAAA GCAGCTCGTT GTGATGACAC | 240 |
| AGATCTGATG AAGAAGTTTT CTGAAGCATT TGAGACGACC CTGGGAAAAA TGGTCCCATC | 300 |
| ATTTTGTAGT GATGCAGAGG ACATTGACTG CAGACTGGAG GAGAACCCTGA CCAAAAAATA | 360 |
| TGCCTAGAA TATAATTATG ACTATGAAAA TGGCTTTGCA ATTGGACCAG GTGGCTGGGG | 420 |
| TGCAGCTAAT AGGCTGGATT ACTCTTACGA TGACTTCCTG GACACTGTGC AAGAAACAGC | 480 |
| CACAAGCATC GGCAATGCCA AGTCCTCAGG GATTAAAAGA AGTGCCCCAT TATCTGACTA | 540 |
| TAAATTAAG TTAATTTTTA ACATCACAGC TAGTGTGCCA TTACCCGATG ATCTCGAG | 598 |

(2) INFORMATION FOR SEQ ID NO:1205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

```

GAATTCGGCC TTCATGGCCT AGTCTAACCA TTATGGAAAG AGAACAGTCC CTTCAATATC      60
CCACTATCTG TAGGGCATGA CACAGCCAAA TCCAAGTCAG ACCATCCCCTT TGATCAATTT      120
CTACCAATAA CTGTTTATTG CACACCCTGT ACAGAGCACT GCGACCAAGC TGTTCCTTGA      180
CCTTCTCCTT TCCTAGTGTT TGGTCACAAC ACTCCCTAAA GCCCTAACTC AAGTTCTTGG      240
GATGATACCA CCAGAAGAGG GAAAAAAGGA GCCGTCTTCC TGAAGTCACC TGGGTAGAGC      300
AGCTGGGGAT TTTCCCTCC TCGAG                                         325
  
```

(2) INFORMATION FOR SEQ ID NO:1206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

```

GAATTCGGCC TTCATGGCCT ACCCACTGCA ATGATGTTTA CCAGCACTAT TAACTTACTG      60
CAGACTCTTT GTCTGTCTGC TGGAGTTCAT GCTGAGATCA TGCAGAGCGA AGCCACCAGA      120
CTCGAG                                         126
  
```

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

```

GAATTCGGCC TTCATGGCCT ACTAATGTGG TTTTGTGAAG TTGGTGTCAA ATTTACGAGC      60
ATAAAATTGT TTGTAATATT CCCTTATATT CTTTTAAAC TGCTATAGGA TCTGTACTGA      120
TGTTCTGTTT CATACCTGAT GTTTTGTGTC TTCTGTTTGT CTTTTTNGT TGTGTGTTGT      180
GTTGTTGTTA GTTTTGATAG AGGCTTACAA ATTTTTTGCT TAATTGATTT TCTCTATTTT      240
CCTCTTTTAT TTCTTCTTTT AATAATTCCT TCCTTCTGCG TTTGGCTTCA TTTTGCTCNT      300
TTTTAGTTTC TTTTGGTAAT TCAATTACTG GTTCGACATC TTTCTCGAG                    349
  
```

(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAGTGATTG TGGGTTATAA TAGAGCAGAT TGTTTTAAAA | 60 |
| AGAGACTTGT GAGCCAAGAC TAAATCCTGG TTTTACTATT TATTAATCTG TATAGCTATA | 120 |
| GCCAAGCTAT TAAAACTCCC TTATTCTCA GTTTTTTCGT TCATGAAGTG GGTACAGTAC | 180 |
| CTAAAGGTTT ATGTTGAG | 198 |

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACAGGGGATG ATTCAGTCCG ATACAGTCAG GGAACCGTAC | 60 |
| ATAGAATAGA ATGACTAGAG TATAATCTGC AAAGGATGGA ATGGCAGAAG TAGTCAGAAG | 120 |
| AGGTATGCAA TGTTGGATC AAAAAGAGCT TTGTATCCAG CGTCACAGGG CCTCAAATTG | 180 |
| TACTGTAATC ATATGTCTTT TACCTGTTCT CTGGCATTTA AATATTCTTG TAAAGAGCTA | 240 |
| AGCCATTACT GATAAAATGT CTGTTGTGTA CAGTTGTACA AATTAAATTC AGTCACAAAA | 300 |
| CTGAAAGAAC AGCAGTGGGA CATCTATCCT AGTGAAAGTT AGAATACTACT TTTGTGGTCT | 360 |
| TTAATAACAG AGTTGATTGT TTACCTTCTC CTTTGGTTAG AAGACTGGTA TGGGGATTGT | 420 |
| TTGGAATGAA GAGGTAGGAG AGAGAAATAA TTCAATTCTG TATTCTCCCA TCATCTTTAT | 480 |
| ATTTGAAC TGAAATGTGT GTTCTATCA TTCATTCAAA TTATTAAACA AAAACAGAGA | 540 |
| CTCGAG | 546 |

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AAAGATATTT TAGCTAACAG GAGAACGGCC CAAGGGGGCA | 60 |
| TTCTCATGTT AATTACCAA TGTGGGCTTG TCAAAATCAA ATAGCTCCAG GAATAATGCA | 120 |
| AGTAGCTCTG CATCATTATA TTGTTTGGCC CTCAACCCAA TATTAGCTAC TTTTAAAT | 180 |
| CTGGGTTTCAT TAGGCTTTTA AATTTAAAAG AGGAATCACT ATTGGGAGCC TTCAGAAGAA | 240 |
| TGTAAAGCAC AGCCAGCACT GCCAGAGTTT AATGTAAATG ACATTAAAAA ATAGTTTCAT | 300 |
| ATCACACACT CGAG | 314 |

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACGCATGAAA | ATTACTTAAA | CGTTGCACAC | AACGTTTCAC | 60 |
| AAAATCTTTT | GTGAAAGAAG | AAAAGGAAAT | TCAGTGTGTG | AGTCTCAGCA | GGAGTTAAGC | 120 |
| TAATGCAGCT | TAAATAATG | CCGAAAAAGA | AGCGTTATC | TGCGGGCAGA | GTGCCCCTGA | 180 |
| TTCTCTTCCT | GTGCCAGATG | ATTAGTGCAC | TGGAAGTACC | TCTTGATCTG | GTACAGCCTC | 240 |
| CAACCATCAC | CCAACAGTCT | CCAAAAGATT | ACATTATTGA | CCCTCGGGAG | AATATTGTAA | 300 |
| TCCAGTGTGA | AGCCAAAGGG | AAACCGCCCC | CAAGCTTTTC | CTGGACCCGT | AATGGGACTC | 360 |
| ATTTTGACAT | CGATAAAGAC | CCTCTGGTCA | CCATGAAGCC | TGGCACAGGG | CTCGAG | 416 |

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGGGAAGCC | TGAGCAGGCC | AGTGGGCTGG | GCGCAGAGCG | 60 |
| GGGTGTGGGG | GCCAGGCTGT | GTGACCATGA | CAGAAAGAAC | CCCAGCTAGC | CCAGCTTGCT | 120 |
| CCCTGGGGCA | GGACTACCA | ACCCCGTGAG | GGCCTGGGGT | AACAGTGGTC | CAGTGGCCAA | 180 |
| GACCAGCAGT | CGCCAGGTAC | CCACTGGCCA | CAAACCAACC | AGAATACTTG | CCGCTGGAGG | 240 |
| CCCCAGCCCA | GGGTCAACCC | AGCCGCCGCC | CTGTCTTTGT | GTGTGGGTGG | GTCAGCCCCA | 300 |
| TCCCTGCCTT | TCGGACTAAA | AACTCGAG | | | | 328 |

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGAGGCATTA | ATATATTTTA | CATTACTGGG | ACCATAGTAC | 60 |
| AGAAATTTCT | AAATGGTTTG | TAAATAACT | TGTTATTTGT | GTTGTTGTAA | AAGCAGTTAA | 120 |
| TACAATGGAA | AAACTCGTAA | TAAGAAGATA | CAGTTTAAAC | TCAAAAAGTT | TACCCAAGGT | 180 |
| AATTATGAGT | ACTACCTGGC | AAAACCTCAC | GGAAGCTGTG | GTATCACTTT | TATGATGGAA | 240 |
| GAATGGTGTT | TGCATTTTGT | GTAAAAGTAC | TTGCGGCTGG | GCGTGGTGGC | TCATGTCCCA | 300 |
| GTGCTTTGGG | AGGCCGAAGC | AGGTGGATCA | TCTGAGCCCA | GGAGTTCGAG | ACCAGCCTAG | 360 |
| GCAACGTGGC | AAGAGCCTGT | CTCTCCAAAA | CCTACAAAAT | TTAGCCAAGC | TTGGTGGTGT | 420 |
| GAGCCTGTAG | TCCCAGCTAC | TTGGGAGACT | CACGCTGGAG | GATCTCTCGA | G | 471 |

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGNC | TTCATGGCCT | AGTCAATGAA | AGAATTCCTG | CAGTTTCATT | ACCTATGAAN | 60 |
| ATTGTGGGGT | CCTCTTGTGG | GACATGAAAG | GGGGACAGAT | AGATGAATAT | TGTTTGGATT | 120 |
| TTTGGTCCTC | AGTGCCATCC | ACAGACTCCA | GAAGGGATCA | GCTATTTGCT | GAACAATCTT | 180 |
| TCAGTTCTCA | TAGAGCCCTG | ATATGTTTTT | AGGGTCCACA | AATGCCTGTG | ACGGTGGCCT | 240 |
| CAAGAACCCA | GTGTCCCCTT | GTAGGTGGGA | TAGCATACCT | CTTAAAGGTC | AGCATGAGAT | 300 |
| TCCACCCATG | TCATCCCCAG | CATTGGTGGG | GTGAGCAGAT | CCTCTCTCTG | GGGTTTCNTT | 360 |
| TTCTGCTCAA | CCTCCCTGCT | TTGATGGACT | GCACAGACAA | GCCCCATCTT | GGTGAAGGG | 420 |
| TCTCCCATG | GGCTGTCTCT | GAGGGTCACT | CCCACAGATA | TGCCCCATCC | TGGTGAAGG | 480 |
| GTCTCCCTGG | GGGCTGTCCT | GGAGGGTCAG | TCCCACAGAC | AAGCCCCATC | CTGTGGGAGG | 540 |
| GTCTCCCCGT | GGGCCATCCT | GGAGGGTCAG | TCCCACAAAC | TCGAG | | 585 |

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GCGATTGAAT | TCTAGACCTA | CCTCGATAAC | CCAAGAGACT | ATGAGCAGAC | ATGACATCAT | 60 |
| TGCATGGGTT | AATGACATAG | TATCTTTAAA | CTACACAAAA | GTGGAACAGC | TTTGTTTCAGG | 120 |
| AGCGGCCTAT | TGCCAATTCA | TGGACATGCT | CTTCCCTGGC | TGCATTAGTT | TGAAGAAAGT | 180 |
| AAAATTTCAA | GCAAAGCTGG | AACATGAATA | TATTCACAAT | TTTAAACTTC | TGCAAGCATC | 240 |
| ATTTAAGCGA | ATGAACGTTG | ATAAGGTAAT | TCCAGTGGAG | AAGCTAGTGA | AAGGACGTTT | 300 |
| CCAGGACAAC | CTGGATTTTA | TTCAATGGTT | TAAGAAATTC | TATGATGCTA | ACTACGATGG | 360 |
| GAAGGAGTAT | GATCCTGTAG | AGGCACGACA | AGGGCAAGAT | GCAATTCCTC | CTCCTGACCC | 420 |
| TGGTGAACAG | ATCTTCAACC | TGCCAAAAAA | GTCTCACCAT | GCAAACCTCC | CCACAGCAGG | 480 |
| TGCAGCTAAA | TCAAGTCCAG | CAGCTAAACC | AGGATCCACA | CTTCTCGAG | | 529 |

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ATCGGCCCCG | CGGCGGAGGG | ANANGATCCT | CCACAGTGCT | 60 |
| CTCTTCAGTN | CCCCTTCAAA | TGCTGTTTTA | TCTCAGCGGA | ANGTACTACG | CCCTGTATTT | 120 |
| CCTCGCCACG | CTCCTGATGA | TCACGTATAA | AAGTCAGGTG | TTCAGCTATC | CTCACCGGTA | 180 |
| CCTGCTCCTC | GATCTTGCTC | TGCTGTTTCT | GATGGGATT | CTAGAAGCAG | TTCGGTTAAA | 240 |
| CCTGGATACA | CCCCGTATGC | CCGATGTCCA | GTGAGGAACC | AAGGCTGCGG | GGAAGGGTGG | 300 |
| CCCCCACCT | TCCTCTTGTT | ATCAGGCCTC | AGACACACTA | GGAGGATGGA | GGCGAGTTCT | 360 |
| CTCAGCTGCC | CATCCCACTG | AGGGGTGCCC | GGCCGTCACT | GTCTTGTTGT | CACTCACGTC | 420 |
| CCAGAACCTC | TAGAGCTTGC | CCCCCAGGGC | GGGCACTGCT | GGGAGGGTGC | GAGCACCGCT | 480 |
| GCGGCACAGA | GGCCCGGTTT | TTGGNTGATC | TTCTGGGGCC | TGGGCCTGCC | CTGAGGTGGT | 540 |
| GGGGACAGGG | TGTGGCCTGG | CCCTGCTGGG | GGCTGCTAGG | CCAACGGGAC | CCTCCCCAAG | 600 |

CGCGCCGCAC ACTGCAGGTG CCTCGAG

627

(2) INFORMATION FOR SEQ ID NO:1217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

| | |
|---|-----|
| GCAAATATTG AACATAATCT AAAATCTGAG GAAGAAAAGG ATCAGGAAAA GCAACAGATG | 60 |
| TTTGAAAATA AGCTTATAAA ATCTGAAGAA ATTAAAGATA CTATTTTGCA AACAGTAGAT | 120 |
| TTAGTTTCTC AAGAGACTGG AGAAAAAGAG GCAAATATTC AGGCAGTTGA TAGTGAAGTT | 180 |
| GGGCTTACAA AGGAAGACAC CCAAGAGAAA TTGGGGGAAG ACGACAAAAC TCAAAAAGAT | 240 |
| GTGATCAGCA ATACAAGTGA TGTGATAGGA ACATGTGAGG CAGCAGATGT GGCTCAGAAA | 300 |
| GTGGATGAAG ACAGTGCTGA GGATACGCAG AGTAATGATG GGAAAGAAGT GGTCCAAGTA | 360 |
| GGCCAGAAAT TAATTAATAA GCCCATGGTG GGTCTGAGG CTGGTGGTAC TAAGGAAGTT | 420 |
| CCTATTAAAG AAATAGTTGA AATGAATGAA ATAGAAGAAG GTAAAAATAA GGAACAAGCA | 480 |
| CTCGAG | 486 |

(2) INFORMATION FOR SEQ ID NO:1218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ATGAATTCTA GACCTGCCTC GAGATCTGAG CAGGAATTAC | 60 |
| TCTCAGATGA CGCTTCATCT GTTTCACAAA TTCAGTCTCA AACTCAGTCA CCGCAAAATG | 120 |
| TCCCTGAAAA ATTAGAAGAA AACCATGAGC TGTTTTCCAA GAGCTTCATC TCCATGGAAG | 180 |
| TGCCTGTCTAT GGTAGTAAAT GGCAAGGATG ATATGCATGA TGTTGAAGAT GAGCTTGCTA | 240 |
| AGCGAGTGAG TAGGTAAAGC ACAAGTACAA CCATAGAAAA CATCGAGATT ACTATTAAGT | 300 |
| CTCCAGAGAA AATCGAAGAA GTCCTGTAC CTGAAGGCTC CCCTTCAAAA TCGCCATCCA | 360 |
| AGAAAAAGAA GAAATTCCGC ACTCCTTCTT TTCTGAAAAA GAACAAAAAA AAGGAGAAAG | 420 |
| TTGAGGCCTA AATAAAGTCT TTTTATAATT ATTATTATAA CAATGTGACA TTGCACATCT | 480 |
| AAATACCACA TCTCGAG | 497 |

(2) INFORMATION FOR SEQ ID NO:1219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

| | |
|---|----|
| GAATTCGGCC TTCATGGCCT AAAAGATGGC GGAGGTGCAG GTCCTGGTGC TTGATGGTGC | 60 |
|---|----|

| | |
|---|-----|
| AGGCCATCTC CTGGGCCGCC TGGCGGCCAT CGTGGCTAAA CAGGTACTGC TGGGCCGGAA | 120 |
| GGTGGTGGTC GTACGCTGTG AAGGCATCAA CATTTCTGGC AATTCTACA GAAACAAGTT | 180 |
| GAAGTACCTG GCTTTCTCC GCAAGCGGAT GAACACCAAC CCTTCCCGAG GCCCCTACCA | 240 |
| CTTCCGGGCC CCCAGCCGCA TCTTCTGGCG GACCGTGCGA GGTATGCTGC CCCACAAAAC | 300 |
| CAAGCGAGGC CAGGCCGCTC TGGACCGTCT CAAGGTGTTT GACGGCATCC CACCACCCTA | 360 |
| CGACAAGAAA AAGCGGATGG TGGTTCCTGC TGCCCTCAAG GTCGTGCGTC TGAAGCCTAC | 420 |
| AAGAAAGTTT GCCTATCTGG GGCGCCTGGC TCACGAGGTT GGCTGGAAGT ACCAGGCAGT | 480 |
| GACAGCCACC CTGGAGGAGA AGAGGAAAGA GAGAGCCACT CGAG | 524 |

(2) INFORMATION FOR SEQ ID NO:1220: ..

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

| | |
|--|-----|
| GAATTCGGC CTTCATGGCC TATGATAAGT TCATTCTGGC TGGAGTATGG TGGAGAGCCA | 60 |
| TGGAGTACTG GTAGGTGAGG GGCTGGAGGA GGGATAGGTT GGAGATGTG AGAAAGGCTT | 120 |
| TAAAGATCGT GGTGAGTTGT TTGGGTTTGT GTTGGCTGTG AGGAGTCATC AGAGGTTTTA | 180 |
| ATGCAGGAAA GTGGTTTGTG CTCTATACTC CAGCAGCAGA GGTGGTTGA GTGGTGCTCA | 240 |
| AACCTTTGTTG TGTATTGGAA TCATCTGAAG AGCTTATAAA AATACCAGTA CCCAGGCTAC | 300 |
| AAACAGTAAA ATCAGATTTT CTGAAGGAGA GGCCAGATA TTGGATTTT GATAATTTCC | 360 |
| CAGGTGATTC CAGTGCGTAT CTGAGTTTGA GAACTACTCT TTTAGAGGGG TCTGATGGAG | 420 |
| TAAGGAATTC AGAGGCCACT CGAG | 444 |

(2) INFORMATION FOR SEQ ID NO:1221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

| | |
|---|-----|
| GCTTGAACAA CACAGGTTTG AACTGTGCAG GTCCACTTAT CCATGAGTAT TTTCAACCAA | 60 |
| ACTAGTATCA AATATACAGT ATACGCGGGA CTTGAAACCC ACGTGTAAGG AGGACGAAGT | 120 |
| TTTCGTGTAA GTCAGCTCCG AAGCACTGAC TTTGGGACTT GAATTTGCAC AGATTTTGAT | 180 |
| ATGAAGTGGG GAAGGGGGTA ACTTGGTACA AATCCCCTGC ATATACTGTG GGATGACTCT | 240 |
| AGTTTGATTC TGGAGTGATA TATGGAAGAC ATAATTCTTC CCATAAAAAA TCATAATCTT | 300 |
| GGTAGTCTAT CATAGTCTAG CATTAGAGC ATGAACTTTG GAGCCGTCCT CGAG | 354 |

(2) INFORMATION FOR SEQ ID NO:1222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCTAGTTCA TGCTTGGCTT GAAAGAGTGG TCGTTTGGCG | 60 |
| TGGGTCATCA CTGTGTAGTA TTGGGGATAC TTAGGTGAGA AAAAAACTTA ACGCTAGAGA | 120 |
| CGTTCACGCA CTAGTGGAGA AGCCAGGATT GTTGCCCTAG AGTTACAGTA GATAAAAGTA | 180 |
| CCTCAGAGAA CTGCGGGGGC TCCCAACCTG GACGCTTGCA CCGGAGTATT AAATCCAGCT | 240 |
| AGAGAATGGC ATGTGCAAAG ATACAGAGCT TTTAGAAGTT GCCTGCATTC CTTGGCCCCA | 300 |
| TCCTCACTCG AG | 312 |

(2) INFORMATION FOR SEQ ID NO:1223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATAAAAACT GGCTGGGCGT GGTGGCGGCA CCTGTAATTG | 60 |
| CAGCTATTTG AGAGGCTGAG CCAGGAGAAT CGCTTGAACC TGGGAGATGG GGGTTGCAGT | 120 |
| GAGCCGAGAC CGCCCCATCG CACTCCAGCC TGGGCAACAA TAGTGAACT CCGTCTCAAA | 180 |
| AAGAAAAAAA GTTTCCTTAG AATGGAAAAT ATTCATTAT GAGCTCTTTT GGCAATCCGT | 240 |
| CATCAGTATA TTCTGAAAAC CAATAAGATG TTGCCAAGTT GGGGGCGAGA GCTATGTAAT | 300 |
| GCAAGGCATA TGCCTGATGA AGTATACAAA TACACCTGAC CAGAAACTTT GTCTCCCAA | 360 |
| TAAGTCTCGA G | 371 |

(2) INFORMATION FOR SEQ ID NO:1224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

| | |
|---|-----|
| GAATTCGGGC TTCATGGNCT AAAGAAAAGT GCTGTAAATG AGGATGTGGC TTGCTGGGCA | 60 |
| ATAATCATTG TAGAGTGGTA CACCCAGTGC CTTACAGGA TGCTTGAATA CTGCCTGCAA | 120 |
| GCCTCGTGTC ATTAGCCAG TAGGCATATG ATAAGCCTCT GGTCATCATT TCCACTGTTA | 180 |
| AGAGTTAGTG TCAGATATGG AGCACCAATA GGCTTGTAAG TGAGAGCATC CCTCAAAGTT | 240 |
| GTCACCTTAG GAGACTCTGA TGACCATGAT GCTGCCATTG TCCAAATGTG CACTCATCTG | 300 |
| TCTTTTGGGG AGTGATTCCC GACAATTTAT AGATTACAAG AGAAAAGCAG TCTGTATTTT | 360 |
| CATCAAATGA TAGTTTAAAT GGAAAATGAA TCAGAAGTCT CGAG | 404 |

(2) INFORMATION FOR SEQ ID NO:1225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGTTGGGGTT | AATTATGGCA | CCTAACTTAT | AGAAGAGGAA | 60 |
| ACCAATTTAG | AGACATTAAA | ATACTTGTTT | AAGGTTACAC | GGCAGGGAAA | AGGCAGAGTC | 120 |
| AGGATCTGTA | TTCTGTAGTC | TGAATCCAAA | GCGAATCCAA | AACCTCTGAGG | TGCTNTGCTC | 180 |
| TGCTACCTGC | TGATGGTTCT | GCTGGGGGAT | GCTCAACCAC | CAGATGTCTT | ACTTGGGAAC | 240 |
| TGCACTGGAG | GTCGAGGGTC | TGCATTCTCC | TTCTGTCGTA | AAATCACAAAC | GTCCCCATCT | 300 |
| TTCAAGCCAT | AAGAAGCCAA | TGATCTGTGG | TTGTCTGTGA | GAGGTCTTTC | CGCATAGACG | 360 |
| ATCTGGCTCT | CGGCTGCGGG | GATGCCAGAC | TCGAG | | | 395 |

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCAAAGGTCC | TTTTGTGGAA | GCGGAGGTGC | CCGATGTTGA | TCTGGAGTGT | CCTGATGCAA | 60 |
| AGTTGAAAGG | GCCCAAGTTT | AAGATGCCTG | AGATGCACTT | CAAGGCCCCC | AAGATCTCCA | 120 |
| TGCCTGATGT | GGACTTACAC | CTGAAAGGCC | CCAAAGTCAA | AGGGGATGCG | GATGTGTCCG | 180 |
| TGCCAAAATT | GGAGGGAGAT | TTAACAGGCC | CCAGTGTGGG | TGTGGAGGTG | CCTGATGTTG | 240 |
| AGCTGGAGTG | TCCTGATGCA | AAGTTGAAAG | GCCCTTGTCT | CGAG | | 284 |

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

| | | | | | | |
|------------|-------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGCAGACGG | GCAGTAGGTC | CCAGAGTTAT | ACTTCGGAGC | 60 |
| ACATGTTCAA | GAGGGAAATG | ACGACCGGCC | CCCACGGTCC | TGGGATGCAG | GTGTGAGGAC | 120 |
| TGAGAATGCT | GGACGGGGTG | TGGTCGAGGC | ATGGTCAGGG | TGGCCCCGAG | CTGTGCCCA | 180 |
| CCCCAGGGAT | GCAGCAAGGG | TGCTCTGTGC | AGGACCCCGA | ACTTGGGCTC | TGCCCACTTT | 240 |
| CAGTGTCTGT | TGCATGTCAC | GCTGGCATCT | TCGGCATGTC | CACAGTTTGT | CACCCCCCAT | 300 |
| TTGGAGAAGC | TGCAGCGGAA | GATGGTTTTCC | TCTGTGCCTT | GCAGGCAACG | TCATCCATCC | 360 |
| AGATCCTCCC | AGTGCCTTGC | CCGAATCGAN | CTGTGCGGTA | CACTCCTCCA | NACCGCGGAA | 420 |
| GCCGAGCATG | CGGCACACCA | CGTCTCCGTC | CTTCTGTGCC | CAGCCGTCGT | CACACACAGT | 480 |
| GCCCCAGCGC | CGGTCTGTGGT | ACACTTCCAC | GCGGCCCTCG | TGCGGACCTG | AGCCATTAC | 540 |
| CAGGCGGATC | ATCATCGGGG | CCTCCACGCC | ACTGCGATCC | CCAGCTCTGT | CTCCTTTCTC | 600 |
| TCCTTTCTCT | CCTTTTGGGC | CTCGGTCACC | TAAAACAGAG | GAGGAAACTG | GCATTAGAAA | 660 |
| TGGAAAGAAA | TCCTAATTGT | GAATAAAATA | TTACCTGCAG | GAGATTGATG | AACTCGAG | 718 |

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

| | | | | | | |
|------------|-------------|-------------|-------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGCTGGGTTG | ACCCTGCAGA | GGCCAGAGAG | CCGAGGGGCC | 60 |
| ATGTGTGCTG | GCAATGGGGCT | CCCTGCCCCCT | TTCTGAGGCT | CAGCACGGAG | GGGAGAAACC | 120 |
| CACATTTTCA | GAGGGAACCA | GCAGCAGAGC | AGAACCAGTA | ACCAAGATCC | CGGCAACCCC | 180 |
| TTGTGCTGAC | CCCACACACG | CTTCCCCTCT | TCCTGGCCAG | GCCACTCCAA | AGCTCTGTGC | 240 |
| ACACAGACAA | TAGACATCAG | GACTTTTCATC | TTCACCTCGTC | ATCTGGCAGC | AGAGAGCCTG | 300 |
| CAGGGCTGGG | CTGCAGGGAG | AAGAGTTCCT | TTCTTCACGC | ATCCAGGCAA | GGGGAGAGCA | 360 |
| GCTCTGTGCC | TGCCACTGGC | CCACTCGAG | -- | | | 389 |

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACACAAACAT | GATTTTATTT | TATTATTTTA | TTTTATTTTT | 60 |
| TTATTTTATT | TTGAGATGGA | GTCTCGCTCT | ATCGCCCAGG | CTGGAGTGTA | GTGGCATGAT | 120 |
| CTCGGCTCAC | TGCAAGCTCC | GCCTCCTGAG | GCGGGAGAAT | TCCTTGGGCC | TGGGAGGCGG | 180 |
| AGGTGCGGT | GAGCTGAGAT | TGCCCATTTG | CACTCCAGCC | GAGGCAACAA | GAGCGAAACT | 240 |
| CCTTCTCAAA | AACAAACAAA | CAACAACAA | CAACAACAA | ACTCTCGAG | | 289 |

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATGTGTTTT | ATGAACGATA | GATCACATCA | GAACTCCTGT | 60 |
| GGGGAGGAAA | CCTTATAAAT | TAAACACATG | GCCCCCTTAG | AGACCACAGG | TGATGTCTGT | 120 |
| CTCCATCCTT | CCCTCTCCTT | TTCTGTCACC | TTTCCCCCTA | GCTGGCTCCT | TTGGACCTAC | 180 |
| CCCTGTCCTT | GCTGACTTGT | GTTGCATTGT | ATTCCAAACG | TGTTTACAGG | TTCTCTTAAG | 240 |
| CAATGTTGTA | TTTGCAGGCT | TTTCTGAATA | CCAAATCTGC | TTTTTGTAAA | GCGTAAAAAC | 300 |
| ATCACAAAGT | AGGTCATTCC | ATCACCACCC | TTGTCTCTCT | ACACATTTTG | CCTTTGGGGA | 360 |
| TCTGGTTGGG | GTTTTGGGTT | TTTTGTTGTT | GTTGTTTATT | TGTTATTTTA | AAGGTAAATT | 420 |
| GCACTTTTAA | AAAAATAATT | GGTTGACTTA | ATATATTTGC | TTTTTTTCTC | ACCTGCACTT | 480 |
| AGAGGAAATT | TGAACAAGTT | GGAAAAAAC | AATTTTTGTT | TCAATTCTAA | GAAACACTTG | 540 |
| CAGCTCTAGT | ATCACTTGA | GTCTTCCTGT | TTTTCCTGTA | CCGGGTTATC | CTGCCTCGAG | 600 |

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGAGGGCCA CATCTGCCAN AGCCTGGAGT CTGCGAAGGC | 60 |
| CGGGACCCGG TTCCCCGGCC CACAGTGGGG GTGTGCAAAC CCGAGAGAAC TGGGTTGCAA | 120 |
| ATTCGTGAAG AATCAGCATC ATGTTTGGCA GCTGAGTATT GGAGCCAGGA GCCTGCCATG | 180 |
| AGGTTTTAG AGAGAGTGC TGTTTTAGAG CTGGCAGCAG CATCTCAGCC CAAGAGAAGG | 240 |
| TTATATCCCC AGAGGATGTC AGTCCCAAGG ACCAGTAGCT GCCATCAGTT TGGATTCTGA | 300 |
| AAACTAAGT GCATCAACAC TGGGTGTAGA AACATGCTTG CCTTATGTAT CAGAGGACAT | 360 |
| GCTCAGCAGA TCCAAGAGAT ATATTTGGCA ACTTTTCTA GAAAAGGCAC CTGCCTCGAG | 420 |

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACCACCCGCG ACAGTTTCCC AGCAGGGCTC ACAGCAGCGT | 60 |
| TCCGCGTCAT GGGGATTGG CAGCGTCTGC TGCTTTTGG TGGGGTGTG CTCCGGGCTG | 120 |
| GTGGCGGGGC CACTGCCCCG CTTGGGGGAA GCCGAGCGAT GGTTTGTGGG CGCCAGTTGT | 180 |
| CTGGCGCCCG GAGTGAGACC CTAACAACAA GAAGAACACA AATCATGTCC CGAGGACTTC | 240 |
| CAAAGCAGAA ACCGATAGAA GGTGTTAAAC AAGTTATAGT TGTGGCTTCT GGAAAGGGTG | 300 |
| GAGTCGGAAT ATCTACTACA GCAGTGAATC TTGCACTTGC ACTAGCAGCG AACGATTCGT | 360 |
| CCAAGGCCAT TGGTTTGCTA GATGTGGATG TGTATGGACC TTCAGTTCCA AAGATGATGA | 420 |
| ATCTGAAAGG AAATCCGGAA TTATCACAGA GCAACCTAAT GAGGCCTCTC TTGAATTATG | 480 |
| GTATTGCTTG TATGTCTATG GGCTTTCTGG TTGAAGAAAG TOAACAGTA GTTTGGAGAG | 540 |
| GCCTTATGGT AATGTCGGCC ATTGAGAAAT TGTGAGGCA GGTAGATTGG GGTCCACTCG | 600 |
| AG | 602 |

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTANACCTG CCTCGTAGTC CAGAAAGATC CCCACGCGCC | 60 |
| TGGGTGGGTC CCGGAGTGA GCCAAGGCCG GTTCCGAGGA NTTGTAATAG CTCCCCAGGA | 120 |
| AGACCAGGAT CCAGAAAGCCG TTGCCCGCGN ANAGCTCGCC CTTCTCCTTC CTGTTACAGT | 180 |
| TCTCCCTGCA CACCCCCAGG GCCCAGCTGG TCGGTTCCCC AACCTCCACC TCCCAGTAGT | 240 |
| GGCGGCTGAG GTGAAGCGCT CCTGGCCCAG CACGCGGGG CCGGGGTCAA AGCGCTCTGG | 300 |
| GCTGTCCGGC ANGGCCTGCC GTANGTCCCC CCGCTGCACG CGTCCGCTG TCTTCAGACA | 360 |
| GGATCAGCTC AGGGTTGGCG GTGTCCGGGT CCAAGGTCAC GTCCCCTCGA AACCTCCGCA | 420 |
| GTGTTTNTAC CAGTCCCGGG ACCCTGCACA CGGTCCTCAG CTCCATAGGC ACAACTNTG | 480 |
| GGGGCTGCAG CTTACATCC TGGACCCTGC NCAGGCGGTC CTTGATGTCC TGCAGCAGCC | 540 |
| CCAGAGCAGG CAGCTGGCAG CGGCCCTCGA G | 571 |

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

```

GAATTCGGCC TTCATGGCCT ACTTAATTTA TAGTCTTTTT CTTGTGAAAT GATCATTGAA      60
GTAGTTACTA ACAGGTAATG AAATAAAATA CCAATTTTGC TAGTGAAAAA TAGTTTTCAA      120
CTGAGAAAAG CACTTGGCAG AAGACCTACA AACATGCAGG CTAATGCTAC ACTCTATTGC      180
AGCTTCAAAT AAGTTGTTTT TGATGCCTTT TGAGAAGAAC AAATAAGAT GAAAATAATT      240
CCTTGAACAT TTATCAGCAT TGCTGTTTAG GTACCCATTA GAAAGTGATT AACATTGAT      300
ACCTACCCCT TCCAAAACAC AAAATCACTG GCAAGCATCA TCACACACTC CTAAACCAGC      360
AACATCTGAG AAGCACAAAA CACCTCCCTT TTTGTCTAAT AACCTGTTGG TTAGTTATTG      420
GAACTGCAAG GCTTACAAAC TCCTCCCTCG TCCTTTATCC TTATGTAAGC TTGCACATTC      480
TCCAGGAATA GCTATTTTCA AAGGTAATTT CAAAAGAATT AATACAATGA ATTCTACTGG      540
GCAGTTTGGG GGAAAATATT GACGATATTA AAATTTAAAA AATGCCTGCC TGACACATAT      600
AAGGCCTCCC CAGTCCCTCA TACAACCTGA G

```

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

```

GAATTCGGCC TTCGTGGCCT AAGGACAGTG TATAAAAAGG CAGCGTCACA CAGGTGGGCT      60
CTGGGGTCTT TGGTCCATTA GGAGATGGCC TTTGCCTCAG GAAGGAAGGC TTCCCAGTAC      120
TTTGCCAGCT GCTGCTGTGA GTAAAGGAGT GTCTCAAGGT ACTTGATGAC GTGGTCTCTG      180
AAGTCCTTGG ATTTCTCTTT CTCAAACCGT ATCACTTCTT TTCGGACCAC TGTGAAATC      240
CTCTCGAAGT CCCTTTCATA TTGAGTCACC CGAGAGTCCC ACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

```

GAATTCGGCC TTCATGGCCT AGGCTGGCGG GGTAGGGGTT GGTTGGTAAG GCTTGAGCAG      60
AAGGTTCTAG ATGCATTGAG GAGATAAAGA TGCATTTGGG GTTATTGCAC TTCTCCTAGA      120
AACATAAACA TTGACTTCCT TTTGTGGAAG AAAAATGTGA TGTTAGCTAT TTGACGTTTC      180
AGGAAGGGTG GCTTCAGCTT GGNATTTNGG GATGTTTGTG TACANGTGGC CAGGCTGCTT      240
TCTGGCTTGG AAGACTATTG TTTCTTGGGA ATTGTCTGTA TCAGACATCA TGGGAGCAGA      300

```


| | |
|---|-----|
| TCCAGGGCGA CATCAAAGG AACATGATTN NCNNAGGACC AGAGGGGCTT GGATGCAGAT | 360 |
| GATCATCATC TGGGCACTGN TGGATACTGA GTAAGCCCCA GCTGCACCCC ACCTCTGCGC | 420 |
| TCTGAGCATG GGAGGCAGCC TGTGCAGCTA TAACTCAGCC TGACTTTTTC CTTCCCTGCA | 480 |
| TACTCTTGAA ATACACTGGA GATGAGTAGG GCGGAGTGAG CTGCACACCA GAATAAG | 537 |

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ATCTCCANAT AATTNGATC ATAGGCCGGA GTGAGTCATT | 60 |
| CCACCTGCAC CTTTCTGTAC AAATACTAAT TCAATTTTAA GTCTTAAGTC ACTTTTTTAA | 120 |
| TATATATGAT CTTCTGCTCT TCCCACTTCC TCCCNNTCT ACTGCTCTCC CATTITCCCT | 180 |
| TGCTGGGAGT AGCCACATGC TTTTGGCCCC CCAACCCTTG TATATGGGGA CAGTGGGGTC | 240 |
| AGTGCAGCTA CCCTTCTTT CCCTCCTGCG GAACAGCGGA CCCAGCAAGA GCATCCACAT | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

| | |
|---|-----|
| GAATTCGCCT TCATGGCCTA ATTCATGCC CCATATTTGG CATATAGTGG AAGGAGAAAG | 60 |
| GTAGTATTTT TGCAGTATTT AATAACATTG AGCCTTGAAG CTGTTTGGCA AAAGGTAAGT | 120 |
| TTCTTTGTG GCTTTGCTGA AAAACAAGGC ATAGATTTAC ATAGATACGT GTTTAATTCT | 180 |
| CTGCTTCACT AAAGAAAGCA AATGCCTATT AAGCCACTTC AGTTGGGATA ATCCCTGATT | 240 |
| ATTGTGAGAT TGAAATTACT TTGTCAATT TACAAATAGT TTTTATCTTT CCATTACAT | 300 |
| ATTTACCATG ACAACTCGAG | 320 |

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

| | |
|---|-----|
| GAATTCGGCC TTCATGCCTA CAGCGATGAG TGCACGAGTG AGATCAAGAT CCAGAGGAAG | 60 |
| AGGAGATGGT CAGGAGGCTC CCGATGTGGT TGCATTCGTG GCTCCCGGTG AATCTCAGCA | 120 |
| AGAGGAACCA CCAACTGACA ATCAGGATAT TGAACCTGGA CAAGAGAGAG AAGGAACACC | 180 |
| TCCGATCGAA GAACGTAAAG TAGAAGGTGA TTGCCAGGAA ATGGATCTGG AAAAGACTCG | 240 |

GAGTGAGCGT GGAGATGGCT CTGATGTAAA AGAGAAGACT CCACCTAATC CTAAGCATGC 300
TAAGACTAAA GAAGCAGGAA GACTCGAG 328

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GGGGATCCTT TTATTTTAAT CACAAAAATG CTGAAAATTT TGGGTTGCAA TTCAATCCA 60
 CAGTAAAGCA TGGGCATTTT TTTTTTTTTT TTAAATCAGA GTGAACTGCC TCGCGTCTTT 120
 CTTTTTAAGG GTTACACTGT ATGTGTTCTG TGTTTTATT AACTGTTCCC CTCCTGAGGG 180
 GCATTCGCT TGTGAGCT TTTCTCCCTC TTGCTGACAG TGCTGCAGTA ATCATTCTTG 240
 TCCATTITAA TCCCTATGTA TTTACACGGT ATTCTCGAG 279

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GAATTCGGCC TTCATGGCCT ACGGAAAAGG AAACCTTGGT GGGATTGCTG TGGATGACAT 60
 TAGTATTAAT AACCACATTT CACAAGAAGA TTGTGCAAAA CCAGCAGACC TGGATAAAAA 120
 GAACCCAGAA ATTAAAATTG ATGAAACAGG GAGCACGCCA GGATACGAAG GTGAAGGAGA 180
 AGGTGACAAG AACATCTCCA GGAAGCCAGG CAATGTGTTG AAGACCTTAG ACCCCATCCT 240
 CATCACCATC ATAGCCATGA GTGCCCTGGG GGTCTCTCTG GGGGCTGTCT GTGGGGTCGT 300
 GCTGTACTGT GCCTGTTGGC ATAATGGGAT GTCAGAAAAGA AACTGTCTG CCCTGGAGAA 360
 CTATACTTT GAACCTGTGG ATGGTGTGAA GTTGAAAAA GACAACTGA ATACACAGAG 420
 TACTTATTCG GAGAGCATT CCGAG 445

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

GAATTCGGCC TTCATGGCCT AATCATGCCT CCTGCTTTTG TCACCTAATA CGTGACAGAC 60
 TTCTTGCCAT ATGTGGAAT AGATAACTCT TTCACTATTC TTAATAATGG ATATTTAGAT 120
 GGCTTCCATT TGTCCTGTT ATTGTTGTA CATATATTCT TGCATACATT TCCTTTTATA 180
 CTTACTCAAT TATTAGCTGA ACTTTGGAGT AAAATCACTA AGTAAATACG TTTTAGGCTT 240
 TTGCTATGTG TTACAAGATT TCCTGTCAGC AATTAAAGAT ACTTTTATTG CTCCTCACAG 300

CCTTGCCAGA ACTCATTGGG ACACTCGAG

329

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAAAATAGTA AATTCACGAG | 60 |
| GAATTTAATT CCTATTTTGT CCATGTTGGT GATGACTGT ACTTCCCTTC CTTTCTCTG | 120 |
| CATCCCCCAT CACCTCATAG AAGACTCTTT GTTGATCATT GTATGTTAAT AATGTATAAA | 180 |
| ATGGCTATCT TGTAAGCGTG CTGTCCTGGT ACTAGTGTAG CGACTTTTTT TCTCCTCTT | 240 |
| CTTCTAGTAC ATATTGATAG GTATAACATA ATTAAGGTTT AAAAAAATT AGACATAGTT | 300 |
| ATTCAGATT AGGACAGTA AGGATAGAAC TTTCTTTAT TTATGAAAAA AAATGCTAAT | 360 |
| AATTTTGGG CAGTTTTTTC CTTAATTAT TTTTTCAT TTCAAGTTTA ATTTATTTT | 420 |
| AGCTGATCTC GAG | 433 |

(2) INFORMATION FOR SEQ ID NO:1244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACATGACTGA GTATATTACC TCTGTTTGAG AGAGAACCAT | 60 |
| TTTCTTCAGA AATTCATATC CTACCGTTCT GCTGTTTTTC ATGATAATTG TTTTCTCCT | 120 |
| AACATTATAT TTCTGTCTTT TAGATTTTAG TATTTACCT TTTAGAATAC ATTTGGATG | 180 |
| ATGAAGTTGT TTTTCTTATT TCTCCTACCC CCTTCCTTC ATCTCAGACA TTATTTCCCA | 240 |
| GCTTTCTTTG TTTAGCTTT TTATTATGAA AAATGTCAA TGTGCAGAAA AATGGAAAGA | 300 |
| ACAGTACAAC ACACCCCAA TCTCGAG | 327 |

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTGAGAATC TTCACCATTA AACTTAGGAG TGTTCTACAA | 60 |
| AATAGTGCCT AGAACAGCTA TTGATACTCA AGAGGGCTGT TTAAGTAGCT AGAAAAAGTCT | 120 |
| AACCTAAAAT CCCATTTGTG ATTAGATTAT GCACTGATGA AAAAATGTTT AATGCCGTTA | 180 |
| AAAAGAATCT ATTACATTAT ATTCTTTCAG GCCATGGTAA AGTTACAAAT TTGAACCTAA | 240 |
| TAGGCTGTGT GTGTATTGT ATGTGTGTAT TTTTCTTCT TTTATTGGCA GTCTCAATAA | 300 |

TTGTTAAGCC ACACACTGCA CAGTATACAC ACACACTGCA CACCACACAC ACACCACAGA 360
 NTGCACACCA CACACAGCAC AACCACCCAC ACTCGAG 397

(2) INFORMATION FOR SEQ ID NO:1246:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

GAATTCGGCC TTCATGGCCT AGTGGGCAGA TCACCTGAAG TCAGGAGTTT GAGAACAACC 60
 TGGCCAACAT GGTGAAACCC TGTCTCTACA AAAAATAAAA AAATTAGCCA GGGGTGAGGG 120
 CAGGTGCCTG TAGTCTTAGC TACTTAGGAG GCTGAGGCGG GAGAATCACT GGAACCCACG 180
 GGGCGGAGGT TGCAGTGAGC CGAGATCACA CCAGTGCACT CCACCCTGGG CGATAGAATG 240
 GGACTTTTTA AAAAAAAAAA AAACGCCTCA CACGGTTTTA GGTGCTATTA ATACAGTAAG 300
 AAACAAATAA ACAAAGCTCA TTGCCCTTGA TGGACTTTAA AAAATGATCC AAGTATATGC 360
 TGTCTGTAAG AGATACACCC TAGACTCAAA GACACAATA AGCAAATCAA AGGATGAAAA 420
 AGATACACTA TATGCTCGAG 440

(2) INFORMATION FOR SEQ ID NO:1247:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 466 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

GAATTCGCCT TTNATGGCCT AGCCNAACAA AATGGCGGCG GCAGCGGTGT CGTTTTGTTT 60
 CCGGGGNTCC TGCGGCGGTG GCAGTGGTAG CGCCCTTTGA GCTGTGGGGA GGTTCCAGCA 120
 GCAGCTACAG TGACGACTAA GACTCCAGTG CATTCTATC GTAACCGGGC GCGGGGGAGC 180
 GCAGATCGGC GCCCAGCAAT CACAGAAGCC GACAAGGCGT TCAAGCGAAA ACATGACCGC 240
 TGAGCCCATG AGTGAAAGCA AGTTGAATAC ATTGGTGAGC AAGCTTCATG ACTTCCTTGC 300
 ACACTCATCA GAAGAATTTG AAGAAACAAG TTTTCCTCCA CGACTTGCAA TGAATCAAAA 360
 CACAGGTAAA TTGAAAAAGA ATGTGCTATA CTTCTAGTC TTTTTTCTAT TTTTTTTTAA 420
 CATTATGGA GGTAACCATT TATTTTATTC AGAGAGCACA CTCGAG 466

(2) INFORMATION FOR SEQ ID NO:1248:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

TTTGTGTTTG TTTGTGTTTG TTTTGGTAG AGTTGGAGTC TTGCTGTGTT GCCCAAGCTG 60
 ATCTCCAATT CCTGACCTCA AACAGGTCTC TCACCTTGGC CTCCCAAAGT GCTGGGAATT 120

CAGGGGTGAA CCACCTCACC CAGCCAAGAT CACATTTTGA ATCTAATTTT TTTTTTTTGA 190
 AACAGTGTCT CGAG 194

(2) INFORMATION FOR SEQ ID NO:1249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GAATTCGGCC TTCATGGCCT ACCTGTGCAA GAACATGAAA CATCTGTGGT TCTTCCTTCT 60
 CCTGGTGGCA GCTCAGAT GGGTCCTGTC CCAGGTGCAG CTGCAGGAGT CGGGCCCAGG 120
 ACTGGTGAAG CCTTCGGAGA CCCTGTCCCT CACTTGCACT GTCTCTGGTG GCTCCATCAG 180
 TGATCACTTC TGGACCTGGA TCCGGCAGCC CCCAGGGAGG ACGCTGGAGT CGCTTGGCTA 240
 TATTCAATAC AGTGGGATCA CCAACTACAA CCCCTCCCTC AAGAGTCGGG TCACCTTTTC 300
 AGTAGACACG TCCAAGAACC AGCTCTCCCT GAAGCTGAAG ACTGTGACCG CTGCGGACAC 360
 GGCCGTGTAT TACTGTGCGA GATTTAGTGG TTATTATACT AACCCTTCCT ACTACTACTA 420
 CATGGACGTC TGGGGCAAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 480
 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACTCTC GAG 523

(2) INFORMATION FOR SEQ ID NO:1250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

GCCAGAGGGA TGACCGGTGG CTGCTGGTGG CACTCCTGGT GCCAACGTGT GTCTTTTGG 60
 TGGTCCTGCT TGCACTGGGC ATCGTGTACT GCACCCGCTG TGGCCCCCAT GCACCCAACA 120
 AGCGCATCAC TGACTGCTAT CGCTGGGTCA TCCATGCTGG GAGCAAGAGC CCAACAGAAC 180
 CCATACCCCT CGAG 194

(2) INFORMATION FOR SEQ ID NO:1251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GAATTCGGCC TTCATGGCCT AAGCCCACTG GCATCAGACA TGCTTTGCTG TAGTGATAC 60
 TTCNTTTTTC NTTTTNTT TTTTTTTT CACACAGAGC CNGGNTCCGT CCCCCAGGCC 120
 TGACTGCAGC GGNANAATCC CACCCACNG CCACNTCCGC CACCCAGGCC CAAGCGGTTC 180
 CCTAACGGCT AATGATGTTG AACATCTCTT CATGGGGTTA CATGCCATCT TTATATCCTC 240
 TTCAGTGAAA TGTTCTTAA CATCTTTTGC TGTTTCTAA TTGGATTACT TGGGGTTTTT 300

| | |
|---|-----|
| TAATACTGAG TTTGGAGTTA TTTATATATT CTAGACAGTA GTCTTTATTG GATATGTGCT | 360 |
| TCAAAAATAT TTTCTCCCAG TCTGTAGTTT GCCTTTTCAG CCTTTTAACA TGGTCTTTAG | 420 |
| CAGACCAAAA TGTTTTAGTT CTTATGAAGT CCAACTTACC AATTTTCCT TTTCTAGATC | 480 |
| ATACTTTTGG TGTCAAGTCT CAG | 503 |

(2) INFORMATION FOR SEQ ID NO:1252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

| | |
|---|-----|
| GAATTCGGGC TTCATGGCCT AATTGAATTC ATGATTGTG TCTCTGCTTG CCTGTTGTTG | 60 |
| GTGTATAGGA ATGCTAGCAA TCTTTGCACA TTCATTTTAT ATCCTGGGTT TCAGTATTTT | 120 |
| AAAAACTTAC TTCAGGTGAT TCTATGTGTG CAACCATGAT TGAGATACAC TGTTATAGAA | 180 |
| TCTAGGATGT GATAAAGTAG AAGAACATAA CTAAAGTTTT GCATTTTTCG GGTGTCTCAG | 240 |
| TTTCCTCATT TATAGATGGA GTTGGTATGT GTACCAAGTT CATAGGCTTG TTCTGAGTAA | 300 |
| ATTAGTGCAT GTAAAGTGCT CCACAGAATG TTAGCTGTTG TGATGCTTTA CTTTCCATTG | 360 |
| CACTTCCTGA CTCCTAGCCT TTCTTTTCCT TGGCTCTTTT TATGCTCATG TCAGATGCCT | 420 |
| CTATTGTTTC TTTCCCCCA GAATATCCTC CACTTTATCT TGCTCTGCTC AACATCTTTA | 480 |
| AAGTATAGAA TCAACAGACT GCCATGCCAC CCAGTCTGTC TGACAATTGA GGCAAATTCC | 540 |
| CTAAGTCCTC TTGTTCTCCT TCTGAGATTT CCACCTGCTC TAACTCGAG | 589 |

(2) INFORMATION FOR SEQ ID NO:1253:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACATTTATCG AGTCTTTAAT TAATGCCCTG GGTAACATA | 60 |
| AGGTGGAAC TGTAATTGTC ACCATATTGA TGATGAGAAA CTTGAGAAAG GATAAGTGAC | 120 |
| TTGTCTAAAA TCACACAGTA AAACCTCAAA TCAAACCCAG GCCCTCTGGC TCCAGACTCT | 180 |
| AAATTATACT CTGAATGATA CTCACTGATT GTCCGAGGAC ACAAAGACTG TCGAGGCACT | 240 |
| ATCTGCTGGG TGTCTGCAGA ACCTTACTGT TCTAAAGCAA AACATTTTAC CCCTGGACAA | 300 |
| GAGCAGCAAA GGTGGCGTTC GGCCCTCCTT GGCTCTCATT TGACTGTTCA AAGCCAGGTG | 360 |
| CTTTTCTTTC TTGGGTCAGA ACGTATTTTC AGCAGCATTT TGAAGCACCC CTGGCGTGCA | 420 |
| CTGCACAGGG AAACCAGGAC CACATTGGTG TGCTGTGTCC TCCTTACCAA CTGGCTCTTG | 480 |
| GAGAAGGTGA GACAGAAGTA GCTGAGACTC CATTCTGAG ATCTTCACTT AACCACTCCT | 540 |
| GCAGCTTGTG CAGAGCCTTA CTAGAAATAC TGAAGGCAGA AGTCCCTGGA AAATAGGGCC | 600 |
| CATAACTAAT TAGTAATTTG TTTTGTAGTA ATTTCTTACC GTTATTTGAG CACATTCTGC | 660 |
| AGTCCAGGCA TTTTGCTAAA CTCTTACATG GCAGGACTCG AG | 702 |

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAGCAAGTAA ACACTGTATA TCTGTAATTG GAAAGTTGGT | 60 |
| GGGAAGATTA CTTTCCATT CTTGATGTGG CAGCCTTAAG TGCCATCACA GCTTGTCTG | 120 |
| TGGTTGCCT TTTTTTTC AGTGACCTCA GCTCACTGCA ACCTCCACCT CCCTGGTTCA | 180 |
| AGCAATTCCC CTCTTCAGC CTCCAAGTA GCTGGGATTT CTGGTGCATG CTACCAGGCC | 240 |
| TGGCTAATTT TTTTTGTAT TTTTAGTATA GACAGGTTT CATCATGTTG GCCAGACTGG | 300 |
| CCTCAAATC CTGACCTCAG GCAATCTGCC CACCTCAGCC TCCCAAAGTG CTGGGATTAT | 360 |
| AGGTGTGAGC CACTGCGCCC AGCCGACTTT CAAATTTTTT AACCACAGCC CAGTGTAAAC | 420 |
| CTGTGTGTAT GTGTGTGAGT GTGCTTGTAT GTGTGTTGA AATAAAATTT TTCATGTGCT | 480 |
| TAAACATTCT GATTTTTTTT TTATCAGAAC CACTAATGAG ATGAGACCAT AGTTTGTAAC | 540 |
| ACCTCATGCT CGAG | 554 |

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCTCCGGCA CATGGCAGGC ACTCAGGGAA AGTATGTAGC | 60 |
| CTTATGAACT GACTGATCTG AGGGAGGCAC TTCTGTAAGC CATAGTATTG GTCAGTGGCA | 120 |
| TGAGGCCACC TACTGGATCC CTGCCATCCA GCCCTGGGAG TAGCATGAAG CAGCATGGCA | 180 |
| CTGGCCTTCT GGAAGCTTGG AGAGGAGTCT TACCCAAGCT TTGCTCCTAG ACATTAACT | 240 |
| TCCCAGCTGG GCACTAACAT GTGGCTGCAG AACCTGCCCT TGCTCAGTCT GTCCCTGGTG | 300 |
| CAGCTGCTGG GAGAGCCTGC CTCGAG | 326 |

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACATTAAGGC AGCTTTGTAA GTAAGTACAA AATATATTTT | 60 |
| AACCTACACA ATTTTATTA GTTCCCTCT CTTTGAAG TACACCGACT CTAAATGAA | 120 |
| TGAAAGTCTG ATTACTTGCC TTAGGTTGGG GGCTTTATCC AAGCTCTACT AAGTGAAGCT | 180 |
| AAAATAAAGG ACATTGTTGT ATATTGTATT TTAATGTATA CATTATTACC TCCTCAGCAA | 240 |
| AGTGAAACAT AGCTAAACT TGAGTATATA TTTCTTCAT TTCTCTTCT AGTTCCTTTT | 300 |
| TGGCATCTCA TGCTGAACAA ATCCAAATA GATTTATTAA TGCCTTCCCC CAACACAAAC | 360 |
| AAAACCAGAA GAGTCTTTCG CTCTAGACC TGCCTCGAG | 399 |

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTGAGTACA GGTTTGGGAT CTACATACCC AGATCAACAG | 60 |
| CATGTGGCAT CACCTGGCCC AGGTGAGCAT GACCAGGTAT ACCCAGATGC AGCTCAGCAT | 120 |
| GGCCATGCTT TCTCTCTCTT TGACAGTCAT GATTCAATGT ATCCTGGTTA TCGTGGCCCCA | 180 |
| GGGTATCTAA GTGCTGATCA GCATGGCCAG GAAGGTTTGG ATCCAAATAG AACACGAGCC | 240 |
| TCCGACCGAC GTGGAATTCC TGCCCGAAG GCCCCAGGCC AAGATGTCAC TCTTTTCAGG | 300 |
| AGTCCAGACT CCGTCGACCG AGTCTTATCA GAAGGGAGCG AAGTCTCGAG | 350 |

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AATTGAATCG AGCTGGTTAA GTTCACTAG GAGGCGCNAA | 60 |
| AAAGGAGCCG TTTTGGACTT AACATTTTAA TTCTAGTAGA GATAAGAAGA GCTTGTGTGG | 120 |
| GCTTACAGTC CTTACCTGA CTGTCCTTCA CCAGTGAGTA GCATACCAGT TCTTCAAATG | 180 |
| TCCTATACTT TGGAAAGCAG ACCCGACTCT GGAGCACTCG CCTTAATTAG ATTCTGAATT | 240 |
| TCCTTGAATT TTGGATGGTC CTTATCAGCT ACCAGCTGAA GCAGAACAGC CTCACTCGTG | 300 |
| GTCACATGA TCCCGGTTCT AGCGAGACGC TCGAG | 335 |

(2) INFORMATION FOR SEQ ID NO:1259:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

| | |
|--|-----|
| TCCAGTTGAA TTTAATAGAA TTCGGCCTTC ATGGCCTAGC CGACCGTTGA CTATTCTCTA | 60 |
| CAAACCACAA AGACATTGGA AACTATATACC TATTATTCCG CGCATGAGCT GGAGTCCTAG | 120 |
| GCACAGCTCT AAGCCTCCTT ATTCGAGCCG AGCTGGGCCA GCCAGGCAAC CTTCTAGGTA | 180 |
| ACGACCACAT CTACAACGTT ATCGTCACAG CCCATGCATT TGTAATAATC TTCTTCATAG | 240 |
| TAATACCCAT CATAATCGGA GGCTTTGGCA ACTGACTAGT TCCCCTAATA ATCGGTGCC | 300 |
| CCGATATGGC GTTTCCCCCG TGATGCTAG TTATATTCT CCAACATAGA TTAATACAT | 360 |
| ACATGACTAT TAAAATCTCA GGGTTCTTCT ATGTGTCCCC TAAAAGCATG ATGTATGCCA | 420 |
| GTGGTCATCT GTCCACCACC ATTTGGGGAC CACGGCATTT AGGTAAAGTG GGTCTCGGAT | 480 |
| GACCTCCTTC AGCTTAACAG CAGGAGTTGA GATGGAGCCC TTGCAATTTT CCCACTGAAT | 540 |
| TCCAGAAGCA AGGAGAAAGA CTGAAGTGAC AAGTACCGCA AGACAGACTT CAGGAACAAT | 600 |
| TCGTTTAAGC TGCAGCTCGA G | 621 |

(2) INFORMATION FOR SEQ ID NO:1260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

```

GTTTGTGAT TCTCCAGGAC AGATGATGAA AAACAGTGTA GATAGTGTC AAAATTCCAC      60
TGTAGCCATA AAATCTCGAC CTGTTTCAAG AGTTACCAAT GGAAGTTCCA ATAAAAAAG      120
TATTCATGAA CAAGACACTA ATGTAAATAA CAGTGTACTA AAGAAAGTCA GTGGCAAAGG      180
ATGTAGTGAG CCAGTACCAC AGGCAATTTT GAAGAAAAGA GGAAGTAGCA ATGGATGTAC      240
TGCAGCTCAG CAGAGGACAA AGAGTACCCC ATCTAATCTT ACTAAACTC AAGGATCCCA      300
AGGAGAGTCA CCAATACTCG AG                                     322
  
```

(2) INFORMATION FOR SEQ ID NO:1261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

```

GCCCTCATGA CTCGGATCCA ACCTGCCTCG CAGGGAGTCG AGCTCTCCGG CCTCTCAGCC      60
GCCATCAGCC ACTTCCTGAA CTGCTTCTCG AGCTCCTACC CAAACCCCGT GGCCCCACCTG      120
CCCCCGCAGC AGCTGGTCTC CAAGAAGCGG AATAAGAGGA GGAAAAACCG GCCCCCGGGG      180
GCTGCAGATA ACACAGCCTG GGCTGTCATG ACCCCCCAGG AGCTCTGGAA GAACATCTGC      240
CAGGAGGCCA AGAACTACTT TGAATTCGAC CTCGAG                                     276
  
```

(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

```

GAATTCGGCC TTCATGGCCT ACAAAGAAAG CAAGCCACAA ACAATAATGA AGCAAAAAAT      60
GGAATCTAAG AATCTTTTTG TATGGAATAT TACTTCTATC AGAAGATGAT CAAGATGTTT      120
CAGTCCAGTG CACATCAGCA TTGCTGACAT TTATGGATT CTAACTTGT GTTGTCTTCTT      180
TTTTAAATCA ACTTTTTAAA AAAATAAAGT GTAAATTAAC CGACTAGAGT ACTTGAAAAA      240
TGTGATCAGT ACAAGTGAAC TTAGGTGTT GCCAACAGGG TCCGTACTCG AG                                     292
  
```

(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

| | |
|---|-----|
| CCGATTGAAT TCTAGACCTG CCTTGATGCC AACTAAGGAA ATTTGTTTAG CATTGAATCT | 60 |
| CTGAAGGCTC TATGAAAGGA ATAGCATGAT GTGCTGTTAG AATCAGATGT TACTGCTAAA | 120 |
| ATTTACATGT TGTGATGTAA ATTGTGTAGA AAACCATTA AATCATTCAA ATAATAAACT | 180 |
| ATTTTATTA GAGAATGTAT ACTTTTAGAA AGCTGTCTCC TTATTAAAT AAAATAGTGT | 240 |
| TTGCTCTGAG TTCAGTGTG GGGCAATCTT GGGGGGGATT CTTCTCTAAT CTTTCAGAAA | 300 |
| CTTTGCTGTC GAACACTCTT TAATGGACCA GATCAGGATT TGAGCGGAAG AACGAATGTA | 360 |
| ACTTTAAGGC AGGAAAGACA AATTTTATTC TTCATAAAGT GATGAGCATA TAATAATTCC | 420 |
| AGGCAATGCG CAACTCGAG | 439 |

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGGGAGGCC GCGNGGGGA AAATGGCGGA CGGGAAGGCG | 60 |
| GGAGACGAGA AGCCTGAAAA GTCGCAGCGA GCTGGAGCCG CCGGAGGTGA ACACAACCCC | 120 |
| AGCGTCGTGG GCAGCGTGGG ATGCTCCGGG CCTTTCTTTG AGCTCCCAAG GTGGGGGGAG | 180 |
| TGGGGTGGGG CGAAAATGGG CGGATCTGGA CCTCACCCGG ACAGGTGTTG GGCCCAGACC | 240 |
| TGCCTCCGGG CNCGCCCCGA TCGGCGCCTC CTGGGCTCCG GGCCTACATC GCCTCCTTGC | 300 |
| CTGGGGAGAG CCGGCCACTG TTCGTCACTT CCTGGCCCCA GCGGAGGCCC TGATTCCGAG | 360 |
| GAGAAGGGAG ATGGGCGCCA GAAAGGGAGA CCGAATCGG GGTGGGACCA GGAGCGGCGG | 420 |
| TGCAGGAGCC GCTACCGCCA CACCGGAGAC GCACATCACA CAAAACACAC ACACCGGATT | 480 |
| CTCGAG | 486 |

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATTTATTGT TGGATCAATC AAAATTTTCA TCACTTAAAA | 60 |
| GAACCATGTC TATTAAAGAA TCTAGCTCAC TGGAGTGCAT TGCCATTCCA AAAAAGAAGA | 120 |
| TGAATTTAAA AGATAAAAGC CATGAAGGTG TTGCTTGTGT CCAGAAAGAA AAATCAGTAG | 180 |
| TTAAACCTG GTTCTGTGAA TGCAATCAGC GATTCCCAAG TGAAGATGCA GTAGAAAAGC | 240 |
| ATGTTTTCTC AGCAACACA ATGGGTTATA AATGTGTGGT CTGTGGAAAG GTATGTGATG | 300 |
| ATTCAAGGGT TCTCGAG | 317 |

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

```

GAATTCGGCC AAAGAGGCCT AATCTTTTCC TTTCTTGTA GTTAGAAGAA ATAACCTCTT      60
CAGTTAAACC TTCAGTGAAG GTTCTTTTAG TTTCTGTTC TGCTTTCTAA AAACATAGAC      120
TCTGTTCTTT AGAGCAACTT ATGACTCTCA TCTCTGCTGC ACGAGAATAT GAGATAGAGT      180
TCATCTATGC GATCTCACCT GGATTGGATA TCACTTTTTC TAACCCCAAG GAAGTATCCA      240
CATTGAAACG TAAATTGGAC CAGGTAACCT CTTACTTTTT ATTCATTTTT CCTGACTATG      300
TACTTGAAAC TAGAAGTTTA CTCAGTTGCT TTTACGATGT TAAAAGGAAA TCAAATTCCT      360
ATTCTTTTGT TTTCTTTTTT TGTTTGTTTG TTTTGTTTT TGAGACAGAG TCTTGCTCTG      420
CACTCCAGCC TTGGGCAACA GAGCAAGGCT CTCAAATAA AAAAGCAGCG ACACTCGAG      479
  
```

(2) INFORMATION FOR SEQ ID NO:1267:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

```

GAATTCGGCC AAAGAGGCCT AGGGTTTATG CCAACAAAAG GAGAGGGAGC CATAGGTTCT      60
CTAGATAACA CTCCTGAGGA AAGAAGAGCA CTTGCCAAAA AATCACAAGA TTTCTGTTGT      120
GAAGGATGTG GCTCTGCCAT GAAGGATGTC CTGTTGCCTT TAAAATCTGG AAGCGATTCA      180
AGCCAAGCTG ACCAAGAAGC CANAGAACTG GCTAGGCAAA TAAGCTTTAA GGCAGAAGTC      240
AATTCATCTG GAAACACTAT CTCTGAGTCA GACTTAAACC ACTCTTTTTC ACTAACTGAT      300
TTACAAGATG ATATACCTAC AACATTCCAG GGTGCTACGG CCAGTACATC GTACGGACTC      360
CAGAATTCCT CAGCAGCATC CTTTCATCAA CCTACCCAAC CTGTAGCTAA GAATACCTCC      420
ATGAGCCCTC GACAGCGCCG GGCCGAGCAG CAGAGTCAGA GAAGGTTGTC TACTTCACCA      480
GATGTAATCC AGGGCCACCA GCCAAGAGAC AACCACACTG ATCATGGTGG GTCAGCTGTA      540
CTGATTGTCA TCCTGACTTT GGCATTGGCA GCTCTTATAT TCCGACGAAT ATATCTGGCA      600
AACGAATACC TCGAG                                     615
  
```

(2) INFORMATION FOR SEQ ID NO:1268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

```

GAATTCGGCC AAAGAGGCCT ACAGAACTTT TGTCAAATGG AGTGTTACCC ACAGTCAGAA      60
TCTAGCCACC AAAATGGGAA GGGAGTGNAG CTGCCCTGTC CACAGGCTTC TCTATGGGAA      120
ANGCTGCTGT TCTGTAAAAC ATGNTGGGGC NGGCTGTGGG GANGAAGGCA TTTTCTGGAC      180
CACATGNACG AATTGGAATT GGGGGACGGT CCTACCCAG TGAGGAAGCT GAAAGAAATG      240
GGCCTGATTT GGTGCAGGAC ANCCCTGAA GACCGTGAGG CCCCTGGCCT CTGCCGCAGA      300
  
```

TGGGAGCCTC AGCAGCANGG TTTAGGGCAG CACCCAGGGC ATCCTTGCCA CGTGAGGCTG 360
 CCGTTGGTGC CTGGGCATCA GTAGCTCAGG CTGGAATAAT TGGAAAGGAA AAGGCAGGAG 420
 GANCCCCCTGA GGCCAGGCCA TTGGGCTGGG GAGCTGTAA GCTGAGGTGG CCCTAGGGCC 480
 TGCCGGGGCT GGGGGTGGCA AGCCAACTC TCGAG 515

(2) INFORMATION FOR SEQ ID NO:1269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GAATTCGGCC AAAGAGGCCT AGTGCAACTG ATCTGTCCAG TTTGTGTATG AAATGGATTT 60
 GATAAAGTTT TTGCTAGTTA TTTACTACAT TTTGGGATTA ATAAGTGATT TATATGCATA 120
 TTTTCTGTGA AATCTACAGT TTTTGTACA AGATATTCTA CAAGTTATGA AGCTAAGGGA 180
 AGAAAATGCC AAAGATACCT CTAGTTATGT TGAACACAGC CAGCTCGAG 229

(2) INFORMATION FOR SEQ ID NO:1270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

GAATTCGGCC AAAGAGGCCT AGTATGCCCT TAAATCTGGT TATTAGGTAA TTCTTTTCCG 60
 AGTAGGAGCC CAGATCAACT CACAGTGTTT CTGAGTCTCG GGAGATTGAA TTCTAGACCC 120
 GCCTCGAG 128

(2) INFORMATION FOR SEQ ID NO:1271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GAATTCGGCC AAAGAGGCCT ATTTAGCACA AATTCTTTT TGCTTGCCTT TTCAGATTTT 60
 AAAACTATTA GAGAAAAACA TACTTGATTG CTAAAATTG TCAAACATAA ATAGTAGACA 120
 CAATTAGTA ATAATCATAT TAATAATCAT AATCATTAAT ACTCATAATA ATCANACAGA 180
 GGACGCCCTA AAATGTACAC TGATTAAATT TTATTTTTTT CCCATGCATA GCTAGCCTGT 240
 TTGTACAAC TTTACTTTTGC TGCTGCATGT AACCAGATGA TTTTAAATC AGATTACTGC 300
 CTTTCTGATT TATTTAGAAT TTTTCTTCTT TTTTCTTCTT AAGAGACGGG ATCTTATTCT 360
 GTCGCTCAGG CTGGGGTGCA GTGATGTGAT CCTAGCTTAC TGTATTCTCG AG 412

(2) INFORMATION FOR SEQ ID NO:1272:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

```

GAATTCGGCC AAAGAGGCCT AGTTTTAAAG GACAGGTTTA AATAGGCTTA CTTTTTCTT      60
TTAAGTTCAG ATACCTAAGC CTTATGTCCC TAGCCGCAGT TTTCAGATAT TTGCAGCTAA      120
TTAATTCTTA GGAAATCTAA TCTGAATTGA ATTAATTTTC CCTTTTAGGG CACACGAAGC      180
AACTTTTtagg TAAGAAAAAA AATGAAAACA GCTTTTGTTG CACATAATTC TTGCAACTAA      240
TGAAAAGTAA TATTGCTGTT CCCTTCAAAT AATGCAATAA CAAAACACCA AATGAGAGCA      300
TTGCATTGTA TTGTTATATT TGCTGTTTAA ATAATTTAGC TGCAAAAATC TGAGGGCTGC      360
TTTAGCTGTA ATTAATTATT CATTAAATGAC ATGCTAATTG CACAATACCT TTGAATATTT      420
AACAAAATGC AAAAACCAGG CTCTGAAGTT ATGTTTTTtag TGCAAGGGGG ACACCTCGAG      480
  
```

(2) INFORMATION FOR SEQ ID NO:1273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

```

GAATTCGGCC AAAGAGGCCT AAGACCAGCC TGGGTGACAG AGCGAGACTC CGTCTCAAAA      60
AAAAAATTGA ATGAAGCAGA AATTTATTCT TTTAAGCCCA TTtagCTGTT ACACACATAG      120
TTATAGCATA TTCTCTCTTG AGATAACTTG CTTTAAATTG GAAAACTAAT TCATTAAATA      180
TCCAAACTCT ATATCATTTT TGAATAAGT GATTTTAGCA ATTTTGTATA CTTATTCTAA      240
CATGATGCAT ATATTGAGTA TGTACTTTTC TTAAATGCA GGCAATACTC GAG              293
  
```

(2) INFORMATION FOR SEQ ID NO:1274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

```

GAATTCGGCC AAAGAGGCCT ACCGCTTTTT TTTTTTTTTT TGATAAAGAG AAGCCACCAC      60
CAGGAGGAGG CTTGAAGCT TGAATTTAAT TACTCCTCCA TCTCCTCATT ATTCCACCCA      120
ACTCCCTACT TCCCCATCTC ATTCACAGC CTCACCAGC TCTCCCTCA GGCCTCCTAG      180
ACATCGCGCT CGAG              194
  
```

(2) INFORMATION FOR SEQ ID NO:1275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGAAGAAGA AAGAAAAATT GGAGAGAAAA AAGGAGTCTT | 60 |
| TAAAAGTTAA AAAGGGTAAA AATTCAATTG ATGCAAGTGA AGAGAAGCCA GTTATGAGGA | 120 |
| AAAAAAGAGG AAGAGAAGAT GAATCATACA ATATTTCAGA GGTC | 164 |

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTGGATGG CAACGAGCTC ACCCTGGCTG ACTGCAACCT | 60 |
| GTTGCCAAAG TTACACATAG TACAGGTGGT GTGTAAGAAG TACCGGGGAT TCACCATCCC | 120 |
| CGAGGCCTTC CGGGGAGTGC ATCGGTACTT GAGCAATGCC TACGCCCGGG AAGAATTGCG | 180 |
| TTCCACCTGT CCAGATGATG AGGAGATCGA GCTCGCCTAT GAGCAAGTGG CAAAGGCCCT | 240 |
| CAAATAAGCC CCTCCTGGGA CTCCTCAAC CCCCTCCATT TTCTCCACAA AGGCCCTGGT | 300 |
| GGTTTCACA TTGCTACCCA ATGGACACAC TCCAAAATGG CCAGTGGGCA GGGAAATCCTG | 360 |
| GAGCACTTGT TCCGGGATGG TGTGGTGGAA GAGGGGATGA GGGAAAGAAA TGGGGGCGCT | 420 |
| GGGTCAGATT TTTATTGTGG GGTGGGATGA GTAGGACAAC TCGAG | 465 |

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AACTGTGGTT CTTACATCCT AACAAAAGCT GCCCTCCCCG | 60 |
| CACATTCTTT TGTATGTTCC TTAAGCTTAA AGATGAATAG ATGCTTAAAG TATGCAACTA | 120 |
| TGGCATTGG AGTGCAAGAC AACTTGAAAA AGAGTGTGAA AACATTGTCA GATATAAAGT | 180 |
| TACTTCAATT CTTTGGAGTC TGTTTCCTGT CATGCTTAGA TGTTTGGAAT CTTAAAGTTA | 240 |
| CAGAGGAAGT GTTCTCTGGT AACAAAGACAT GTCTGAGTTT GTGGACTGCA CGCGATCTCG | 300 |
| AG | 302 |

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGGGT TAGCCTAAAG GAGAAAAAAG | 60 |
| CAAGGCTCAA GAGAAATTAG ACAGCAGCTT TCAAATATTT TTAGAGAAAGT AGGTTAATTA | 120 |
| TGSTAGTCAT TCAACAAGGT AGAAATCATA CCAAGCATGA AGTCACAGGA ATGTCCCAGG | 180 |
| AGTGTGCAAC CATTGGAAGT GTCCATAGTA AAATGGGCCA GCTTGAGCAA TAAAAGTCTC | 240 |
| CTAGTACCAG GAAATGCTTA GAGGTGGGG AAAGTGAAAA AAAGGGGGAA AGTTTGGTCA | 300 |
| GGTTGGGGAG CAGTCACACT TCTTCCTGAG AGGTAGTAAA TACCAGGCTC TCCATCTGGA | 360 |
| GGAGGGGTCA GTAAATCAGG TTTGCAAAGG AATATCTCGA G | 401 |

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACCCACCCT ACTCCTCAAC ACTTCTGGTT TGCCCTGACT | 60 |
| TCTCTACGGC TCTGGCTTCT TCCCGAAGAG ATATAGGAGC CATGTAAGCA CGCAGTGGGT | 120 |
| GAAGTCTTA ATTTCACTAC ATGTTGATGT ACTTGTCTTC CGTCTGTAG GTCTTTTCTA | 180 |
| TATAACTTTA TGCCACCCTT AAATGAATCA TTGGGTATAC CTGTCTGTT GGATCCTGTA | 240 |
| ATCACAGTTT TCCCTGCTCA CCTTTTGTG TAAGATCTAT TGAGAAAGG AAATATGGGA | 300 |
| AGGAGAACCA TTTGATCAGA ATACAACCAA TAGTCTTTAA GCATTGTTAA AGTATGAAAC | 360 |
| TGAAATACAT TCAAAACACT TTACACTCGA G | 391 |

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGACTCCAC ACTCCCCAGA TCCAGTATG ACTACATCTT | 60 |
| GCCTCAAGTT TCTTTCACCG CAGTGGGCTA CCATAAACAC ATCACCTTGA TTTTAAATCC | 120 |
| CACGAGGAAG CTGCCTGAAC AGGACATCGC ACAAGGATCC TACATTGCC TGCCATTGAC | 180 |
| GCTGCTGGTT CTGCTGGCCG GTTACAACCA TGACAAGCTC ATTCCTTTGC TGCTGCAGTT | 240 |
| GACAAGCCGG CTACAGGGAG TCCGCGCGCT CGGCCAGGCA GCCTCTGACA ATAGCGGCC | 300 |
| AGAAGATGCA AAGAGACAAC CTCGAG | 326 |

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACAGATGCAG ACACGGTGTC CGACGAGTAT TCTGACGAGG | 60 |
| AGGTGCTGGA GGACGTGGAT GATGCCGCCT ACTCCATGGT CAGTGCCTCC CATGTGACCG | 120 |
| CCCGCACCTG GGCCGCTGTC CGTCTAGCCG TCTAACAGTC TTACACCTTG GCTTTCTCTG | 180 |
| TCCCTTGAAA GAATTAATA TATCTACTGT GGACTGTTTC ATAAAACCAA CCTATGGTGT | 240 |
| TGCCGGGCAC AGAACAAAGC TGTGTTTCAC TACTGAAGGG ATGATTGGGT TTCTATATCA | 300 |
| TAATTACTTT TAGCTTCAGA ACAGACCCTT GTTCAAACAT CTCATGATCT TCGCTAACCA | 360 |
| TCTCGAG | 367 |

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGAGAAGTG TCAGCCTCAC CTGATTTTTA TTAGTAATGA | 60 |
| GGACTGCGCT CAACTCCCTC TTTCTGGAGT GAAGCATCCG AAGGAATGCT TGAAGTACCC | 120 |
| CTGGGCTTCT CTTAACATTT AAGCAAGCTG TTTTATAGC AGCTCTTAAT AATAAAGCCC | 180 |
| AAATCTCAAG CGGTGCTTGA AGGGGAGGGA AAGGGGGAAA GCGGGCAACC ACTTTTCCCT | 240 |
| AGCTTTTCCA GAAGCCTGTT AAAAGCAAGG TCTCCCCACA AGCAACTTCT CTGCCACATC | 300 |
| GCCACCCCGT GCCTTTTGAT CTAGCACAGA CCCTTCACCC CTCACCTCGA TGCAGCCAGT | 360 |
| AGCTTGGATC CTTGTGGGCA TGATCCATAA TCGGTTTCAA GGTAACGATG GTGTCGAGGT | 420 |
| CTTTGGTGGG TTGAACTATG TTAGAAAAGG CCATTAATTT GCCTGCAAAT TGTTAACAGA | 480 |
| AGGTATTAA AACCACAGCT AAGTAGCTCT ATTATAATAC TTATCCAGTG ACTAAAACCA | 540 |
| ACTTAAACCA GTAACGAG | 560 |

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTCATCA ATAGTAAGTT TTTATTGTCT GCTAATTGG | 60 |
| TAGATAAGTT GAGACATCTC ATTGTACTT TAATTTGCAT TTTCTCCACA TTAGAAAATA | 120 |
| TTTTCATTGG TTTATTGACC ATTTGCATT CTCTTCTATA AATTGACTTT TTATATTTAT | 180 |
| TTGTCTCTAT TTCTGTATTC TGTGATAGT CAATTTATAG GAACCTTCTG ACAGATATGC | 240 |
| ATATTCATTT TATGTGTGAG TTATTTTGT GGCACCTACT CGAG | 284 |

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACTTCGGTTG CGGGATTCTT CCTCTGCCTG GGTCATTCTT | 60 |
| TCTCGTGTCA TCTGATACGA GTCGTTTGTG GCACACACTG TAATTTTATC TTGTATAAAT | 120 |
| CCCAGGCAAT TGAGCTGGGA GGCTCCAGAG CTGGAGAAATG TTTGCTGGAT GCAGTCAAAG | 180 |
| CTGCCCTGAG GGTGTCTTT GCCCACATTT GACAAATAAA AGTTAAAGTT ATGAACTTCA | 240 |
| TTGAGGGGAT CATTTTGGG AATTTTGACA AGCCCGTGA GTCTTGGA CTGGATTGAA | 300 |
| GGTCGAAAAG GAATTAAAT CTTGTGGCTC TGGTAAGTCT CGAG | 344 |

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGGAATTTG TTTTGCATA GGGGAATAGG TAAACCAAAA | 60 |
| GTGGTATTAA AAGCAGTGCT ATAGTAAAAG GAGATTTTTT TTAAGTCCAC AATAAAAAGT | 120 |
| TTAGGCCCAA TTTCATAGTA AACTATTCT AATTAAGGAT TGAACATATT ATCACTTGCC | 180 |
| TTGATTTTGA CCAGTGACAT TTTTGGCTT CTCATTTC ACTGTGACCA TCTGAATGCT | 240 |
| TTCTATTGG CTCTTAAATG CCCAGATTTT ATTGACATG GTGGCGAATC CCTATTCTA | 300 |
| CACAGACAAA GCATCTGACT TTGTCCAAGA AGCAAGCATG CTGCAGGCCA CTATGACGAA | 360 |
| GCAAGAAGCC GATGACATGA GCATTCCCAT CTCCACATT GACGATGTTT TCGACATGGT | 420 |
| GGATGTCCTG GTGGAGGGCA GTGAAGGCTT GGATGAGGAA ATAGGGTTCA CGTTGAGTGA | 480 |
| AGACATGATC CTGCTCACGT TCCCATTCAG TGCGGTAGTC CCTGCGGCCC TGGAAGCCAG | 540 |
| GAATAAGTTG CTCCTTGGGA CAGGCAATGA AGCAGATACC CTCGAG | 586 |

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTTGAACAT AACTGTAGT GTGAATATGG TTAACAACAA | 60 |
| GGACACCTGA TGTCTGTGAA GTCTGCTAAG GACAGGTACA AAATTTATGC ATTGCTTTTT | 120 |
| AAAAAGTTTA AAATGAGGAA TGCTTTTGAT AATCAGAAAG ACTAATGTAA AGTGCTGACT | 180 |
| GATGTCCTGT CTGCAGTTAA GGAAGACACC CAACTCTCTT CTTCTCATC ATGGTATTCT | 240 |
| CTATGTATAG ATCTCTAAAA ATGCAAACTT CCTATGGACA AGACAATATG ATTGCTATA | 300 |
| ATATGAATTA AGATATGGTA ATATCTAATA GTCTCCACTG CTAGGATTCT GAGTAACACA | 360 |
| AAAAATAGGT TTTATAAAAA GCCCATGCAC TTCAATTGGT GGGGAAAAG AATAAAGTCA | 420 |
| TTTTCAGTCG ACTGACTCTG TAAAACAGAT TACCAATATA ACAAGCTATG TTATCTAAAT | 480 |
| TGCCCTGGCT ACTCGAG | 497 |

(2) INFORMATION FOR SEQ ID NO:1287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

```
GAATTCGGCC AAAGAGGCCT ACAGGAGTTC ATTTTCATCC AAAACAAACA CTGGA CTTC      60
TGCGGAGTGA CATGGCTAAT TCCAAAATCA CAGAAGAGGT GAAAAGGAGT ATAGTAA AAC      120
AGTATCTAGA TTTCAA ACTT CT CATGGAAC ATCTGGACCC TGATGAAGAA GAAGAAGAAG      180
GGGAGGTTTC AGCTAGCACA AATGCTCGGA ACAAAGCAAT TACCTCACTG CTTGGAGGAG      240
GCAGCCCTAA AAATAATACA GCAGCAGAGA CAGAAGATGA TGAAAGTGAT GGGGAGGATA      300
GAGGAGGAGG CACTCCCGGG GAACTCGAG                                     329
```

(2) INFORMATION FOR SEQ ID NO:1288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

```
GAATTCGGCC AAAGAGGCCT ATGCATCGCG GGAGGCGCAT GGCGGGGATG GCGCTGGCGC      60
GGGCCTGGAA GCAGATGTCC TGGTTCTACT ACCAGTACCT GCTGGTCACG GCGCTCTACA      120
TGCTGGAGCC CTGGGAGCGG ACGGTGTTCA ATTCCATCCT GGTTTCCATT GTGGGGATGG      180
CACTATACAC AGGATACGTC TTCATGCCCC AGCACATCAT GCGGATATTG CACTACTTTG      240
AAATCGTACA ATGACCAAGA TGCGACCAGG ATCAGAGGTT CCTTGGGGAA GACCCACCCCT      300
ACGAAGTTGG AATGAGACCA TCAGATGTGA TAAGAAATC TTCTAGATGT CAACATAACC      360
AACCTTATAA AGACTAAAT TCATGAGTAG AACAGGAAA TCATCCTGAC TCATGTGTTG      420
TGTTCTTTAT TTTTAATTT CAAAGAGGCT CAGCTCGAG                                     459
```

(2) INFORMATION FOR SEQ ID NO:1289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

```
GAATTCGGCC AAAGAGGCCT ACTACCTGCC TGAAATTC AA TGCCGTGTTT CTTCTGGACC      60
AGTTTAAAGC CATCTCTTCT GTTGTTCCTT TCCTCCCAA GATGTAGACT TTTCCACTTA      120
AAAGCATTTC CAAGATTCTA TTTTTCATC CTTTTTCTG TCCCTATTCT CTTTCACTCC      180
CCACACTGT TCCTAGCCTG TCTCTGTTGC TCTGATGTCC ATGTTGATGG TGGCGGTCTT      240
CAACCATGCC ATCCGTGTGC CAACCCAGCA CTTTCTGCC ATCCCTGTAG CCCTTGCCCC      300
AACATCTGTG CATTTGACTC CCCACCACTC GAG                                     333
```

(2) INFORMATION FOR SEQ ID NO:1290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

```

GAATTCGGCC AAAGAGGCCT ATCCACCCGC CTCAGCCTCC CAAAGTGTG GGATTGCAGG      60
TGTGAGCCAC TGCGCCTGGC CTAAACAAAC TTTTGA AAA GCTGTTTCTA AAAGATTCTT      120
TAAATTCAGA TATGACAGCT AATTACCTCA TCATAAATTA CTTTATACT AATTGTTTCC      180
AGGGTTTTAG AGTAGTTGAA TGTTTATTC ACAAGGCACC CTAAATTCTA TAGAAATAAA      240
ACCTCAGATG AGTCTCCTTC TTAGAGTGTT ACAATGAATG GGAGTTTACA ACTTTTATGT      300
GTCATGTTTC CAACAGCTAT CTCGAG                                         326
  
```

(2) INFORMATION FOR SEQ ID NO:1291:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

```

GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCTG CTTCTGCTC GTCCAGTACA      60
TTGGCTTTGA AATATACTTG AATTGTGGA GGCAGGGTGT AGAATGACAA AAACAAACAA      120
AAACCCACA ATACAGACCA AATTGGGTA CACACGGACA GATTGGTTTT AATTTTATTT      180
TAATTTTGA GTTTCTATGA GAAGAAGAAT GAGGAGAGAC AAAAAAGGGG AAGAGTGAGA      240
GATAGTATAT TTAGGGTATG ACAAATCAGG GATGGCTCGA G                                         281
  
```

(2) INFORMATION FOR SEQ ID NO:1292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

```

GAATTCGGCC AAAGAGGCCT AATTAACTA AATCTTAGGG ACTTAGGGAT TTAACTAAA      60
TCCCCACCAC ATCTGATTTC CCCTTCCTCG AAATACCAAT AGTACGTGCA ACACAGACTT      120
GTAGCTCAGA GGTGCGATGC TGTTCAAAT TCTTGGGATA TGCATGTTAC TTTTITTTAA      180
AGAAGTGGTA TATCAGACAC CTGAAGGTCA AGTCTCTCTG TGCCACCAAC AAATCTCTGT      240
GACCTTGAGC CCCTCCTCTC AATTCCTCTT CGGTAAAAGA AATACCTCAC AGTGGCTGTG      300
CAATCACCAA ATAGGAACTA CAGGTGGCAT TATTTATCTT TTGCCCTTGT GTAAGAAAAG      360
ACTCGAG                                         367
  
```

(2) INFORMATION FOR SEQ ID NO:1293:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGATATTTT AAATTTTGTT AATTTTGTTT CGTGGTCTCT | 60 |
| GCCTGAATAG ACAGGCACCT GCCTGGAACG TAATACTGTT TCACTGCCTC GTTTTACCT | 120 |
| GTTTAATCTA GAACCAAATT GTGTCAATGT GTCAGCCCGT TTGTGCTTTT ATAACAAAAT | 180 |
| ACTACAGACA GTAATTTATA AAGAATAGAT ATTTATTTCT TCACAGTTCT CGAG | 234 |

(2) INFORMATION FOR SEQ ID NO:1294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 562 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ATACTGATCC TCTCCCCTTG TGCATCACTT TTTCAGTGCA | 60 |
| GATATCTTGT AGCTCCGTGT CTAGAGGTAG CCAAGGTATC CTCCTAGCTT GCCTTCTTGG | 120 |
| TTTTATACAT GCTTCAGTAT GTAAGACAGC TTGTAGTCCA AACTCATGAG ATGACTATTC | 180 |
| TGCCTGCCCC ATCTTACCTC AACAAAGTGAG CCTGCATGCA TGTGCTCCTC AGTCTAGTCC | 240 |
| CAGGATAGGA GGTAGGGGTC TCACATCGAC CTCAAGTTCA TATGACTTTT TCTAACTCAC | 300 |
| CTTTACCACA CAGCCCCTAC TGTGGGGCTT ATAAAGTGTC ATGGAGATTT GTGAAGTCAA | 360 |
| TGTTTCCTTT CCTTGTTTAT GTGCTTTATA AATTAGGTCC CTCTCCAAA CTTTTCATC | 420 |
| ATCCTAACT GAAACACTAT GCCCATGAAG AAGTCATTAA ATAAAGACT GATAAATTG | 480 |
| ACTCCATAAA AATTAAAATT TTCTATATAG GAAAAAATGC CTCAAAGTCA AAAGTCAATC | 540 |
| ACCAAAGTGG GAGTTACTCG AG | 562 |

(2) INFORMATION FOR SEQ ID NO:1295:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGACACCCGT CATTGCAATT TATATTTTAA CAAAGGCTTC | 60 |
| TGATCCTAAT TTCAGGAAAT AGCCTCTAAA CTCATCTATT AGTCCCAAAT TCTTTACCCA | 120 |
| TTAAATCTGC TATTTTATGC CTCCTATATT CTTACCTTCA GATGTTGAGA GGTGGGGCA | 180 |
| TAAAACCTTG CAGCAGTCT GCAGTCTTCC CTCTAGAGTG AACTTGATCC TGCTGTTTGT | 240 |
| TCTTTTATT CTCTTCAAAG TTAAATCATA TTCCAGCATT CATGGTATTT CTCCAGCTTG | 300 |
| TCCTCCACAC TCACCCCTCG AG | 322 |

(2) INFORMATION FOR SEQ ID NO:1296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AAGCTGTTCT GGTACTTGTC AAAAATGGCT TCCAAATATA | 60 |
| TTCCTTTTAA TACAGGATGT GAAAACACTT CCTAATAAAT TCCTGC AAAA TTAGATGATA | 120 |
| CTGTATGTAC TTCTGAAGGA CAGACAAGAA AGTAACCTAA GACCAAAACA ATAGAGGTCT | 180 |
| CCTACTACTG GGGAGAAGGA GGATTATCAA GAATAGAGGA AAACAGAGCC TGCCTAAGAC | 240 |
| TAATACTGGT CTAGAACAAA AGAGAAAGCT CAATTCCTAC CACCACAAAG CTAAACAGCA | 300 |
| TCCAAGGCCT CGG | 313 |

(2) INFORMATION FOR SEQ ID NO:1297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGATTTTTGT CTTTAATTCT CTGTGTTTTT AGNACCTTGC | 60 |
| GATTTTTTAA GTATATTAAC CTTTCTCCT AGATGTTTAC CTTTGAAATA CCTCTCTCTC | 120 |
| CTAATGATT AGACCTATGT GTCCAACCTAC TTTTCGGACA TGTTTCCCTA GATGTCTCAT | 180 |
| GGTTAACTCC AATTTAACAT TTCCAAAGTT AAATTTATTT TATTTTACCA GACTTGGGTT | 240 |
| TTTGTTTTT TTTGTTTTT CTTTTCCT TTTTAAGATA TCCTGGAGTC ACCAGAATCC | 300 |
| TATCTAGATA CCCTTGGTTA GAGTTGCTCA TGATCTCGAG | 340 |

(2) INFORMATION FOR SEQ ID NO:1298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGCTTCTTCT GAGAGAGTCT CTAGAAGACA TGATGCTACA | 60 |
| CTCAGCTTTG GGTCTCTGCC TCTTACTCGT CACAGTTTCT TCCAACCTTG CCATTGCAAT | 120 |
| AAAAAAGGAA AAGAGGCCTC CTCAGACACT CTCAAGAGGA TGGGGAGATG ACATCACTTG | 180 |
| GGTACAACT TATGAAGAAG GTCTCTTTTA TGCTCAAAAA AGTAAGAAGC CATTAATGGT | 240 |
| TATTCATCAC CTGGAGGATT GTCAATACTC TCAAGCACTA AAGAAAGTAT TTGCCCCAAA | 300 |
| TGAAGAAATA CAAGAAATGG CTCAGAATAA GTTCATCATG CTAAACCTTA TGCATGAAAC | 360 |
| CACGCTCGAG | 370 |

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTTGGAGTT TGCTGATAGA AGGACTAGCT AAAGGCGTCA | 60 |
| CTGCAGGAAT TACAACTGA AGAGGACTCT GTTGGACTGT TTTTCTTTTC TTTTNCCTTT | 120 |
| TTTAAAGAAA AACCCATTTT TTTCTTAAAG GACTTACTAG CCAAAATTC TTAACTTCG | 180 |
| AGGACTCTAC TAGCCATGGC CGAGCCATTC TTGTCAGAAT ATCAACACCA GCCTCAAAC | 240 |
| AGCAACTGTA CAGGTGCTGC TGCTGTCCAG GAAGAGCTGA ACCCTGAGCG CCCCCAGGC | 300 |
| GCGGAGGAGC GGGTGCCCGA GGAGGACAGT AGGCATCTCG AG | 342 |

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTT GGTCTATCCT ATGCTTTATA | 60 |
| CGTAAGAGA GACCACATTT TATTGCTGT GTCCACACA GGAATTTAAT AAATGTTGAT | 120 |
| TTTAGGAATG CCTCAAGTT CCTCTTTATC TTTATATCTC TTTCTACTTT GGCTTCTCCT | 180 |
| CTCTAGAGAA GTTCTAGATC TTTCCCAAC TCTCGAG | 217 |

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

| | |
|---|-----|
| CCTTCGGAGA GAGGCACGCC CGGCCCGGAC AGTTCAGGCT CTCTCGGCTC CGGGGAGTTT | 60 |
| ACTGGCGTGA AGGAGCTTGA TGACATCAGT CAAGAGATTG CCCAGTTACA AAGAGAGAAA | 120 |
| TATTCAGTGG AACAGACAT TCGAGAAAAG GAAGAGGCAA TCAGACAGAA AACCANCGAG | 180 |
| GTGCAGGAAT TACAAATGA CCTAGACCGG GAAACAAGCA GTTGCAGGA GCTCGAG | 237 |

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACAAAGGAGA CCCTTCATAT CAAAATACAG TTATCAAAAT | 60 |
| ATTTTAAAGT TATATATAAT TATGTGCTTC TNTACTAATG TCTTAAATAA TGAGATCAAA | 120 |
| CAGCAGATCT TAAAACTGT CATAATATTT GGAGTAGTGA TGGGCATAAA AGTTATTCTG | 180 |
| AGATCTCCGC AGGAACTGTA ATGTGATATG AAAAAGTCTG TGA CTCTGT TACCAACAAA | 240 |
| GTCTCAAGTC TCAAGTCTAC TACTAGGGTA TGTTACCTAC ATTCCTAAG TGAGGGAAAT | 300 |
| GTTATGTTTC AGTTGAGGGC AAATGATGGC AATGATGTA TTTTTTCTC TTCAAGTTC | 360 |
| ACAGCCCCC CCGCTCGAG | 379 |

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTGCTGA TTTCTCTTA CATATGAATT ATGTGGGTAT | 60 |
| GTTTAATTTT AAGTTAGGAT AAACAGGCGT TAAGTAAGGG TTAGTGTAGA ATTTAAGCAT | 120 |
| GTCATTTTTG TAATCTCATC GGGCCTTGAT TTCATTAGTT TAGGCCCTCC ATTTTATAGA | 180 |
| TAGTGGTTCC CAGACTTCCC GGCTGCCTCA ATCTCCTGGG TCTTTGTTAA ATAACCTTAA | 240 |
| GCAAGCTCAT TTCCCCAGT GTGTTCAATT CACAGAAAGC TCGAG | 285 |

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCTT AGTTGGTATC TGCCAGGGA TAATTGCTCT TAGGGTAAGA | 60 |
| CTTTTAACAT GTAAGCCAGC CTGTCAAAG TGCACCTAAA AGTTCTCTT CAGTCATTTT | 120 |
| CTGAGTTACT GATAGGAACA TAGGTACTGT GTGAATCAGA TCTGAGAGGA TTATGAATGT | 180 |
| TATAGAATGC CTTTGTGTAG GGAATTTAAG CCCAGAAGAA GTTGGGAAAG TGACAGATTT | 240 |
| ATATAAATGC GAGTGACAAA ACCAGTTAAA ATGTTCTGAC TCAACCTGAA ATATGTTGGA | 300 |
| CTATATAATA AATATAATAT TGTGAGATAT TCTGAAC TAG ACTCAACTCG CTCGAG | 356 |

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

| | |
|---|----|
| CTCGAGTACG TAGCGTAGAA ATAGAGAATA GGTCAACAGG TTGGAGGTGG AGTGTTTAAG | 60 |
|---|----|

| | |
|---|-----|
| GACAAAGTTA TAAAGAAGTT TTTTGGTTTG AAAAATTAGA GGATAGGTTT GTACCATAGA | 120 |
| CAAATGGATA AGTTCGGAAA AAATCTTTTT TTTTTTTTAA AAAAAAGCC | 180 |
| ACGGTCTCAC TATGTTGACC AGGCTACCAG GTCGTCTCA AACTGCTGGC CTCAAGCAAT | 240 |
| CCTCCACCT AGGTCTCCA AACTGCTGGG ACTACAGGCA TGAGGCAGAA TCGCCCGAAC | 300 |
| CCAGGAGGCA GAGGCTGCAG CGAGCCAAGA TCACGCCACT GCACTCCAGC CTGGGTGACA | 360 |
| GAGCAAGAAT CCGTCTCCA AAAAAAAGA AATAAATAA ATAAAAAGG GTGTTCCATA | 420 |
| GGGGTGATGG GGAGGATGAA ACGTCATCAA ACAAGTTTAA GAAACATCTA GGCCTCTTG | 480 |
| CCCGAATTC | 489 |

(2) INFORMATION FOR SEQ ID NO:1306:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAATCAAAT AAAGAAGAAA TACAGGAAAA GGAGACAATC | 60 |
| ATTGAAGAAT TAAACACAAA AATAATAGAA GAAGAAAAGA AAATCTTGA GCTAAAGGAT | 120 |
| AAATTAACAA CTGCTGATAA ATTACTAGGA GAATTACAAG AACAGATTGT GCNAAAGAAC | 180 |
| CAAGAAATAA AAAACATGAA ATTAGAGCTG ACTAATTCTA AGCAAAAAGA AAGACAGTCT | 240 |
| TCTGAAGAAA TAAACAGTT AATGGGGACA GTCGAAGAAC TTCAGAAGAG AAATCATAAA | 300 |
| GACAGCCAAC TCGAG | 315 |

(2) INFORMATION FOR SEQ ID NO:1307:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

| | |
|---|-----|
| GAATCTAGA CCTGCCTCGA GTAAAGCCTG TAGGTAAAT GGAGACAGAT TTGAAAGAAA | 60 |
| TTAGAGAAGA AATTCCCAA AGGGAAAAGG TGCTAGCAGA GATCAGTGCT ATAAGGGAAA | 120 |
| AGGAGATTGA TTTGAAAGAA ACTGGAAAAA GAGACATTCC CATGATGGAG AAAGTATCAG | 180 |
| GAAAGATGGC TGTGTTGAA GGACATCTCG AG | 212 |

(2) INFORMATION FOR SEQ ID NO:1308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAAATATTA ATGAAATCGC TGAAAAGCTT TGCCTTCGAG | 60 |
| AGGCCAGAAG CCTCGCGGAA TGTCTGCAAG TCCTAAGACG CGTGTGGGTT GTGCCCTGAA | 120 |

GTGCCGTCCA GCAGGCGCGT GCGGCCGGGC CGGCCTGTGC GTGTGGCCTT TGCCTTCTTC 180
 CCTTTCTTCC TGTCTTCTGT TTTTAAATT TGGGGACTGG TGAGGGCTCG TCCATGCTCT 240
 TTGTCAGGTC TTCTTGCTCC TCCCCTCGAG 270

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

GAATTCGGCC AAAGAGGCCT AGTCTTATAC CTGGGATGTA GCTGACAAAT TATTGCATTG 60
 TAAATGAGT CACGTGAATC ACGGAAGCTT TAACTTTTT CTCTTTATAG CCCTACCTGA 120
 ACCCATCCTT CCATCCCTCC AAAAAATTTA CCCAGTAAGT GTTCTTTATA AATTATTATA 180
 ATACATTTTA TGTCAAGTGT ATGTAGAACT ATTATAAGTA GTATTAATGT GATTATAAAA 240
 GTAGTAAGGC TAAGTACATG ATAACATTTT CTATATATAC CAAGAGAACA TTTAAAATGT 300
 TTCATATACT GTTTCAGAAA ACTCTCTTAC TTGTTATTTT GTTATTGGCA GACAGTCTGG 360
 TCAGTTGTGT TAATGGTGGA CTCGAG 386

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

GAATTCGGCC AAAGAGGCCT ACCATTTTAG CCTGCAGGCT TCCTTGGGCT TTCTCTGTGT 60
 GTGTAGTTTT GTAAACACTA TAGCATCTGT TAAGATCCAG TGCCATGGA AACATTCCCA 120
 CATGCCGTGA CTCTGGACTA TATCAGTTTT TGGAAGCAG GGTTCTCTG CCTGCTAACA 180
 AGCCACGTG GACCACTCTG AATGTCTTTC CTTTACACCT ATGTTTTTAA GTAGTCAAAC 240
 TTCAAGAAAC AATCTAAACA AGTTTCTGTT GCATATGTGT TTGTGAACCT GTATTTGTAT 300
 TTAGTAGGCT TCTATATTGC ATTTAACTTG TTTTGTAAAC TCCTGATTCT TCCTTTTCGG 360
 ATACTATCTC GAG 373

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

GAATTCGGCC AAAGAGGCC TAAACAGATA TTTACTGAGC ATTTACCATG TTCAGTAACC 60
 AGGGCCCTGG GAATATAATA GGAGAAGGCA GATGAGATCC TTGCCTTCAC CAAGCTTATG 120
 TTTTCTATT TTAAGTAAAA TTTGCCATGA CAAAATTTCT ATCAGCGGAA GAGCCAGTAA 180

CTCTTATTGT AATAGGTTTT ACCCAGTTTT AGAAAAGGAA AGTAGCTAAA CTCTTGTTTC 240
 CTTGGTGTGT GTTTTTGTTT GTTCATTTCT AGTACTTGT TATGTCTTTG GGGTAATTTT 300
 TGATTTAGAA TTTTGTAGAA ATTACTCGGC ACAGTGTAGT TGAGGTGAAT ATAGGCAAGA 360
 AGGCTTAGGA AGCCTACAAC AAAGGAATCT GACACACTCG AG 402

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

GAATTCGGCC AAAGACGCCT AATTGAATTC TAGACCTGCC TCGAGTTGGA CCCTGAGTGT 60
 ATCACTCCCA AGTGTGTACT ATTTATACAC AGCAGTTTCC AATGTACTCA AATCAACCTC 120
 ATGTTCTTTG CTGTAGTAAG CTGAATGAAC ATGACTCTTG AATCACCTTA AATATGCTTG 180
 ATAACATGTC AGGATTCAGA ACAGCAAAAA AGAAAGCTTT AAAGGGAGAT ATGCTGGGCT 240
 CATTACATC AAACCTGCAGG GGAAACCTGG TTTATGTCCC ATAGCTACTA GAATTCCTAC 300
 ACTTGGCCAG CTTATTTTAA TAGACCATT CTCAACTACT CTAGCTGTTC TGTCTAGTTC 360
 TAAATAAAAA GCTAGGTAGT TGGGTACTAA AAGGCAAATA TGAATATATC AGTGGCTCTG 420
 TATCATCTGC AGCAGTGGTT CTCAGTGTGA TTCCTGGACA GGCAGCACA GCATCATCAG 480
 GGAACCACTC GGTAAATGCA ACTCTGGGGC GCACTCGAG 519

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

GAATTCGGCC TTCATGGCCT ACGAGGACGT GAGCAGATAT ACCAGCCCAG TGAACCCAGC 60
 TGTCTTCCCC CATCTGACCG TGGTGCTTTT GGCCATTGGC ATGTTCTTCA CCGCCTGGTT 120
 CTTCTTTTAC GAGGTCACCT CTACCAAGAC ACTCGAG 157

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

CTCGAGTTCA CTACCATGAC AATCATTAAT TAATTTGGTT TCTCTAGTGA GGTTAGTTGC 60
 TTTCTTCCCT TCCTCCAGCA TCTGACCAAG GTCTGATTCT ACAGCTATTT GGGAAACAGT 120
 AGTTTCTGGT GACATAGCTG AAGACCCTGA TGCTGTCATA GTCTGAATTC CAGAATCTTT 180
 AGAATCTTGA GTTTCAGTAT CAGTTTGCTT TTCAGTAACA GGTTTTCCTT CTTGAAATAT 240

| | |
|---|-----|
| TAATTGTGCA TCATTACCAA ACATGTCCAG TTTTTCACCG GCTTCAGATG CAGCTGGAGA | 300 |
| CAAACTGTGA TCTTGGAGCT CTGTGGGTAG ATTAGCTTCC TCAGTAGGAC TGCCTTCTAC | 360 |
| TTTCAGTTCC ACATAATCAT CATCTTCCTC TTCCTCTACT ATAGATTTAT CCAAGAATTC | 420 |
| TGGCATCTCT GAGGCAGGTC TAGAAATTC | 449 |

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGTGAATAC TAGGATATTT GTTTGGCAGC AATAGAGCGG | 60 |
| CAACACCCCTT CTCAGACTCG TGGTACTACC CGTCCTATCC TCCCTCCTAC CCTGGCACGT | 120 |
| GGAATAGGGC TTACTCACCC CTTTCATGGAG GCTCGGGCAG CTATTCGGTA TGTTCAAAC | 180 |
| CAGACACGAA AACCAGAACT GCATCAGGAT ATGGTGGTAC CAGGAGACGA TAAAGTAGAA | 240 |
| AGTTGGAGTC AAACACTGGA TGCAGAAATT TTGGATTTT CATCACTTTC TCTTTAGAAA | 300 |
| AAAAGTACTA CCTGGTTAAC AATTGGGAAA AGGGGATATT CAAAAGTTCT GTGGTGTAT | 360 |
| GTCCAGTGTA GCTTTTGTGA TTCTATTATT TGAGGCTAAA AGTTGATGTG T | 411 |

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACATCCAACA AGAAGCCATA ACTTTATTTA TGATAGAAAC | 60 |
| AGTACAAATT TCAAACCAAG CTGCAGTTAC TCCTTTGAGA CACCAAAAAA AGTTGCCTCC | 120 |
| ATATGGTTAC ATTGTTAATT CCATAATCGC ATTTACAATA TCATTACTGT TGTCTTCAG | 180 |
| GGCTCGGACT GCCTTTGCTC TCGACACATT TGCTTGTGAC ATGACCAATT CTATGTCCTT | 240 |
| AACTTCTACA CCTGTTTCAC TTCCTCTTCT CGAG | 274 |

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGCGGAGGT GCAGGTCCTG GTGCTTGATG GTCGAGGCCA | 60 |
| TCTCCTGGGC CGCTTGGCGG CCATCGTGGC TAAACAGGTA CTGCTGGGCC GGAAGGTGGT | 120 |
| GGTCGTACGC TGTGAAGGCA TCAACATTTT TGGCAATTTT TACAGAAACA AGTTGAAGTA | 180 |
| CCTGGCTTTC CTCCGCAAGC GGATGAACAC CAACCCCTTC CGAGGCCCTT ACCACTTCCG | 240 |

GGCCCCCAGC CGCATCTTCT GCGGGACCGT GCGAGGTATG CTGCCCCACA AAACCAAGCG 300
 AGGCCCCAGCC GCTCCTCGAG 320

(2) INFORMATION FOR SEQ ID NO:1318:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GAATTCGGCC AAAGAGGCCT ATAATTTTTC CCATCATTTC CCCTGATAAT CTGCCTCTTC 60
 TCCATTTCTC CTTCCCTTAC TACCTTTCTT TGAATTACTG TAACTGATTG GTCCCACCAA 120
 AATTTTAAAG TACATGAAGT ATCTTCATTG GTTCATCCTC TTGCCCCCTC CAGATGTCAA 180
 AAAACTTTAT CCTGCCCCCT TGCCTCCACC CGATGGCCCA CTCGAG 226

(2) INFORMATION FOR SEQ ID NO:1319:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GAATTCGGCC AAAGAGGCCT ATGAAGCTTC TGAGTTCTGC GGCCTCACNT CTGAGAAAAC 60
 CTCTTTGCCA CCAATACCAT GAANCTCTGC GTGACTGTCC TGTCTCTCCT CGTGCTAGTA 120
 GCTGCCTTCT GCTCTCCAGC GCTCTCAGCA CCAATGGGCT CAGACCCTCC CCCCCTGGC 180
 AAATCTCTCG AG 192

(2) INFORMATION FOR SEQ ID NO:1320:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

GAATTCGGCC AAAGAGGCCT ATTTATTACA ACAGATCTTT TAATGACTAT TTTTAACATA 60
 AAGATTGTTG TTTTGGGAAA CATCTATTCT CTTTGAACAT TTCCTAAAT TTTCAATGTA 120
 TTAAATAACT GACAGAAATA AGTTCTGTGT TCTGTACAAA TTAAAGGTCC CATGAATACA 180
 TAACCCCCAC CCCCCCCCCG TCCACTCGAG 210

(2) INFORMATION FOR SEQ ID NO:1321:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTGTGTA TGAATCTATGA ATGATTTATT AGATAAATTC | 60 |
| TATACATACA AAGTACAGAT TCTTCATTGA GCATTGATTT ACTTCTTAGT TTTCATCTTT | 120 |
| CTGACTATCC AAACCGCTGA CTCGAGGCAG GTCGAG | 156 |

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTGTGTA CACTATGTGA CAGAACAGCT TATAAACTA | 60 |
| GGTATGAACA TTAAGTGTGA GTGTAAACAG TAGGACTACC ACTTGTCAAA AGTTTAAAC | 120 |
| ACTTGAAGTGA GAAGTGGTAC TGGTTATTCA TCATTTTCAT TGTCTTCTAT TTCATCCCC | 180 |
| CCACACCCCT CTGCTCGAG | 199 |

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACACGGTACC AAACACAAC CAAGCATCGA CTCCTCCGCA | 60 |
| GACCCAGACC CCTCAGCCGA ATCCTCCTCC TGTGCAGGCC AGGCCTCACC CTTCCCTGC | 120 |
| CGTCACCCCG GACCTCATCG TCCAGACCCC TGTCATGACA GTGGTGCCTC CCCAGCCACT | 180 |
| GCAGACGCCC CGCCACTCAG CGCCTCGAG | 209 |

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

| | |
|---|----|
| GAATTCGGCC AAAGAGGCCT AATCACTACT CACAGTAACC TCAACTCCTG CCACAATGTA | 60 |
|---|----|

CAGGATGCAA CTCCTGTCTT GCATTGCACT AAGTCTTGCA CTTGTCACAA ACAGTGCACC 120
 TACTTCAAGT TCTACAAAGA AAACACAGCT ACAACTGGAG CATTACTTC TGGATTTACA 180
 GATGATTTTG AATGGAATTA ATAATTACAA GGCTCCAAAC TCACTCGAG 229

(2) INFORMATION FOR SEQ ID NO:1325:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

GAATTCGGCC TTCATGGCCT AGCTTTCCCA ATCTCTCGGA GCATGCACAT CAGGGCCACG 60
 TTGGTCTTCC CAGCACCAGT AGGAGCACAC AGCAGCAGAT TCTCATCCGT CTCAGGGGCA 120
 GCACGGTAGA GCTTACTCTG GATCCGATTC AGTGTTTTGA AGCCCTCAAA CCCAGCCTGG 180
 ATTGAATTCT AGACCTGCCT CGAG 204

(2) INFORMATION FOR SEQ ID NO:1326:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

GAATTCGGCC AAAGAGGCCT AGCCGATCTC CAGCCCAAGA TGATTCCAGC AGTGGTCTTG 60
 CTCTTACTCC TTTTGTTGA ACAAGCAGCG GCCCTGGGAG AGCCTCAGCT CTGCTATATC 120
 CTGGATGCCA TCCTGTTTCT GTATGGAATT GTCATCCCC CAGAGCGTCT CGAGGCAGGT 180
 CTAGAATTCT AG 192

(2) INFORMATION FOR SEQ ID NO:1327:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

GAATTCTAGA CCTGCCTCGA GAATAGGATA GCATTTAGTA ATCACTTAA CAATTTTAT 60
 TGAATATCTA TTGTTTATT GAATATGCTT GTTCTCACCT TAGCACATT GCCCTGTGTC 120
 TCCCTGGGAT ACTATCCCC TAGATCTGAT TTTTGGTTTT TGTGTTTGT TGTTTTAATT 180
 CTCTGCCATC TTTCTCCAGT CAAATGTCAC CACACTCTCG AG 222

(2) INFORMATION FOR SEQ ID NO:1328:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

```
GAATTCGGCC TTCATGGCCT AAGAAATGTT CACTTTTCCA ACTTAAAAGG ATTTTAAAAA    60
ATACAAACAT AATTGACCTA CCTGGTTCAA AGAACAGAAG TGAGGAGAAC TTGCTTAAAG    120
GTATTGATGT TATATTTTCT CTTGACTGAG TGCTTGAAAA AAAATTTTAT TGAACATATG    180
TTCTCCTTCC GTGGCTTTT TGTCTTGCT TTTTGTGTT GTTTGTGTT TTTTCTTT    240
GAGATGGAGT CCACTCTCT GCTCGAG                                     267
```

(2) INFORMATION FOR SEQ ID NO:1329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

```
GAATTCGGCC TATGGCCTAA AAAAAAAG AAAGAAATAG GATTGATACA GGTATAGATA    60
CATAGATACA TGAGAAGGGA TTTATTATGG GAATGGGCTC ATATGATTAC AATGATTACA    120
GAGGCTGAAA ATTCCCACAA TAGGCCATCT GCAAGCTGGG GACCAGGGAA GCCATTTATG    180
TGGTACAGTC TAAGCGTCAA TCAGGAAAGC CAGTTGGGTA ACTCTCAGTC TGCAGCTGAA    240
GGCCTGAGAC CCGGAGGTCC ACTCGAG                                     267
```

(2) INFORMATION FOR SEQ ID NO:1330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

```
GAATTCGGCC TATGGCCTAA AAAAAAAG AAAGAAATAG GATTGATACA GGTATAGATA    60
CATAGATACA TGAGAAGGGA TTTATTATGG GAATGGGCTC ATATGATTAC AATGATTACA    120
GAGGCTGAAA ATTCCCACAA TAGGCCATCT GCAAGCTGGG GACCAGGGAA GCCATTTATG    180
TGGTACAGTC TAAGCGTCAA TCAGGAAAGC CAGTTGGGTA ACTCTCAGTC TGCAGCTGAA    240
GGCCTGAGAC CCGGAGGTCC ACTCGAG                                     267
```

(2) INFORMATION FOR SEQ ID NO:1331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

| | |
|---|-----|
| ATGGATTGGT TGCCGTGGTC TTTACTGCTT TTCTCCCTGA TGTGTGAAAC AAGCGCCTTC | 60 |
| TATGTGCTGT GGGTCGCGCC TATCAACTTC CACCAGAACG ATCCCGTAGA AATCAAGGCT | 120 |
| GTGAAGCTCA CCAGCTCTCG AACCCAGCTA CCTTATGAAT ACTATTCACT GCCCTTCTGC | 180 |
| CAGCCCAGCA AGATAACCTA CAAGGCAGAG AATCTGGGAG AGGTGCTGAG AGGGACCGGA | 240 |
| TTGTCAACAC CCCTTTCCAG GTTCTCATGA ACAGCGAGAA GAAGTGTGAA GTTCTGTGCA | 300 |
| GCCAGTCCAA CAAGCCAGTG ACCCTGACAG TGGAGCAGAG CCGACTCGTG GCCGAGCGGA | 360 |
| TCACAGAAGA CTACTACGTC CACCTCATTG CTGACAACCT GCCTGTGGCC ACCCGGCTGG | 420 |
| AGCTCTACTC CAACCGAGAC AGCGATGACA AGAAGAAGGA AAAAGATGTG CAGTTTGAAC | 480 |
| ACGGCTTACT CGAG | 494 |

(2) INFORMATION FOR SEQ ID NO:1332:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AGCTGATATT ATTTCTGAGT TTTTGCTTAT TTGCTTTCTA | 60 |
| CATAGAATCA ATAAAATTGA CAACTAGCAT TGCCTATATA TGCAGGTGTG ATACTATTCA | 120 |
| GGGTACTAGT ATATTGGCCA CTCATTATGA AACTTTCAGG TCCTCATATA TTTTCTTTTA | 180 |
| TTACAATGAT CTACTTATTT CTGATAAATA TTGGATTTCAT AGAGGCTAAA GGGCTGGGAA | 240 |
| AGGAAAACAT TCGTGACTAC TTACAACCAT TTGATACGAG TTGTGTCAAT ACAGACCTCA | 300 |
| CACAGCAGCA CCTCGAG | 317 |

(2) INFORMATION FOR SEQ ID NO:1333:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCTTTTCTA GCCTTTCTCA AAGAAATGCA AACAGCTTGT | 60 |
| GTTTTTCCC CTTGGGTCCT ATTGTACCTA CTTTGTGTTG ATGGTCTCTC TGTCTCCCAT | 120 |
| GATGCCAGTG AATGTAGCAG TTTCTCTCCA CTTCCACCAG TGCCTGGGGA AAATTTGGTA | 180 |
| TTGGCAAATT TGAGTTCTGC CTTTTGTCAG CTTGCATTGC TGGATTCAAC CTTAGGAGCC | 240 |
| TCAGTTACCC TCGAG | 255 |

(2) INFORMATION FOR SEQ ID NO:1334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTCTTCCCC AAAAGGAAGC ATTTACTCTG CCTCTTACAG | 60 |
| TGCAGAGTGA CAGAATGGAC ACAGAAAAAC ATAGGTGGGT CAGAACAGAT CTCAGTTTGA | 120 |
| ACCCAGTAGC TACTGGCTAT AGGGTCTCTG GGCAAGTGAT TTGACCTCTC TGGGCTCTGT | 180 |
| CTTCTCAAAT GTAAAAACGG GTCAGGCGCA GTGGCTCATG CCTATAATCC CAACACTCCG | 240 |
| GGAAGCCAAA GTGGGAGGAC TCTCGAG | 267 |

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACAAATGTAA AAATAACTGG GCACTGAAGT TTTCTATCAT | 60 |
| ATTATTATAC ATTTTGTGTG CCTTGCTAAC AATCACAGTA GCCATTTTGG GATATAAAGT | 120 |
| TGTAGAGAAA ATGGACAATG TCACAGGTGG CATGGAAACA TCTCGCCAAA CCTATGATGA | 180 |
| CAAGCTCACA GCAGTGGAAG GTGACCTGAA AAAATTAGGT GACCAAACCTG GGAAGAAAGC | 240 |
| TATCAGCACC AACTCAGAAC TCTCCACCTT CAGATCAGAC ATTCTAGATC TCCGTCAGCA | 300 |
| ACTTCGTGAG ATTACAGAAA AAACCAGCAA GAACAAGGAT ACGCTGGAGA AGTTACAGGC | 360 |
| GAGCGGGGAT GCTCTGGTGG ACAGGCAGAG TCAATTGAAA GAACTTTGG AGAATAACTC | 420 |
| TTTCTCATC ACCACTGTAA ACAAACCCCT CCAGGCACTC GAG | 463 |

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAATTCTAGA CCTGCATCGA GGGCGGCGAC CTGATGATGA | 60 |
| CCAGCTTCGA GAGGATGCTG TCCAGAAAG ACNTGGAGAT CGAGGAGCGC CACAAGCGCC | 120 |
| ACAAGGAGAG GATGAAGCAA ATGGAGAAGC TGAGGCACCG GTCCGGAGAC CCCAAGCTCA | 180 |
| AGGAGAAGGC GAAGCCGGCA GACGACGGGC GGAAGAAGGG TCTGGACATT CCTGCTAAGA | 240 |
| AACCCCGGGG GCTGGACCCT CCATTTAAAG ACAAAAAGCT CTCGAG | 286 |

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

| | |
|---|-----|
| CTCGAGGGTT TTTGTTTGGC TGGTTGTGTG TACACAGTGT ATACAAGTTG AGTTGTACAG | 60 |
| AAGCCCAAGA AAGAGCAAGA GACAAAGGGT AGTGGGAGCA GGGGGTGGG CGGGGGCGAG | 120 |
| AACGGGGAGG AGGGGAAAGG AGACCGATAA AAAATAGAAC CACATCCAGA CAACAATGGG | 180 |
| GGATGGGCAG TGGGTGGGGG CCAGACACAG ACAAATCGCC GTAGAAAAGG AGTGGGAGGG | 240 |
| GCAGAGAGTA GAGGG | 255 |

(2) INFORMATION FOR SEQ ID NO:1338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AAGAGAAAGC ATTTAACTT TTATAGTAA CAATAAAAA | 60 |
| GCCTCATAAA GCTTCTCACA ACAACTTCAT TCGTTTCAGA AGTTAAGATA TATTCCTTAT | 120 |
| GAATACCAAC ATTGTGACAT TTGTGTTGCC AATTATTTTC TCTGGAATCA TTCTTTTAAC | 180 |
| TTCACTTCCT GTTGTGTTGGG AAGACTTTGC AGAGAACATA TTTTAAATAG GCTATAATCA | 240 |
| CACGGGCAAC AGACTCGAG | 259 |

(2) INFORMATION FOR SEQ ID NO:1339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

| | |
|---|-----|
| GAATTAGAAG TATTGTTTAA TAAGTCCTTT TTTTCTACTC AACATTAAGT AGTAATCAAC | 60 |
| TTTTACCTCC GCCAGTTTTT CTGCTTTTTT GCTGGTACGA TCTCTCTTC TAAATTGAAT | 120 |
| CAAAGACCTA GGTGGAAGT GAAACTTAGG AGGGAAAGAC AAAATGAGGC TTGTTTCATGA | 180 |
| TCAAATCTG TGTACTCTAG TTGCTTCTTT CCCTTGGAGT GACAGGTACT TTTATATCCA | 240 |
| GGATGATTAC AGTGATGACA TCCATTCTTT TTTGGGGGCC CTCGAG | 286 |

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGAATCAGT AGTGTACTTT GATTGTATTG TATAAGGTAT | 60 |
| TTTCAAATAG AAAAGCAGGT AGCAGAAATA CTAAAAGAAT TTTTGTCTTT AGTGTAAGT | 120 |
| AGATAATGAG AGGTAGATGC CTAATTCTTT AGTTTCTTT TTAAATATAT GCTAAATAT | 180 |
| ATCATATCAT TTACCATTTT GACTATTTTA AAAGTATACA GTTCCGTGGC AAGTCTCGAG | 240 |

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

```

GAATTCGGCC TTCATGGCCT AAAAAATTGT GTCTTTTTTT TGGCAATGTT GTCTTGCCAA      60
TCCCATCCCT CCCCAGCTC TCCGAACAGC AGGATTTCCT AACGGCAGCT TGGGANAAAG      120
ACCCAGTGGC AGCTTGGGGA AAAGACCCAG CGCTCCGTTT AGAAGCAACG TGTATCAGCC      180
AACTGAGATG GCCGTCGTGC TCAACGGTGG GACCATCCCT ATTGCTCGGC CAAGTCACAC      240
TCGAG                                     245

```

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

```

GCGATTGAAT TCTAGACCTG CCTCGAGACT GACGCCGCAC CATGACCCTC CTGCTGCTGC      60
CCCTTCTGCT GGCCTCTCTG CTCGCGTCTT GCTCCTGTAA CAAAGCCAAC AAGCACAAGC      120
CACCGCATCT CGAG                                     134

```

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

```

GAATTCGGCC AAAGAGGCCT AAAAAGCTTC CAGCAGCAGA TGCAGAATTA CCTTAAAGAC      60
AACAAAACAG CCACTATTTT GGACAAATTG CAGAAAGAAA ATAAGTCTG TGGAGCTTCT      120
AACTACACAG ACTGGGAAAA CATCCCCGGC ATGGCCAAGG ACAGAGTCCC CGATTCTTGC      180
TGCATCAACA TAACTGTGGG CTGTGGGAAT GATTCAAGG AATCCACTAT CCATACCCAG      240
GGCTGCGTGG AGACTATAGC AATATGGCTA AGGAAGAACA TACTGCTGGT GGCTGCAGCG      300
GCCCTGGGCA TTGCTTTTGT GGAGGTCTTG GGAATTATCT TCTCCTGCTG TCTGGTGAAG      360
AGTATTCGAA GTGATGTCGA G                                     381

```

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

```
GACCAGATGG AANGGTCACC GAACAGTTCT GAGTCATTG AGCATATAGC TCGATCTGCA      60
AGAGATCAGC CAATTCCCT TTCTGAGCCT CGTATGCTGT GGGGGTCAGA TCCCTATCCT      120
CATGCTGAGC CTCAACAAGC AACTACTCCC AAAGGAACAG AAGAGCCTGA GGATGTAAGG      180
TCTGAAGCTG CGTTGGACCA GGAACAGATT ACTGCTGCTT ATTCTGTAGA ACATAATCAA      240
TTAGAGGCTC ACCCAAAGGC AGACTTTATC AGAGAATCAA GTGAGGCACA AGTACAAAAG      300
TTTTTAAGCA GATCTGTGGA AGATGTTAGA CCTCACCATA CTGATGCAAA TAATCAGTCT      360
GCTTGTTTTG AAGCACCTGA TCAAAGACC TTATCCGCTC CTCAAGAGGA GCGGATTTC      420
GCTGTAGAAA GTCAGCCTTC CCGGAAAAGA AGTGTTCCTC ATGGATCTAA CCATACGCGC      480
CTCGAG
```

(2) INFORMATION FOR SEQ ID NO:1345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

```
GAATTCTAGA CCTGACTCGA GGTGCTGGAA TTACAGATAA AAGCCACCAC ACGCAGCCCA      60
CATAAAGTGT TTATGGGAGC AACTAACAGT TGGTTGCGAG GCAGCCTAAA TAGGGGATGG      120
CAAGGTTGGG TTTTCCAAGG TTTTCTAATC TTTCTATTTT TTCTAGTGAG TCTTCAGGTT      180
ATTATGACTT GTGTTACCAG ACTATCAACA AAAGTGGGTA CCTCTTAAA TCAGAGCCTC      240
GAG
```

(2) INFORMATION FOR SEQ ID NO:1346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

```
GAATTCTAGA CCTACCCCAT CCACATGCAC AGCCAGCTGG ACCACCTTAG CCTCTATTAC      60
TGCAGGTGTA CTCTGCCAGA GAATCCAAAC AATCACACCC TCCAGTACTG GAAGGACCAC      120
AACATCGTGA CAGCAGAAGT CCACTGGGCT AACCTGACTG TCAGTGAATG CCAGGAGATG      180
CATGGAGAGT TCATGGGATC TCGGTGCGGC CATCATGGAC CCTACACTCC TGATGTCCTC      240
TTTTGGTCCT GTATTCTCTT TTCACCACC TTCATCCTCC CAAGCACCTT CGAG
```

(2) INFORMATION FOR SEQ ID NO:1347:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

| | |
|---|-----|
| AGTTTCTCCA TTTTAGAATT TTGTTGTCCT CCTTAATCAT CTGCTTACCT AGTCATTACT | 60 |
| CAATCTGCAG AAACCTCATA AAGGAAAAGT GCTGCATTGT TTTTACAAAT AACAGTTTGT | 120 |
| AGGGAAAATA TGACAAACCT CAACTATGGG AGTTGTCCAC AATACAAAT TTTGAAAAAA | 180 |
| CATTACATAG TGATAATATC ATACTTGGTT GTTAGGCTTG TTGCTTCCCC ACCACTCGAG | 240 |

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

| | |
|---|-----|
| AAGTATTCTT TCAATTGCAA AGTGGCAACA GCTTTTATAT GCTAAGTCTG ACAAGTTTGC | 60 |
| AGTCAGTGAA TGATGGCACA TGGCACGAAG TGACCCTTTC CATGACAGAC CCACTGTCCC | 120 |
| AGACCTCCAG GTGGCAAATG GAAGTGGACA ACGAAACACC TTTTGTGACC AGCACAATTG | 180 |
| CTACTGGAAG CCTCAACTTT TTGAAGGATA ATACAGATAT TTATGTGGGA GACAGAGCTA | 240 |
| TTGACAATAT AAAGGGCCTG CAAGGGTGTC TAAGTACAAT AGAAATCGGA GGCATTTATC | 300 |
| TCTCTTACTT TGAAAATGTT CATGGTTTCA TTAATAAACC TCAGGACGAG CTCGAG | 356 |

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

| | |
|---|-----|
| GAATTCTAGA CCTGCCTCGA GACCTTTCTC CTGGTCTAAT GCTCCTTTTA AGGAAGGTGG | 60 |
| AAGGAACAAT GGAAGAATGC TTGTAAAGTA ATGTATTCTT AAGAACTAAA GCTATTTGCA | 120 |
| GAAGGGCCGA AGCTATGTGG TGTGAAAGGG AAATGAAGAG GGTGAGTTGG GGGGCTCGAG | 180 |

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCTAGA | CCTGCCTCGA | GCTTTCCTCG | ATCTTCTTCC | ATCCCTTACT | GACAGTGTTT | 60 |
| ACCAAGGATT | TCCCTTGGCC | TGCTTCTTTC | TTTGACGCTC | ATTTAAACCT | TTCCTTTCAG | 120 |
| TTGCAGACCT | CGTCTGCTTC | TCCCAGCTAT | TCCATTCTTC | AGTTGCTTGT | TAAACACGGC | 180 |
| CCACCATCAC | CTCAAAAATG | ATGTTAAAAT | GTCCCATTT | TTTATCAAAC | TTAAGTTTCT | 240 |
| TCCTGTGCAT | CTGTTGCTCA | GTACTCTCAT | CTTTCGATC | ACTCGAG | | 287 |

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAAAAATTCT | TTTTTAATGG | GTTTTAAACA | CTAACACTGA | 60 |
| GAATTTTTCT | TGATTCCCAT | CTGTTGGTTT | ACTTGATTGC | TATAGCTGTA | TGGTAAATCT | 120 |
| CAAAATTAGG | TAATGTGATT | TCTTTTTTCT | TACTATTTTT | ATTTAAAATT | CATTTAGCAT | 180 |
| TCCTAGTTTG | ACTTCCATA | TACACTTTAG | GAITGGTTTT | TCTGTTTTTC | AAATATTCTT | 240 |
| GCTTGGATTT | TGATAGAAAT | TGAGTTAAAT | CTATAGATCA | ATGTGTTGGA | AATTGGCATC | 300 |
| TTAGTCTTCC | AATTCATGAA | CATAGCCTAC | TCGAG | | | 335 |

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACGTATGAGA | CAGTGATAT | GACACTGTAT | ATGTGTGAGA | 60 |
| CTGTGTGTGT | GAAACACTAT | ATGACACTGT | ATATGTGTGA | CAGTGATAT | GACACTATAT | 120 |
| GTGGAGACTA | TGTGTGAGAC | ACTATGTATA | TGTGACACTA | TGTATGTGTG | TGACACTGTG | 180 |
| AGAGACACTG | TGAGACACCA | AGACAGTATA | TGTATGAGAC | ACCCTGTGTG | TGTGACACAG | 240 |
| CGTGTGACTG | TGTGAAACAT | GCTCGAG | | | | 267 |

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

| | | | | | | |
|------------|------------|------------|-----------|------------|------------|-----|
| GAATTCGGCC | AAAGAGGCCT | ACCCAGAACC | AGTTTACTG | AGGGTCCTGA | GATCTGCTAT | 60 |
| AACATCACCA | TCCTTCAAC | CCAGAGGTGT | GTGTTGTGG | GCCATTCATT | TGGCCCTCAC | 120 |
| CACATCCTGC | CTTGATTGTC | TAGTTTATCT | TTTATTGTC | TTTGTTCTCC | CCCAACCTCC | 180 |
| TGCGCCATAC | AGACTCCTCG | AG | | | | 202 |

(2) INFORMATION FOR SEQ ID NO:1354:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

```

GGTTTGATA TCCTGAAAGA TCAATGGGCA GCTGCAATGA CTCTCCGCAC GGTATTATTG      60
TCATTGCAAG CACTATTGGC AGCTGCAGAG CCAGATGATC CACAGGATGC TGTAGTAGCA      120
AATCAGACGA GCAAAAATCA AATTAAAGTA GATCTTGTAG ATGAGAATTT TACAGAATTA      180
AGAGGAGAAA TAGCAGGACC TCCAGACACA CCATATGAAG GAGGAAGATA CCAACTAGAG      240
ATAAAAATAC CAGAAACATA CCCATTTAAT CCCCCTGATC TCGAG                      285

```

(2) INFORMATION FOR SEQ ID NO:1355:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```

GAATTCGGCC TTCATGGCCT AGTTATTTCG TCACTGTCGC AAACAGCAGG CAAAGTTTGA      60
CGAGTGTGTG CTGGACAAAC TGGGCTGGGT GCGGCCTGAC CTGGGAGAAC TGTCAAAGGT      120
CACCAAAGTG AAAACAGATC GACCTTTACC GGAGAATCCC TATCACTCAA GACCAAGACC      180
GGATCCCAGC CCTGAGATCG AGGGAGATCT GCAGCCTGCC ACACATGGCA GCCGCTTTTA      240
TTTCTGGACC AAGTAAAGAT GGGTCCGTGG CCCACACTCG GTCATGTGCT CAGACAACAA      300
CTCGAG                      306

```

(2) INFORMATION FOR SEQ ID NO:1356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

```

GGAATGATGT CACTCACGTC CAGCAAAGCC AAAGAGCTGA AGGACCGGCA CCGGGACTTC      60
CCAGACGTGA TCTCAGGAGC GTATATAATT GAAGTAATTC CTGATACCCC AGCAGAAGCT      120
GGTGGTCTCA AGGAAAACGA CGTCATAATC AGCATCAATG GACAGTCCGT GGTCTCCGCC      180
AATGATGTCA GCGACGTCAT TAAAAGGGAA AGCACCCTGA ACATGGTGGT CCGCAGGGGT      240
AATGAAGATA TCATGATCAC AGTGATTCCC GAAGAAATNG ACCCAGGC TCTCGAG      297

```

(2) INFORMATION FOR SEQ ID NO:1357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

| | |
|---|-----|
| GTCCCGCTAA ACCGGCAGGC GATGAGAAAG GAAACCATCA CTAAGATGCT CTGGAGTACC | 60 |
| CGCACCTGT TGAATATCAC CAAGGAGCAG GTACCACTTG TGGTGGAGGA GTACCTGGAC | 120 |
| AATGTCAATG AGCATGACTG GAAGATGCTA CGAAACCGTA TGATGGACAT AGTTCAAGAT | 180 |
| GCCACTTTCG TGTATGCCAC ACTGCAGACT GCTCACTACC ACCGAGATGC CGGCCTCCCT | 240 |
| GTCTACCTGT ATGAATTTGA GCACCACACG CTCGAG | 276 |

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGGGGAGCAT AAAAATACAA AAAACATTG GCTTTATTCA | 60 |
| CAACGTATTT TGTGAAACT CAGGAATAAC TCTTTGAATT TTGGGAAAC CAACAACATT | 120 |
| CTCAAAAACG ATGATAATCA ATTTTATTGT GCACCTCTGC ACCCTGCCTC CATGGTCCCA | 180 |
| CCACCAGGTT CCTCTCCTC CACAGTCAGA AGTTCCTCCC TGCATTCAA CACTGGGTCT | 240 |
| CGAG | 244 |

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

| | |
|---|-----|
| GCGATTGAAT TCTANACCTG CCTCGAGGAC CCAAATATTT CTTGAGATC TTTCTTTCAA | 60 |
| TTCTTTTGGA CATATACTCA GAAGAGAGAT CATTGGATTA TTTTGTGTT TTTCAGAAAC | 120 |
| TGCTACCGT ATTCCAAAGC AGCTGCACCA TTTCACATTC CCACCAACAT TGCATCAGGG | 180 |
| TTCCAATTTT CCCACATCCT TGTCACATT TGTTATGTTG TTTTGTGTT TTTGTTTTTT | 240 |
| TTTGTTCGC TTTGTTTGT TTTGTTTTGT TTTGTGCACA CAGTCTCGCT CTGTTGCACA | 300 |
| GGCTGGAGTG CAGTGGTACA GATCTCAGCT CACTGCAGCC TCTACCTCTC CAGTTCAAGC | 360 |
| AATTCTCCTA CCTCAGCCTC CCCGGCTCGA G | 391 |

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

```
GAATTCGGCC TTCATGGCCT ACATTTTTTT CCTAGTATGG ATATGCTTAT TAATGCACTT      60
GTTTCAAAAT CCCAAATTGC ACAAATGTGT TAATATTTTA AGAAACAAAA TGAATCCTAC      120
AAGGAGAATG ATTTTATAGCC ACACATAGGG TTGGATCTTG AGAGTGACCT ACAGAATAAA      180
AGTACTTTTA AAATAAAGTA GTCAGAGGCT ATTCAAAGGG TAAAATAATC ATAGTACCAC      240
ATTGGTCCAC TTGACACTCG AG                                         262
```

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

```
GAATTCGGCC TTCATGGCCT AGACAACCTG AAACTGGATG ACATGCTGAG TGAAGTCTAG      60
GACAAATGGG ATACCATATG TGGAAAATCT GTGGAAAGGT AAAATGTTCT TTAAGACAGT      120
TTGGTTACTC TGTAGACCTC TTTCAAATAC ACAGTAATGG TGCTTTGCGG GGACATTTTCG      180
GGAACCTTAA ATATTTCTCT TGCCTGAGGA ACTTCTGCTT GTCCTAAGTA TCCCACACAC      240
ATAGCACTCG AG                                         252
```

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

```
GAATTCGGCC TTCATGGCCT ACATAGCAGT ACACAGAAAC TCATCTTTGG TCTTAAAACT      60
GCATAGGTAC TTTAGTCCTC TGTTGACAAA TGTTGGGTTG TTTCAGTCTT CTGCTATCAC      120
AAATAATGCT GCAAAGAATA CATTTGTTCA TATGTCATTT CATCCTTGGC AATTTTGCCT      180
CTGGAAAGTT CCTAGAAGTC AGATTCCCAG GTCAAAGGTT AAATGCGCAT GTAATTTTGC      240
TGGATATTGT TAAATCCCCC TACAGAGCAT GCACCACTCA GCATTCCCCT CAGCTCGAG      299
```

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGCGAGATCT | GCGTGAAAAA | TACAGCAATT | TTGGCAATAA | 50 |
| CTCTTATCAC | TCCTCAAGAC | CCTCATCTGG | ATCCAGTGTG | CCCACCACCC | CCACATCATC | 120 |
| CGTCTCACCC | CCACAGGAGG | CCAGGTTGGA | AAGGTCATCA | CCGAGTGGTC | TTCTCACATC | 180 |
| ATCCTTCAGG | CAGCACCAAG | AGTCACTGGC | AGCAGAGAGA | GAGAGGCGGC | GGCAGGAGAG | 240 |
| AGAAGAAAGG | TTGCAGAGAG | AGCTCGAG | | | | 268 |

(2) INFORMATION FOR SEQ ID NO:1364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCT | TCATGGCCTA | CCAACCCCCC | CATTTCTCCC | TTCTCCAGC | CACTGGCAAC | 60 |
| CACCATTTCA | TGTTCTTTTT | GTTTGTTTGT | TTTGTTTTT | GTTTTTTGTT | TTTGTTATT | 120 |
| ATTATACTTC | AAGTTTTAGG | GTACATGTGC | ACAACGTGCA | GGTTTGTTAC | ATATGTATAC | 180 |
| ATGTGCCATG | TTGGTGTGCT | GCACCCATTA | ACTGGTCATT | TAGCATCAGG | TATATCTCTT | 240 |
| AATGCTATCC | CTCCCCACTC | CCCCCAGCTC | GAG | | | 273 |

(2) INFORMATION FOR SEQ ID NO:1365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATCGGTGTC | TTTGGTAAAA | ATTCTATGAG | GATGACATAT | 60 |
| TCCATCATGT | TATTCGTTTC | ACATTTCTT | TTGCTCAGTC | TCCAATGCAA | GCACAGCTTG | 120 |
| TGGTATAACC | TATTGTTTTT | CCATTCTAAT | AACTTCTCAA | TCGATCTTCG | TGTTCTTTTA | 180 |
| CTGAGGCAAA | TAACTGGCCA | CATACTGCAA | CCTAATGTGC | AGCAGCAACA | AAGGCAGCCA | 240 |
| CAAAGTAGCC | AACGTACATT | AACAGGAAGG | TTCTTCTTAA | GACAACTGTT | AACTCTGTNG | 300 |
| ATGCTGGCTT | TAAATTCTTC | AGGAGCTACT | TTTTCAGTTA | ATGAAGAAGG | GAATTCAGAT | 360 |
| TCAAAT | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:1366:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTTGTTAGGC | TGGTGTGTT | ATGTTGCTGT | TGTTATGCTG | GTCGTGCTGC | TCCATGTTCT | 60 |
| CCAGGTGTTT | TTCCCTTTTA | TCGTACAGT | TACCCCGTAC | ACCTGACAAC | TGGACATCTG | 120 |
| CGCCTGGGGT | CTTCAGCCTA | AACACACCTA | AACCCTCCAC | CAAACCCCTC | TGCTTCCGCC | 180 |

TCCCCGTGTC TGTGAGCGCC TCCACTGCCC ATCCCTCTGC TCAGGCCCCA TTTCCAGGGC 240
TCGAG 245

(2) INFORMATION FOR SEQ ID NO:1367:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

GTATTTTGT GACTGAAGTC ACCTTCTAAA TAATTTCTAG AATAAAATTT TTATATTGAA 60
 GAAGTTGGTC TTAACCATTT TTTTTCAGG AGCATGCATT TTGAAATCAT TCTGTGGGAA 120
 GATGAAAACA AATTTAGTTC TATGTCTCCC CTTTITAGAG ATGTTGACAC TTTCTTAAA 180
 TGTACCATGC ATGATTGTGC TACCACCCAG ACTCGAG 217

(2) INFORMATION FOR SEQ ID NO:1368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

GGCTAGAAGC AAGATGGCTG AACTCAATAC TCATGTGAAT GTCAAGGAAA AGATCTATGC 60
 AGTTAGATCA GTTGTTCCTA ACAAAGCAA TAATGAAATA TCCTGGTGC TCCAACAGTT 120
 TGATTTTAAT GTGGATAAAG CCGTGCAAGC CTTTGTGGAT GGCAGTGCAA TTCAAGTTCT 180
 AAAAGAATGG AATATGACAG GAAAAAGAA GAACAATAAA AGAAAAAGAA GCAAGTCCAA 240
 GCAGCATCAA GGCAACAAAG ATGCTAAAGA CAAGGTAGGG AGTCTCGAG 289

(2) INFORMATION FOR SEQ ID NO:1369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

GCGATTGAAT TCTAGACCTG CCTCGAGTGT TTTTAAAAA CTCTCTCTCT TCACTGACAC 60
 CAGGTGTTGC TATTAATGTG CTCAAATCTC TCACTTATAA AAAAGAATAA AACCTCTCTC 120
 TTTTCTAGTT ACTGGTCTGT TTATTCTTTT GTAGAATGAT CTTTGGGAAG AGTGTTTTCA 180
 TTTATCCAG TCTCTTCATC TTTTATTCCT TACTGCACTG TCATCTCGAG 230

(2) INFORMATION FOR SEQ ID NO:1370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAACAAACAA AAAGAAGAAA ACACTCAACA AAACCAATCT | 60 |
| ACATGTTTTG GACTAAAAAA AAAAATAGAG GTTGTTATTCT CAGTGTCGA CTCGGAATTA | 120 |
| TGTTGCTGCC TCTCTGTGCT TTTGGCCTCT GTGTGGCCGT GTTTGGCCAG CATGAGATAC | 180 |
| TGTCCCTCT GGAGGATTT AGGGGAGGAA GAGCCACGTC CCCAGGGATT GGAGGAGGCT | 240 |
| CCGGCACCT CGAG | 254 |

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

| | |
|---|-----|
| GAATTCAGCT ACACTTGAGT ATTAGGAAGC CATATAGAAT TCGCAGGGTC CAACTTCATA | 60 |
| GACTCTATTC ACATTATTAG AGTAGTAGTG GGGACCGTTA CTTTGGGAA AGGATCAGTG | 120 |
| AGACAGTATA AACTTTTGAA ATAATACATT TTTGTATTCC AGAATTATTA GATAATACTA | 180 |
| AAGCAAACTT TTTTAATGGA ACATTTTGAA GTCCTGTGTA TTTATTTTAT TTTTATTAT | 240 |
| TTTGTGAGA CAGAGTTGCA CTCACGCACG CTCGAG | 276 |

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTCGAATCA TAGTGATTAA AATAGTTGGG GTAAAGTTGT | 60 |
| AGCTTATATG CAATACTACT TGGAGGAATT CTTCTACTAA TTTGTATTTA ATGTGGAAAT | 120 |
| TGTATAGTTT CATTGATTGA ATCATAAATA ATGGAAATGG TCTCCAAGAA GTTTTATTTT | 180 |
| TCATTTT TTTT GCTTATACAC TCTGATTCCT ATAATACAGT GCTATAAGCT ATGCACAGAA | 240 |
| AATCTCGAG | 249 |

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

| | |
|---|-----|
| CCCGTTGTCA ATCTTTGGGT TTTATTCCTT TTAAAGAAAG AAAGAAGTTC TGCTGAATTT | 60 |
| GGAAATAAAT TCTTTATTTA AACTTTCCTT CCCAGTTTAA TAGTTTCTGG TTCTGAGGAC | 120 |
| TGATGAAAAT CATCTTCCAT CAGCAGATTT TCTTGCACTG TTTGCTGTGC CCCTCAAATA | 180 |
| TAATGTCTTG GGTTTTAAGA TCGAGCAGAG AGCTCGAG | 218 |

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS: --

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCTT GGGTCTCTCT TCCCATTTT TGCTTCTTGT TCTCCAGAT | 60 |
| CTTCCCAAAA ATAAGCTCAG TGCCAGAAAC TTGTGTGGCT TTGGGATATT CCACTGCCCC | 120 |
| GGCAACAGGC AATCTCGAG | 139 |

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGCAAGACGC AGCAAAAGTG GAACTTCCAA GATACTAATC | 60 |
| TGAGAAGTTT TCAACAAGAA ACAGGTTTAG AATTAAAAAT CAAAACCTCT TTTAATTGTA | 120 |
| TTAAGAGTAA ATCATATTTT AAGACAACTT TCTTTTAAA CAAGGGACCA AAATTTAGAA | 180 |
| AGACTTTTAT AAATAATTTT AATTATAGCC AACTTAATCC CACACAAAAT GCTTTTCATA | 240 |
| AGTATTCTCT CACAAACACT CGAG | 264 |

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

| | |
|---|-----|
| CTTAAACCCA GGAGTTAGAG ACCAGACTGG ACAATATAGC GAGACCTCAT TTCTAACCCC | 60 |
| CAAAAAATA TACACACGCA CACACACACA CACAAACACA CACACACACA CACGCATGCA | 120 |
| AACTATATTA AAAAAACGGT CATGCTGCAT GGTTTTTTAT TTGTGTTATT TTTATTGTTG | 180 |
| TAATGTTACT TTATTTTCTA ATATTTTCTG TTTGCGGTTG GTTGAATCCT CAGCTGTGGA | 240 |
| ACAGCTCGAG | 250 |

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

```

GAATTCGGCC TTCATGGCCT AATTTCCTT TCTCTTTTT TTTGGTTTT GGTAAATTTG      60
TAATTTTGGT TCGTCCTGA TGTATATGGA CTGCCAGAAT AGGGGGGGTG GTGGTTTGGT      120
CGTGGTGTCT GGGGGAGGAA GGAATCCTTA CCCTGGCTTC CTTAATCGGG GAAGGCTTCC      180
TGAAGGAGGT GGGCTCAGAG GTGAGTTGTG AATGAAGCGG GTAGGGAGTG GGCTGGGTGG      240
ATGGTTTGGG GATGTTTGGG GGAGGTGAGT AAAGGGTAAC TCGAG                      285

```

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

```

GAATTCGGCC TTCATGGCCT AGAAAGAGCA AATATAATGA AGACTTTGAA AGAGCTTGGG      60
GAGAAGATCT CACAATTAAA AGATGAATTA AAAACATCTT CTGCAGTCTC CACACCATCT      120
AAAGTGAAGA CAAAAACGGA GGCCCAAGAAG GAGTTATTAG ATACTGAACT GGACCTCCAC      180
AAGAGGCTGT CCTCAGGAGA AGACACCACA GAATTACGGA AAAAACTCAG TCAGTTACAG      240
GTTGAGGCTG CACGGTTAGG TATTTTACCT GTGGGTCGAG GAAAGACCAT GTCCTCTCAA      300
GGTCGAGGAA GAGGCCGAGG GCGTGGAGGA AGAGGAAGGG GCTCACTAAA TCACATGGTG      360
GTGGACCATC GTCCCAAAC CGAG                      384

```

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

```

GAATTCGGCC TTCATGGCCT AGTCAGGAAC TCCAGTTTGC TTTTCTGTTT TGTGTCCTGG      60
TAGCAGCTGT TGAGTAACTT TCATTGGAGG TTGGGAAGGA AGTGAGGAGA AAGTGTCTCT      120
GTTTAGTGTT TTATTTCTTA TAATAGGATG CTGCCTAACC CAGTTCATCT CTATGTCCTG      180
TTCACTGAAT ATTCCGGGTA ATTGAAAGAA AATATAATGG ATGGGCTCCA TTAAACCAG      240
CTCAAAAATA AATTCTTGTC AGTAAAGATT TCTTGCAAG ATGTCTTGGA TTGCACTTTT      300
GTTGAGGAAA GACAGTGTA ATAGTTAAAG AATGTTGATA AAATTGAAAC ATTTGGGCCT      360
TCATGGCCTA                                     370

```

(2) INFORMATION FOR SEQ ID NO:1380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCTAGA | CCTGCCTCGA | GTTGCTGAAC | GGTTTAGATC | CTCAAAAAAT | AAAGCAATTG | 60 |
| AACCTGGCCA | TGATTAATA | TGTNTTGGTC | GTCTATGGAC | TTGCCATTTC | TCTCCTTGGA | 120 |
| ATAGGACAGC | CTGAGGAATT | ATCTGAAGCC | GAAAACCACT | TTAAGAGGAT | TATTGAACAC | 180 |
| TACCCCACTG | AGGGCCTTGA | TTGCTTGGCC | TACTGTGGAA | TTGGAAAAGT | ATATTTGAAA | 240 |
| AAAAACAGAT | TTCTAGAAGC | TCTCAATCAC | TTNGAGAAAG | CAAGAACCCT | GATTTATCGT | 300 |
| CTTCCTGGAG | TGTTAACTTG | GCCACGAGT | AATGTGATTA | TTGAAGAGTC | TCAGCCACCC | 360 |
| CTCGAG | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:1381:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACTTTAATGA | GATAGGAACT | AGTATATTCA | CCGTCTATGA | 60 |
| GGCCGCCTCA | CAGGAAGGCT | GGGTGTTTCT | CATGTACAGA | GCAATTGACA | GCTTTCCCCG | 120 |
| TTGGCGTTCC | TACTTCTATT | TCATCACTCT | CATTTTCTTC | CTCGCCTGGC | TTGTGAAGAA | 180 |
| CGTGTTTATT | GCTGTTATCA | TTGAAACATT | TGCAGAAATC | AGAGTACAGT | TTCAACAAAT | 240 |
| GTGGGGATCG | AGAAGCAGCA | CTACCTCAAC | AGCCACCACC | CAGATGTTTC | ATGAAGATGC | 300 |
| TGCTGGAGGT | TGGCAGCTGG | TAGCTGTGGA | TGTCAACAAG | CCCCAGGGAC | GCGCCCCAGC | 360 |
| CTGCCTCCAG | AAAATGATGC | GGTCATCCGT | TTTCCACATG | TTCATCCTGA | GCATGGTGAC | 420 |
| CGTGACGTG | ATCGTGGCGG | CTAGCAACTA | CTACAAAGAA | GAAAACCTCG | AG | 472 |

(2) INFORMATION FOR SEQ ID NO:1382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGAGTTTAACT | CCAGAACTGG | TGCTGGTCTC | AGCTGGCTTT | 60 |
| GATGCTGCAC | GGGGGGATCC | GCTGGGGGGC | TGCCAGGTGT | CACCTGAGGG | TTATGCCCAC | 120 |
| CTCACCCACC | TGCTGATGGG | CCTTGCCAGT | GGCCGCATTA | TCCTTATCCT | AGAGGGTGGC | 180 |
| TATAACCTGA | CATCCATCTC | AGAGTCCATG | GCTGCCTGCA | CTCGCTCCCT | CCTTGGAGAC | 240 |
| CCACCACCCC | TGCTGACCCT | GCCACGGCCC | CCACTATCAG | GGGCCCTGGC | CTCAATCACT | 300 |
| GAGACCATCC | AAGTCCATCG | CAGATACTGG | CGCAGCTTAC | GGGTCATGAA | GGTAGAAGAC | 360 |
| AGAGAAGGAC | CCTCCAGTTC | TAAGTTGGTC | ACCAAGAAGG | CACCCCAACC | ACCCAAACCT | 420 |
| CGAG | | | | | | 424 |

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

```

GAATTCGGCC TTCATGGCCT AGGCAGCGGC CTCTGTCCCA GGCCCCGGG TGCCAGCGTC      60
CTGCGAGCAC CCAGCTGACC AAAGATGTTT CCCTCTGTAG AAGACTCTGC TAGACTGGGT      120
CTGAAGCTTG AGTTTCTAA CAGGTGCTGC TGCACAGGTG GAAAGGAGCC GTGGGAATGT      180
GTGTGTGGCA CGGCCAGAC AAGGGCAGGG CTGAGGGCCT CCGACTCAGC TGGGGGTAGA      240
CGGGCTCGAA TGTGGCCTGG GAGAGCCTAG GGGGCCCCAG GGTCTGCTT TTCTATGTGA      300
GCCTTTAAAC TTCAGACAGG CCACCACCCT GCACCTGCAG GGGCTTTGGC ACAGGAGTGC      360
TGGCTTTGGA GGGACTGTGG CCTTCATCGT GGTCTCTGC CCACACCTCC ACGCACACAG      420
ACAGTGCCTT AGGAGGGAAA CAGAACTAAT TACGAGGGGG AGGCAAGAGG ACGCCAAGCA      480
AGGAGTGACT CGAG

```

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

```

GCTCGAGAGT GGGGCGTGGC AGTGTGTGCC TGTAGTCCCA GCCACCTGGG AGGCTGAGGC      60
AGAAAAATTG CCTGAACCCG GGGGTGCGAG GTTACAGAGA GAGACTCTGT CTCCCCAAAA      120
AAAAAAAAAA AAAAAAAAAA NNGTCTAAGG GTTANACAAT TCTTGATATA ATCTCTCCAC      180
AATACATTCA GAAATCTACT TTTGCTGTTG GAGTTGTATC TGAGAGCTGG GGAATTTAAA      240
ATTGCTGAAA ACAGATATAA GGGGAAAGTG AGATAAAAGC AGAAGCTGCC AAAAGGAGGT      300
ATTAGCATCA TCCTCAATTT ACACAGAATC ACATGCTAAG AGAGGCTAAG TATCTTTCCC      360
AAGATTACTC AGCCAAGTTG TGAAGCCAAG ATTTAACTGT ATCTATTCAA CTCTTATCTA      420
ATTATAAAAG CCTATGTTAT TTCCCACTGT GCTACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

```

GCAGGAGTAT CTGAGGATGG AGAACTCAGC ATAGAAAACC CCTTTGGTGA AACATTTGGA      60
AAAATACAAG AAGTGAAAA AACTCTTATG ATGAACACAT TATATAAGCT TCATGATCGA      120
TTGGCACAGC TTGCAGGAGA TCATGAATGT GGCAGTTCTA GTCAAAGAAC GCTTTCTGTT      180
CAAGAGGCAG CTGCGTATTT AAAAGATTTA GGTCTGAAT ATGAAGGTAT ATTTAACACT      240

```


| | |
|--|-----|
| TCATTGCAGT GGATCTTAGA AAATGGAAAA GATGTTGGAA TAAGGTGTGT TGGTTTTGGC | 300 |
| CCTGAGGAAG AATTGACAAA TATAACTGAT GTGCAGTTTT TACAGTCCAC AAGACCACTG | 360 |
| ATGTCTTTTT GGTGTCGTTT TCGACGTGCT TTTGTTACTG TAACTCACAG ATTATTGTTG | 420 |
| TTATGCTTAG GTGTAGTGAT GGTGTTGTGTC GTTCTGCGTT ACATGAAATA TCGATGGACA | 480 |
| AAAGAAGGGG AGGATCTCGA G | 501 |

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid --

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT ACTCCAAGAG GCAGTTCTAC ATCAAGATCT CAGACGTGCA | 60 |
| GGTGTGTTGGG TATAGCCTGA GGTTCAACGC CGACCTCCTG CGCAGTGCAG TGCAGCAGGT | 120 |
| CAACCACTCC TACACACAGG GCGGCCAGTT CTATTCCTCT TCGTCAGTGA TGCTCCTCTT | 180 |
| GTTGGATATT CCGGACCGAA TTAATCGCCT GGCCCTCCT GTGGCCCCGG GGAAACCCCA | 240 |
| GCTGGACTTG TTCTCCTGTA TGCTGAAACA CCGCTGAAA CTGACCAACA GCGAGATCAT | 300 |
| CAGGTGAAC CACGCCTTGG ACCTGTACAA CACGGAGATC CTCAAACAGT CCGACCAGAT | 360 |
| GACAGCCAAC ACTCGAG | 377 |

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGACGACGCC TATGAAGCCC TTAGTCCTTC TAGTTGCGCT | 60 |
| TTTGCTATGG CCTTCGTCTG TGCCGGCTTA TCCGACATCA AAGGGATCAA AATTAAAGGA | 120 |
| GCTAGTTACA CATGGAGACG CTTCAACTGA GAATGATGTT TTAACCAATC CTATCAGTGA | 180 |
| AGAAACTACA ACTTTCCTA CAGGAGGCTT CACACCGGAA ATAGGAAAGA AAAAACACAC | 240 |
| GGAAAGTACC CCATTCTGGT CGATCAAACC AAACAATGTT TCCATTGTTT TGCATGCAGA | 300 |
| GGAACCTTAT ATTGAAAATG AAGAGCCAGA GCCAGAGCCG GAGCCAGCTG CAAAACAAAC | 360 |
| TGAGGCACCA AGAATGTTGC CAGTTGTTAC TGAATCATCT ACAAGTCCAT ATGTTACCTC | 420 |
| ATACAAGTCA CCGTCCACCA CTTTAGATAA GAGCACTGGC ATTGAGATCT CTACAGAATC | 480 |
| AGAAGATGTT CCTCAGCTCT CAGGTGAAAC TGCGATAGAA AAACCCGAAG CACTCGAG | 538 |

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACCTATTTTC | CATATTCCTG | GTGACTCATA | ATGTACTCCT | 60 |
| GCTGTTGCTG | ACGGGCAGTG | GTCGGTCAGA | GCAGAAGCTC | AGCTGTGATT | GCTGGGGGAG | 120 |
| TTCTGAGCTC | CATGAGCCAC | TCTGGCCACG | ACACCATCTT | TACTTGAAAG | AAAAACTTCC | 180 |
| CTTTGATGCT | GAGGCCTCCA | GTGTCATAGA | CGATGCCTTT | GCCCACCCAG | GCGATGGTCT | 240 |
| GCGTGGCTCC | ATCTGGGGTG | TGGCTGAGGA | CGGCCAGGGC | TGGGGGATGC | AGGGCGGCTT | 300 |
| TGCCAACCCC | ATAGATTTCCT | CCAAATCCTC | TCGTCTTCAG | TTCTCATCC | CGGATGATGG | 360 |
| TTGGGATGAT | CCCCAGCTCC | TTTCCAACCT | TGTTAATCTC | CTCGAG | | 406 |

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAATTAACCT | TAATGGGCAA | TCATAAGAAT | AATTGAAAAT | 60 |
| AAGGAATTCA | GGGGAGCTTA | ATTCAATTTG | AGGTTTTAGG | TGATACCATT | GCTATTCAGA | 120 |
| TTGCTTTGGG | CAATTTATGT | AATTTTTTCC | AATGACATCC | AATTTTCATAT | CACTGTAAC | 180 |
| GAAGAAACAG | AAAATTTAGT | TCAGATTTTA | AATCATCATT | CCCTGATGCC | ACCTCATCCA | 240 |
| ATGATGTTTC | ATAAACGATG | AAATCACGTA | AGAACCACCT | AAACCAGGAC | TGATAGTCTA | 300 |
| TTGCTAGAAA | CTTGAATAA | TTTCCACTGA | TTTCTGTTTT | CACTGGAAAC | AGAACAGAGA | 360 |
| CTCCTCGAG | | | | | | 369 |

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AAGACCAAAA | CTAAACTGAA | ATTTAAAATG | TTCTTCGGGG | 60 |
| GAGAAGGGAG | CTTGACTTAC | ACTTTGGTAA | TAATTTGCTT | CCTGACACTA | AGGCTGTCTG | 120 |
| CTAGTCAGAA | TTGCCTCAAA | AAGAGTCTAG | AAGATGTTGT | CATTGACATC | CAGTCATCTC | 180 |
| TTTCTAAGGG | AATCAGAGGC | AATGAGCCCG | TATATACTTC | AACTCAAGAA | GACTGCATTA | 240 |
| ATTCTTGCTG | TTCAACAAAA | AACATATCAG | GGACAAAGCA | TGTAACCTGA | TGATCTTCGA | 300 |
| CACTCGAAAA | ACAGCTAGAC | AACCCAACTG | CTACCTATTT | TTCTGTCCCC | AACGAGGAAG | 360 |
| CCTGTCCATT | GAAACCAGCA | AAAGGACTTA | TGAGTTACAG | GATAATTACA | GATTTTCCAT | 420 |
| CTTTGACCAG | AAATTTGCCA | AGCCAAGAGT | TACCCAGGA | AGATTCTCTC | TTACATGGCC | 480 |
| AATTTTCACA | AGCAGTCACT | CCCCTAGCCC | ATCATCACAC | AGATTATTCA | AAGCCCACCG | 540 |
| AGCTCGAG | | | | | | 548 |

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

| | |
|---|-----|
| GTTTATTTTC ATCATCTACA GAACCAAACCT CCCTTTTCATG TGCACGAGTG AGAATCTCTT | 60 |
| TGTACAGTGT TTCTGCTTGC TTGAACTTTC CTTGTTTCAA ATAGCAGGAT GCCAGGTTAT | 120 |
| TTTTCGTCTT AGCCACGTTG GGGTCATCAG GTCCCAGTTT TGTCTGGTAG ATCTCGAG | 178 |

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGGCCCTAT ACCTCCAGCC GTGAATGCCA GACTTTAAGA | 60 |
| TTGCCCGGAG GAAGCAAACCT CTTCTGATAA AAAAAGCAGG CCATCTGCTT AACCTTGGC | 120 |
| TCCACCATAA GGCAGTGGGA CTCGGATTTC TCTATCTGAT AGAGGTATTT TCTGTGGCCC | 180 |
| TGGGAGCTGT CTGTCTTTCC CCTACCCCA AGGATGCCAG GAAGACGTCC ACCATTAGCC | 240 |
| ATGTGGCAAC CTTTACTTCT ATGCCTCACA AGTGCCTTTC AGAGAGCCCC AATTCTGCTT | 300 |
| TCCCACAAA TAAACCCAAT GCACTCGAG | 329 |

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTCCTTTCC TTTTCCCTTT GAGATTTTTT TGTGTGTGT | 60 |
| TCCTTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT | 120 |
| ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCCAATCCGG | 180 |
| AGAAGGTTC AGCAGGTCCC CCACCTCCC CTCCTCTCC TACTTCTCCT CTTGACAGCG | 240 |
| AGGACAGGAG GGGGACAAGG GGACACCTGG GCAGACCCGC CGGNTCTCCC CCCACCCAC | 300 |
| CCCGCCCTC GCATCATACT CGAG | 324 |

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AACTGCAACG GAGAGACTCA AGATGATTCT CTTTTTACCC | 60 |
| ATGTTTTCTC TACTATTGCT GCTTATTGTT AACCTATAA ACGCCAACAA TCATTATGAC | 120 |

```

AAGATCTTGG CTCATAGTCG TATCAGGGGT CGGGACCAAG GCCCAAATGT CTGTGCCCTT 180
CAACAGATTT TGGGCACCAA AAAGAAATAC TTCAGCACTT GTAAGAACTG GTATAAAAAG 240
TCCATCTGTG GACAGAAAAC GACTGTGTTA TATGAATGTT GCCCTGGTTA TATGAGAATG 300
GAAGGAATGA AAGGCTGCCC AGCAGTTTTG CCCATTGACC ATGTTTATGG CACTCTGGGC 360
ATCGTGGGAG CCACCACAAC GCAGCGCTAT TCTGACGCCT CAAAAGTGAG GGAGGAGATC 420
GAGGGAAAGG GATCCTTCAC TTACTTTGCA CCGAGGCTCG AG 462

```

(2) INFORMATION FOR SEQ ID NO:1395:

- (i) SEQUENCE CHARACTERISTICS: ..
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

```

GAATTCGGCC AAAGAGGCCT AGAACTGCCA TCATGAGGTC TGACAAGTCA GCTTTGGTAT 60
TTCTGCTCCT GCAGCTCTTC TGTGTTGGCT GTGGATTCTG TGGGAAAGTC CTGGTGTGGC 120
CCTGTGACAT GAGCCATTGG CTTAATGTCA AGGTCATTCT AGAAGAGCTC ATAGTGAGAG 180
GCCATGAGGT AACAGTATTG ACTCACTCAA AGCCTTCGTT AATTGACTAC AGGAAGCCTT 240
CTGCATTGAA ATTTGAGGTG GTCCATATGC CACAGGACAG AACAGAAGAA AATGAAATAT 300
TTGTTGACCT AGCTCTGAAT GTCTTGCCAG GCTTATCAAC CTGGCAATCA GTTATAAAAT 360
TAAATGATT TTTTGTGAA ATAAGAGGAA CTTTAAAAAT GATGTGTGAG AGCTTTATCT 420
ACAATCAGAC GCTTATGAAG AAGCTACAGG AAACCAACTA CGATGTAATG CTTATAGACC 480
CTGTGATTCC CTGTGGAGAC CTGATAGCTC TCGAG 515

```

(2) INFORMATION FOR SEQ ID NO:1396:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

```

GAATTCGGCC AAAGAGGCCT AGTCCTTCAC TAGACTATAT GCATTTTATC TTACCTTATT 60
CCTCATTTTA GTGTCCAGTG GCTGGCGTGT ATAAACCCTG AATGTTTTTA AAGATAATAT 120
TTTAAAAGAT CACTTTAGTT ATAATACGGC TTCAGTTGGT GGAATAAAGA AATTTTTTTC 180
TTTTTTTTTA TTTTGAGTAA AAATGATAAC TTCTCTCCAC CCTCTCTATA GTTAAAGCCT 240
TCCATCTGAA GTATGATGAA GTTCGTCTGG ATCCAAATGT TCAGAAATGG GATGTNACAG 300
TATTAGAACT CAGCTATCAC AAACGTCATT TGGATAGACC AGTGTTCTTA CGGTTTTGGG 360
AAACATTGGA CAGGTACATG GTAAAGCATA AATCGCACAT CTCGAG 406

```

(2) INFORMATION FOR SEQ ID NO:1397:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

| | |
|---|-----|
| GAATTCGGCC AAAGGGGCCT AAGAATAGCA AATATCTTGT GCTTAGCAAA AAATAATCTT | 60 |
| GAAAAATTTT TCTGAAATAA ATGTTATTGA AAAATGCAAA TAATTAGAAT TAAATACCAG | 120 |
| CTGCAGTTCT ACATCCTCTT ATTGGCCAAT GTAAAGAGAA ATCAGGCATG TTAATCCAA | 180 |
| AAAAGGACAA TTCAACAACA TGGAAACCAT GACTAATATA TGGAGAATAC AAAGAAAGAC | 240 |
| TAAAGATTTA GATCAGGCTA ATTTCTTTT ATTCCCATCA AATCCAAGTA CCACTCGAG | 299 |

(2) INFORMATION FOR SEQ ID NO:1398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs --
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

| | |
|---|-----|
| GAATTCGGAC AAAGAGGCCT AGGAGAGGCG GGAGCCTGGG AGAGCCTCTG CTAGACCTTT | 60 |
| CCTGGCACTT CCCCAGGAAA GGCAAGGCAG GGCAGATGTG CGGCTGGCCA GCTGGAGTGA | 120 |
| TTCCATGGG CTCCAAGCTG TAGGAGTGGT CCCTGGCTGC CAGAGTGCTC TGGCCAGATA | 180 |
| CAGGTGGGCT CTGGACTGGT GAGGCTGCAT TCGGAGGCG CGCACACCCA GCTGGGCCCT | 240 |
| TATCTGTAAG GACTGGCTGG CCTGGGAGGG GCAGTCTCCC ANCCAGAANG TGGAAATTTT | 300 |
| TTTTTTTTTT TGAGATATCA AAACATCCTA AGGTACAGGA AAGAAATTGT CNACACACAC | 360 |
| GGCTCGAG | 368 |

(2) INFORMATION FOR SEQ ID NO:1399:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTTTTGG AGATGTTGAT CAGATGTTCA CTGATAAACT | 60 |
| TGAGCCCCCT TTTCTTCCTC TGGTCTACCC ATCTAGAATG CTATGACCCA TCTCAGACAC | 120 |
| ACCCCTCTGG GAAGCTGCCT GAGCTCGAG | 149 |

(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGTCGATGGA GATAAGTGT TTAATTACTT TTTTAATGTC | 60 |
| TGTGCTTTTG TATTTTCTC CTCTCTTCC TTTTATTTCC TGCTGTNGAG ATTACTGCCT | 120 |
| CATCTCCACA GCAGGTGGCT GTTGCAAATT TGTTTCTTT GTAAGCCTGG AAGATTTATT | 180 |
| TTGTAATATA ACTGTTCTT TTTAGTATTT TATTATTAAT GATTTCCTTA CTTTGGGATA | 240 |

| | |
|---|-----|
| TAGTGTACTT ACACAGTCCT AACAGTAAT TTCCTAACAC TATCTAAGAA CTCCAATCAT | 300 |
| TAAGAAAAAA AATCTTTGCC TGAGGCGTAT TGTTTGAGAT TTTTGCTTAC CCTTACTTCA | 360 |
| CAATGCCGGG ATTAAAATTT AAGGAAATTG TTTTATAGCA AAAGCCAAAT GAGAAAAAGA | 420 |
| AACAGAGAAA ATAGAAGGGA GGGAAATAAA GAAAAGGAGA AGAGAAAAGG CTCAAGAGAC | 480 |
| AAAGTATACT TTAATAAATA ATACCATAAA GCAGAGTAAT GAGGATAAAT TTATGGCTGA | 540 |
| AATATGAAAT TACATTAACA TCTTTTCTAG AAATGTTTCA ACTAAACCAA ATGCTCGAG | 599 |

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs..
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT ACAGTCACCC TATAAAATAG ATTAAGTGTT CCGAGTTCGG | 60 |
| TTGGGTTTTT CGCAATTAAA AATTGTGTTA ACAGTTTAGT GTTTCCTTACA GATAACACTG | 120 |
| ATAACACTTT TTTGTTTTCA TTGGGTCTTA TCATTGGTAC AGACTGATCC AAAAATCCAA | 180 |
| TTGGCTTGCT AGTAATTTTT TCCTGTGAAT TGCTAAGATT TATGGGTAAA TTAAATTTTT | 240 |
| TTTTCTTTT CTTTTTTTTT TTTTAAAGCA TTTGCTCCTT AAATGCAAAT CGTACCACTA | 300 |
| AGATCCTCTC ACAACAGATT AAGGTCGAAT TTGCAGAGAC ACTCGAG | 347 |

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATATAAATC AACTTTTCTT TGTCTCTCTT GCCTGTGATG | 60 |
| AGTAACAGAA ACCATCTTCC CAGAAACTAT CCCCACCCAC CCCCAGCCCA GCCCAGCAG | 120 |
| CCCAGACCCA GGAAGGAGGT CAGAGCCTGC GTGACTGTGT GGCAAGGATC CCCCTCAAAG | 180 |
| CAGGCAGTGA TCCCCCTCAA AGCAGGCAGT GATGACCAGG CTCCCCAGGG GAAGGAAAAA | 240 |
| TGGTTGATTA CCCCACCTCA CTTTCTCAAG TTCCTGAAAG CCTCCCATCT TTTCAGGATG | 300 |
| TTTTCCTTCT GCTTCCTTTC TGGGGTGATA TTGCAATGCA TGTGTCAGTC CCTCGAG | 357 |

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AAGGATTGTC ATAGCCAGGA CCACACTATT GCTTTTTTCAT | 60 |
| AACATTTTCT TTTTGGTTCT TTCTTTTGAA TTTCTTACAG GGCTGCAAAG TATGCCAGGG | 120 |

| | |
|---|-----|
| GAGTATGTAG CCCGGGGTGG TCCAATGGGT GTGAGTATGG GACAGCCAAG TTATACCCAA | 180 |
| CCCCAGATGC CCCCCCATCC TGCTCAGCTG CGTCATGGGC CCCCCATGCA TACGTACATT | 240 |
| CCTGGACACC CTCACCACC AACTCTCGAG | 270 |

(2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACAGCCTTTC TTCCCACTTT TAACTATAGA ACTTGCTTTT | 60 |
| AATTTCACTG ATATATGGAC ACAGTCAGAC GAGAACTCCT TCATGCTCCT ATTACCACAG | 120 |
| CTACTCGAG | 129 |

(2) INFORMATION FOR SEQ ID NO:1405:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATTGCTTAA GTCCTCAAG TTCTTTTAT TAAGAGTTGT | 60 |
| AAGTAAATT TAATAACAA TAACATAGTC TCTGCTATTT TGATCCTTGC TCTTTGCCAT | 120 |
| GCTGTTTTAC TTATTCTTTA TTGCATGTTT CACATCTATC AATTTTGGGA TATGCTTCTC | 180 |
| ACCTTCCTTA CTAAAATGTG AGCTCCGTAA ACGCAACAGC TACCTCGAG | 229 |

(2) INFORMATION FOR SEQ ID NO:1406:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGGAGGTA TTTTGAAAAT ACAATTTAAC TACAACAACA | 60 |
| TTTGCTTATT TTTAGAGTCT TTTATGACAT CAAGAGAAAT GATCCCAGAA AGAAAAAATC | 120 |
| AAGAAAAAGA ATCTGATGAT GCCTTAACTG TGAATGAAGA GACTTCTGAG GAAAATAATC | 180 |
| AAATGGAGGA ATCTGATGTG TCTCAAGCTG AGAAAGATTT GCTACATTCT GAAGGTAGTG | 240 |
| AAAACGAAGG CCCTGTAAGT AGTAGTTCTT CTGACTGCCG TGAAACAGAA GAATTAGTAG | 300 |
| GATCCAATTC CAGTAAACT GGAGAGATTC TTTCAGAATC ATCCATGGAA AATGATGACC | 360 |
| AAGCCACAGA AGTCACCGAT GAACCAATGG AACTCGAG | 398 |

(2) INFORMATION FOR SEQ ID NO:1407:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTAAAGTG TCTGA ⁺ CTGA AACATAATAC CCTCCCTTTT | 60 |
| CAATCCTGAT GTACCTTCTT CTAGTCTTGG TCTTTGGCAC CTTTTTTTCA AGAAGAAACC | 120 |
| ATACTCTCGA G | 131 |

(2) INFORMATION FOR SEQ ID NO:1408:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGTCCAGGC TGTAGGGTCC CTGGTCACAG AGGACCCGGG | 60 |
| TCACCCGGGA CTCATCTTTC ACTTATTGTT TTTCAAGTCC AGGGCCCCAT GGATGCCACT | 120 |
| GAGATGATTT CAGATGTTAC AGTCATCAAG AGGGATTGGG GCCGCATTCT GCCTCATTCC | 180 |
| TTGGCTTTTG AAATCAGAGA CGACATTTTC ACTTTAAACA AACCCAAACC ATTCCTGCTG | 240 |
| GTGGAGGATT TCTCCTGCAT CTCGGGGGTG GATTTTCACT GATTTATGTC TGCAGCGTGA | 300 |
| GCAGTCTCTG GGCTTTTCTG CAGCTCCAGA TGTTAGATGT TTTATCTCTC CGTCTTTTAT | 360 |
| CNGCTTCAGT CCTTGCCCCA GTCTATCCTC GCATGCTCCN TCCTNNGGGA GGGCTTCCTG | 420 |
| TCTTCACAGC CGCACCTTCC TCCCACTGCT ACCAGTGCCA TGGACCCACT GTATGTTTCC | 480 |
| TGGGGGCCAT GCAGAAGGTC CCCAGACCAG TGCTGGCCTG CGACAAATAA GTACAGAAAT | 540 |
| GGAGAATAAC CCCTTTCAAA CACATAATAG CATTGATAG AATCAATCAG GAGACTCAAG | 600 |
| TTTTTACTGC GTGCGTCTCG AG | 622 |

(2) INFORMATION FOR SEQ ID NO:1409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAATCATGCA GATTTTTCCT CTAGAAAACC CCTCCCCAC | 60 |
| ATTCAGCTTA TTAGAAATCC TTAACAGCAG GTAACCACCA ATGCTCCTGC CTTCTAGCCA | 120 |
| CAGTCTGCTC CTGCCCCTAC AGGCTTTGAA CATGCAGATT TTCCTCTAG AAAACCCCTT | 180 |
| CCCTGCATAT TCTCTCCTCT CCCCACTCAC ACAAACACCT GGCCTGCCAG GCCCCGTGGG | 240 |
| GCTGCCGGGC TTCTGTGAAC CTGCCGCCTG CCTTGGAGCT TCGGCCTATG CCTCTGCCCC | 300 |
| CCTTACAGAG CCTGGATCCA AACTCGAG | 328 |

(2) INFORMATION FOR SEQ ID NO:1410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT NNAAAAAAAAA AAACCAAAAA AAAAGAAAAA GCTGACACAG | 60 |
| TTCTCTGAAA AAAGCCTAGA GAACACAAGG GTGACACAAA CTCCAGAGAG TATGCTGCTT | 120 |
| GCAGCTTTGA TGATTGTATC AACAGTGGTA AGTCACCCCA TGTCTGCAGG AGCAGCTGCA | 180 |
| GCTAATTATA CCTACTGGGC CTATGTGCCT TTCCCACCCT TAATTCGGGC AGTCACATGG | 240 |
| ATGGATAATC CTATTGAAGT ATATGTTAAT AATAGTGCAT GGGTACCTGG CCCCATAGAG | 300 |
| GATCGTTGCC CAGCCCAACT CGAG | 324 |

(2) INFORMATION FOR SEQ ID NO:1411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGAAGTTGAG TGAAGGAGAA AGAGAGGGAA GTAGAAAAGA | 60 |
| GGAGAAAAAT GTTAAGCAAA AAAGGTATTT TCCCTTGGAT ATTAAGTTGC ATATCTGAAG | 120 |
| AAATGGCATT CCGGACAATT TCGTGTGG TTGGAGTATT TATTTGTTCT ATCTGTGTGA | 180 |
| AAGGATCTTC CCAGCCCCAA GCAAGAGTTT ATTAAACATT TGATGAACTT CGAGAAACCA | 240 |
| AGACCTCTGA ATACTTCAGC CTTTCCCACC ATCCTTTAGA CTACAGGATT TTATTAATGG | 300 |
| ATGAAGATCA GGAACAATC GAG | 323 |

(2) INFORMATION FOR SEQ ID NO:1412:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTTAGTTGC TCTCCTTTTT TCTTTTTTTT GTCGTGCATA | 60 |
| TTTTATTCT GTAGTTCTG GTTAGCTACC CTAAGTGAT TTAATAATT AGAATGCTTT | 120 |
| GTGTTTCTA TTTGGTAATC AACTCGAG | 149 |

(2) INFORMATION FOR SEQ ID NO:1413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AATAAGAATT ACTTGTAAC TTAGGGGGCA TTTAGAATTA | 60 |
| TATTGTCTT ATTTGAGATT TGGATTTAAA TTTTATTTTA GACCATTTT TAAAAAATAA | 120 |
| ATAGAAGTGA GGCTAATATT GTTAATTATT CTCTTTAAAA AATACAGTAT TTGCTTTGGG | 180 |
| TTAAAATTTT CTGCCCCAAC ATCATTATCA AGAGTCAGCA TATTACAATG ATAAATTTAG | 240 |
| CATTACTGT GTGGCAGGCA TTGTTCTATA TACTTTATTC GTTAAATCA CCAGCGAACA | 300 |
| CGCTCGAG | 308 |

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ACTCAGAGCT GTTACGACTA GTCAGAGAGA GCGAGGTGGC | 60 |
| TGGTTCATGT TTGCAGATAG AGACCTCACT GTGTGGTGA CTTCCCCACT TCCTGTCTGC | 120 |
| TTATCCTGA TGGGTGGCTG CCTTCATCCT GATGGGTGGC AGCCTTGCCC TGCAGTGGGA | 180 |
| GACCCAGGTA ATGTAGTTT TTGTTTGTGA TCCCTGATCT CTTCTTGCG TTTTGGCCG | 240 |
| GCAGGTCTCG AG | 252 |

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGATTCAG AACCATTGTA TAATAGCTTG AAAGCCTAGA | 60 |
| TNGACTCTCT GCATTGCCAC CCCTCCCTAT TCTTTAAGC CCACTCCATT CACGCTGTCA | 120 |
| TCCACACCAC TCGGCCACCA ATTTCACT GCGAAATCCA GTTCCAGTT CCTCATCGTG | 180 |
| TTTATNGCA ACATTTGAAA CAAGTGATCA ATCCCTTTT CATGAAAAAC CTTCTTTGCA | 240 |
| CAGTTTCCAG AATTCTAAAC TTTCTGGTT TTCCTCCTAC TTCAACTTTC CAATTACCGT | 300 |
| CCCTCATTTT TACCTCATCA GCCCACTCG AG | 332 |

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

| | |
|---|-----|
| GAATTCGGGC CAAAGAAGCC TACAANAAAN TATATATATN TGGATCTTCT GAAAAGTTTT | 60 |
| TTGAGGTGCA AGTTTTCTCT CTTTTTTTTT TTTTTTTTTT TTCTCATTGA TTAATGGACA | 120 |
| TGATGCTGAG ATTCAATCAC TACATGAAAC ACCTGGCTGT GAAAACAAAA CAACCCAGAG | 180 |
| GGCTGTGTTT CAAGCAGCGC TGGGGAAGCT ACGTAACAGT CGGATGCCAG TTTTGAAGA | 240 |
| TTCACCATGC GTTCTGACCC TCTGTTCGTC TCTTCTCTCT CCTCTTCTT CAAGAAGGAA | 300 |
| ATTGATCCTA GTGATTTCAG CCCATGCATT AAACAGGAAA CTCGAG | 346 |

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

| | |
|--|-----|
| GAATTCGCCA AAGAGCCTAA GGGCAAGCAG CATTCATATA TCATATGACT TCTACAACCTA | 60 |
| AAATGAAGCT ATTAGCACTA GTATTTAGTA ATCTAGTAAC TCTCCTTCCA GCCCTCTTCA | 120 |
| CCCTCGAG | 128 |

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

| | |
|---|-----|
| GAATTCGGCC AAAGAGCCTA GGGAAGCGCT CTTACGGCA CTGGGATCCG CATCTGCCTG | 60 |
| GGATCATCAA GCCCTAGAAG CTGGGTTTCT TTAAATTAGG GCTGCCGTTT TCTGTTTCTC | 120 |
| CCTGGGCTGC GGAAAGCCAG AAGATTTTAT CTAGCTTATA CAAGGCTGCT GGTGTTCCCT | 180 |
| CTTTTTTCC ACGAGGGTGT TTTTGGCTGC AATTGCATGA AATCCCAATG GTGTAGACCA | 240 |
| GTGGCGATGG ATCTAGGAGT TTACCAACTG AGACATTTT CAATTTCTTT CTGTGCATCC | 300 |
| TTGCTGGGGA CTGAAAACGC TTCTGTGAGA CTTGATAATA GCTCCTCTGG TGCAAGTGTG | 360 |
| GTAGCTATTG ACAACATCAC TCGAG | 385 |

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

| | |
|--|-----|
| GAATTCGGCC AAAGAGCCCT AGTAGGTTTA TAAACAGAAG TTAAACTTG TAAGCTTAAG | 60 |
| CTCCGTTTA TAAACAGAAG TTTAAAATTA TAGGTCCTGT TTAACATTCA GCTCTGTAA | 120 |
| CTCACTCATC TTTTGTGTT TTTACACTT GTCAAGATT CTTTACATAT TCATCAATGT | 180 |

| | |
|---|-----|
| CTGAAGAAGT TACTTATGCA GATCTTCAAT TCCAGAACTC CAGTGAGATG GAAAAAATCC | 240 |
| CAGAAATTGG CAAATTTGGG GAAAAAGCAC CTCCAGCTCC CTCTCATGTA TGGCGTCCAG | 300 |
| CAGCCTTGTT TCTGACTCTT CTGTGCCTTC TGTGCTCAT TGGATTGGGA GTCTTGCCAA | 360 |
| GCATGTTTCA TGTAACCTTG AAGATAGAAA TGAAAAAAT GAACAACTA CAAAACATCC | 420 |
| TCGAG | 425 |

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGACGCATG CCTGTAATCC CAGCAACTCG GGAAGCTGAG | 60 |
| GCGGGAGAAT CGCTTGAACC CGGGAGCGGA GGTTCGGTG AGTTGAGATG GCGCCACTGC | 120 |
| ACTCCAGCCT TGGCAAAAAG AGCAAACTT CATCTCAAAA AAAAAAAG AATGTGTGGA | 180 |
| ATAATGGGGG TTTTTCCTT ACTTTGTGG CTTATTCTCA CTTACATGGG GATAGCCTTG | 240 |
| GTCTTTGACT TGGATAGCCT CGAG | 264 |

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAGTGAATCG ATGTTCTGGC TTGGCTGTCT TTGGTGTITT | 60 |
| CATTCTTTCA TTTCTTTCTC CCTGTCTCA TCTCTCTCTC CCCGTGCCCT GCTCCCTACA | 120 |
| CCTATCCCTC CCCCTACCCT CGAG | 144 |

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGAGAGAATA AAATACATAT AGTTGATTAA AGGAAGGAAG | 60 |
| TTTATTACTT AGGGAAAAGG AAGGTAAAAA AAGACCCTAA GCAATAAAGG CAATTCTTTT | 120 |
| TTAAGCAGAA TACTTTTATT TTATTTTATT TTTGTTTACC AGTGTGTGTA CGAAAACCTGC | 180 |
| TGCTGGGGCT ACTTCAGCTG AGATGATTG GCTCTTTT GTGGCTTTCT TCTTGTCTG | 240 |
| TACATCAGCA CTGTGGTTAT TACACCAGCT ACCAAGTCAT CTCGAG | 286 |

(2) INFORMATION FOR SEQ ID NO:1423:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

```

GCGATTGAAT TCTAGACCTG CCTCGAGACA GAGCAAGATT CCGTTCCCAA GAAAAAAAAA    60
TTGTTCAACA ATAAGGGCAA AGGGAGAGAA TCATAACATC TGATTAAACA GAAAAAGCAA    120
GATTTTTTAAA ACTAACTATA TAAGGATGCA TCTCGAG                                157
  
```

(2) INFORMATION FOR SEQ ID NO:1424:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 408 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

```

GAATTCGGCC AAAGAGGCCT ACTCAAAAGA CAAAAAGAT ACATTAGGCA GTGTTCTGTA    60
AACATGGGAA AATTATTTTA GGTAAATGG GCTGAGAAGA AATTGCTAA ATTTTGCTTT    120
TGTTACCACG TTTCTGAAA TGATGATAAT AAATAATATT TTAAAAGGGT GAATAGAAGG    180
ATCTTTATTG TAGGTACTGG TGTTAAATTT TAGGTTTCTG AATAATACTG TAAAGCTACT    240
TTCTTTACAC AGATTACAC ATTTATCTTC TTGAATTATT TAATAATGAA TGTCAAAAAA    300
TTCGAAATCT CATATAAGAT CTCACTTTGA AACAAAGTAT ATAACTGTT GATTGCACAA    360
TTTGGGTTTT GTGAAGCACT CAGTTTGTAC TATAAGTGGC AGCTCGAG                    408
  
```

(2) INFORMATION FOR SEQ ID NO:1425:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

```

GAATTCGGCC AAAGAGGCCT ATTCTGTCT CTAAGAATA ACTGTGCTTG AAGAAGAAAA    60
TTCCCAACAT GGACAAACCA CGCAAAGAAA ATGAAGAAGA GCCGCAGAGC GCGCCCAAGA    120
CCGATGAGGA GAGGCCTCCG GTGGAGCACT CTCCCGAAAA GCAGTCCCCC GAGGAGCAGT    180
CTTCGGAGGA GCAGTCCTCG GAGGGAGGAG TTCTTTCCTG AGGAGCTCTT GCCTGAGCTC    240
CTGCCCTGAG TGCTCCTCTC GGAGGAGCGC CCTCCGCAGG AGGGTCTTTC CAGGAAGGAC    300
CTGTTTGAGG GCGCCCTCC CATGGAGCAG CCTCCTTGTT GAGTAGGAAA ACATAAGCTT    360
GAAGAAGGAA GCTTTAAAGA AAGGTTGGCT CGTTCTCGCC CGCAATTTAG AGGGGACATA    420
CATGGCAGAA ATTTAAGCAA TGAGGAGATG ATACAGGCAA CTCTCGAG                    468
  
```

(2) INFORMATION FOR SEQ ID NO:1426:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

| | |
|---|-----|
| TTTGACCAGA TTATTCTTCT ATGCTTTTTT GCAATAAATC AAATCCCACA TATCTACAAG | 60 |
| TGGTATGAAG TCCTGCACCC CCCAGGAGGC CTGTCCAGGC ATGTCTTCAG AGGCAGGGTG | 120 |
| GGTTACACTC ATTTACCTCC CCTCTCCCCA CCAAATTATG ACACAAACGA GTATGTTTCC | 180 |
| TCTCTAGAAC CCGTAATGC CTCCTCCCC ATCCCAGAG CTCCTTACTG TAGGTCTTAC | 240 |
| CCTGGACAAG GATTTTTTCA AGTTGGAGGC ACAGAACATG AGCAATCTGA CATTCCCACA | 300 |
| GGCCTCGAG | 309 |

(2) INFORMATION FOR SEQ ID NO:1427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AAGTGAGGAC AGGGCAAAGA TTTTATAGTC TCCTGTA AAC | 60 |
| AGGAAGTGTCTAGTCTGAC GTAAGTCTGTA CGTTGTACCT GGATGGCCTC TTTCTTGATC | 120 |
| TTACAGGGTA CGTGTCTTCC AGCCAGGGTA GGTGTCTTCC GGCCGGCTTT CTCCTGCTT | 180 |
| CTGCTATTTT GCTGGCCAC ACTGCTGGCG CAAGGCTTGC GCCTTGGTAC TGGGCCTGAG | 240 |
| AAGGGAGGAG TTATTCATCC CCTTAAGCTT TCAGGCCCCA GGGAGAATCT TACACTACTG | 300 |
| GGCTGCATTT CCAGACAATT AGGGCATTCT AAGGCACAGG ATGAGGTAGG AGGTCCGCAC | 360 |
| AAGATACAGG TCATAAAGAC CTTGCAGATA AACAGCTTG CAGTAAATAA GCTGGCCCAA | 420 |
| ACCCACGAAA ATCAAGATT TGACCAGAGT GACCCTCTGG TCATCCTCAC TGCTACACTC | 480 |
| CCACCAGCAT CAGACTCGA G | 501 |

(2) INFORMATION FOR SEQ ID NO:1428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AGACCTTGTT TAGTGTGTA AAGTTCTTCC AGTCTCGGAA | 60 |
| TGGTAAGGAA TTTATGCATG CTTACTCCAT TTTCAATAAG AAGTTTACA AATGCAACTC | 120 |
| TATCCATTAC TCGAG | 135 |

(2) INFORMATION FOR SEQ ID NO:1429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGGGGCAGCG AATGTTTTTA GAAGCAGAAA ACTTTCCAAA | 60 |
| TTTGGTGAAA GACATAAATT TACAGATTTC AAGAAGCTCC ACAAATTCCA AATATGATAA | 120 |
| ATATGAAGAA ACTCATAGCA AGGATGCTAT ACCACACACT TCTGAATAAT CCACAGGTCA | 180 |
| AAGAAGTCAG ACTCTCCGGT CTGACATGTA AAGGCCTGG AAGTCGTCAC TCCCATCCTC | 240 |
| TCGAG | 245 |

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

| | |
|--|-----|
| GAATTCGGCC ANNAGAGGCC TAAGAACTG GAAGTCCTT TCATCTCCTC CCCCACCTAA | 60 |
| CTCCCCGAG TTAATCAGCA ATACTTTTGT GTGTATATTG TTCTGGAAAT TGTAATGTT | 120 |
| TAAACAAATC TACTAAGTA TACTCTCTG AAATTTTCCT TTGAAAATTT AGTTTATAAT | 180 |
| TTGGATTAT TTCTTGATGA GCACATGCTA AACTCATTCC ACCCTTTTTT GATGAAAATT | 240 |
| ATTACATGTT TATTAATATA TCACATTCCC TCCCTCCCTG TCCCTTTTTT CCCCATAAA | 300 |
| ACACAATACT GTCAACTCGA G | 321 |

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AGTGTGAGAC ATTTGTCATT GCTCAGAATT TTAAAATTGC | 60 |
| ATTCCAAGCT GTTGGATTG AGTTTAAGTG AGGCCAACT GGGCGGAGAT CAAACACACC | 120 |
| ATCAAAGAAT TACACACATA TCCTTGTTGG CACATCGCTT TTGTTGTTG TTTCAAGGAT | 180 |
| GCTGTGTGTG TTACTAGGGT TAAGACTCTT CTCCTTGGCT GAGGGATCTC CTCTGGAGAT | 240 |
| TTTGAAAACA GGAAACAGAT TTCTCTCTCC CTTCTCTGGT AGTCTTCCTA TTCGTGTTAG | 300 |
| AAACAATCAA CTCGAG | 316 |

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

```

GAATTCGGCC AAAGAGGCCT ATAAAAATGC AAAAAATCCA GTCTAAATAT TGTCTATAGT      60
TTTTTAGGAT TATAGTGTA TCTGCTCTTT TAACCTATGT ATCTCTACAG CCTGCCACCA      120
TATAAGCTTT TAATTATAAA ATTATGATGC TTGACATTGG GGAGAAAGGA ACATAAGCAC      180
CCATAATGAG TCATTTTTGT TGA CTGTATA AATGAGTCAG AGTTACATGT AAGGATGAGA      240
ATATCCTCCT ACAATTTTGG TTTTGTATCT TGATTTTTTC CCATTGACTC TCTTTTCTCC      300
CCGCCATTCT CTCTCTTGCA CGTAGCACAC TTTTGCCTC TGTCTGCTAT TACTGCTATT      360
ATAAACCTTT TACTGGACTT CAGTTGTAGT GACCATTAGG TCCTAAACAT AGAACTAAGA      420
GCGTAAGTGG ACTTTAATAG AATACTTATT AATTTTAATA ACTAGAGTTC ATAATTTAGA      480
ATTAATATAT GAGAATTAC TGTATAATCC TCGAG                                     515

```

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

```

GAATTCGGCC TTCATGGCCT ACTGCTTTTT TTTCTCTTTT TTCTTTTCC CTTTIGACTT      60
TTGAGGCTCC TGTCTTTGG CAGCACCAGC TCCTTCTATT TCTGCAGCCA AGGCATCAAG      120
ATCAATGTCA TCCTTGGTGC TGTCTCGCT CTGTCTTTTC TGTTTCTTCC CCATTGCTTG      180
TCAATGGCGC TCGTGGCCCC AGCCCTCTA TTCGGTCTCT CACAGACCCA CTGTCTCCCG      240
GCTGACTTTG GTCTCCGCTC AGCTCTTTTC CCCTCGTGCT GCCGCCGCTC GCACCCGGCT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

```

GAATTCGGCC AAAGAGGCCT AGAATTTATG TAATCCAGG GTGGCTACCT ATTTCACTAG      60
TATCCCTC GCCTCAGTTT TAAATTTATT TTAGAAGCTT GGATTTCTCC CTAAGAGTTC      120
AAATTTTCCC AATTATATTT GGCTTCCAGT TGACTTTGAT ACTGGAATTC TCTGCCAGGA      180
AGGAGTGAGG CCATCATGTT TCCACTTATG CCATCAGTGG CATCTCTGAT ATTTTGCCAC      240
GTGTTGCCCC TGTACAGCCC TGAGGTGTTG GGCAGAGGAG GCCAACCTGA G                                     291

```

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

```

GAATTCGGCC AAAGAGGCCT AAGACCCCCC TCAGCCTCCC GGAGTGCTGG GATTACAGGT      60
GTGAGCCAAT GCATCCAGCT GACTTTTGGG CTCTATCTTG AGGTAGCTGG GAGCCACTGA      120
CATATGTCAA GCAAGGGATT GACATGATCA GATTATTATG TAGAAAGGCC AGTCGCTCTG      180
TCTACAGTGT GGAGAGTGA TTGGGAGGCA GAATGACCAG TCTGGAGGCT ATTATAGTAA      240
TCCAGGTTAC AGATGGGGT AATGAGACCT AGGCAGGTAA TAGCGTGGCT AGAAGGAATG      300
GATAGATTCC AGAGACATTT GGAGGTGAAA TCAGGGGCTG GCGATTTAAC TGGGTATGAA      360
TAAAGAGGTA GAAAGAAGAT TTGAGGATGA TGCTCAGCAT TGAACAAGAG GGTAGACTCG      420
AG                                                                                   422

```

(2) INFORMATION FOR SEQ ID NO:1436:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

```

GAATTCGGCC AAAGAGGCCT AAGCTAGTTA TATGTTATTC TGGGAAAAAA TATTATTTGT      60
AGTTATTGCT ATCATGAAAA ATAAATTTT ATGTGTCCTA AATTTAATTA TATTTTATGA      120
AACATTAACC CTGACACTCG AG                                                                                   142

```

(2) INFORMATION FOR SEQ ID NO:1437:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

```

GAATTCGGCC AAAGAGGCCT ACGTACATTT ACTCTTTATA CATGTTTTTT TTGTATGTCA      60
TACCTTTACA GTCATTATTC TTCTTGATGT TCATATCTCC CCATCTTTGG CCAGTTAGAG      120
CATTTCCAAG TGAGCTCCTG TGTCCTTTTG ACAAGACCCC AGTAATCGTT CTGCTTTTAG      180
ATAGAATAAG ATGTTTGAGG ATTCTTTTAT ACAACTTTAC CCTAGACCTG AACTCAGACA      240
TCTCTCCAAG GAGCGAACTC GAG                                                                                   263

```

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

```

GAATTCGGCC AAAGAGGCCT AGCAGCCTCT GCCTCCCGGG TTCAAGTGAT TCTCCTGCCG      60

```

CAGCCTCCTG AGGATCTGGG ATTACAGAGG CTATTGGA GCTCCAGACT GTTTAGAAGA 120
 CCTGGACAGC CAGAAAGTCA TTAGTCCTAT CCAAAATGAA GCAATTTGTG CAGGAAAAAC 180
 AGATATTTTA TGGAAGAACT GTGAGTTTCT GGTAATCGA ATGTGCCGTC TTGAAAGCCT 240
 CATGCACTCC TTGAAGATGA ACATCTTTCG GCTGCAAACT GAAAAGGATT TGAATCCTCA 300
 GAAAACAGCT TTTCTGAAAG ATCGACTGAA TGCAATACAG GAAGAGCATT CTAAGGACCT 360
 GAAGCTGTTG CATCTCGAAG TTATGAATTT GCGCCAGCAA CTGAGAGCTG TAAAAGAGGA 420
 AGAAGACAAG GCACAAGATG AGGTGCAAAG GTTGACTGCC CCCTCGA 467

(2) INFORMATION FOR SEQ ID NO:1439:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GAATTCGGCC AAAGAGGCCT AGGCAGATCT GGCAACTTTC ATATCTGATA TTATGTTACT 60
 GAAACTAATT TTAGGTCGCT TTGCATCTCT CTGTGCCCTC GAG 103

(2) INFORMATION FOR SEQ ID NO:1440:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

GAATTCGGCC AAAGAGGCCT ACATNTTTGA ATCTTAACT GNNTTTTTCT CTTAGTATTG 60
 CTAATGAGTA AAGAAAAGTC TCATAAGGTA GCCAAATGAA AAAGAATGAA AGGGAAAGTG 120
 AAAAATTAAG GGGACNAAAG ATGGGATGTG AAAAGAAGAA TTCTAGTTTG ATGGTGACTC 180
 ATATTCACGA TAGGATACAA AGTGTGATTT GTTGGAACA TGTCCTCAAT TTCTAAATTT 240
 CTGCTTCTCT GCCAAAAGCA ATGTCTTTCT TGGTTGATAT TTGAGTTTAA AAAGGGTCAA 300
 ATCTTTCTAA TTTTTTGTAT CTNNAGAGGG CAGCACTAGA AGAAATCAGC AGGTCTAATC 360
 CCACCAGTAA GAAACTACC ACTTCTTGAT TTTTACAGAT TTAATAAAAT CTTTTCAGTG 420
 ACCTTTCTTT TTAATGTAAA TACAAATTTA AACCTTAGGC TCGAG 465

(2) INFORMATION FOR SEQ ID NO:1441:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GAATTCGGCC AANGAGGCCT AGAATTATAC AGGTAGAGAT GTATGCAGAT GTGTCCATAT 60
 ATGTCCATAT TTACATTTTG ATAGCCATTG ATGTATGCAT CTCTGGCTG TACTATAAGA 120
 ACACATTAAT TCAATGGAAA TACACTTTGC TAATATTTTA ATGGTATAGA TCTGCTAATG 180

AATTCTCTTA AAAACATACT GTATTCTGTT GCTGTGTGTT TCATTTTAAA TTGAGCATT 240
 AGGGAATGCA GCATTTAAAT CAGAACTCTG CCAATGCTTT TATCTAGAGG CGTGTGCGCA 300
 TTTTGTCTT ATATGAAATT TCTAATCCCT CTCGAG 336

(2) INFORMATION FOR SEQ ID NO:1442:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

GAATTCGGCC AAAGAGGCCT ATGATTTTTA GACATCCAGA AAGCAAACCTT TAACTGTCTG 60
 TGAGGTACAG AGACTGGATG ATGTTAAAGA AAACCATAGT TGGACACAAG ATACTCGAG 119

(2) INFORMATION FOR SEQ ID NO:1443:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

GAATTCGGCC AAAGAGGCCT AGAGAAATTT TAAAAAGCAT AGTTGAGGCA TATTTTTC 60
 TAATTATATA CTTATCTGTT TATTGCCCAT GGAAATATA TGTGTAGAAG TATTTCTTCT 120
 GTTATTTGTT ACTATCTTCT TAATTTGTTT CAAAGAAAAT GTTGCCATAC TGCATTCCTT 180
 CTGGAAGGAA ACAAACAAA ACAAACTCT CGAG 214

(2) INFORMATION FOR SEQ ID NO:1444:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

GAATTCGGCC AAAGAGGCCT AGGAAAGGAA AAATTA AAAA CCCTAGATCT CTGGTACACA 60
 TAAGTCTGGG TTTGCGATTG CTATTTGTGC TGGGGCAGTG TGATTGAGAC TGACATTGAG 120
 GAAAGAAGCA GCTATGAAGA CCAGGGGGTT CAGCTTTCCA AGACAAAGGC AAGTCCTGTT 180
 TCTTTTCTT TTCTGGGGAG TGTCTTGGC AGGTTCTGGG TTTGGACGTT ATTCGGGTGAC 240
 TGAGGAAACA GAGAAAGGAT CCTTTGTGGT CAATCTGGCA AAGGATCTGG GACTAGCAGA 300
 GGGGAGCTG GCTGCAAGGG GAACCAAGGT GGTTCGGAT GATAACAAAC AATACCTGCT 360
 CCTGGATTCA CATACCGGGA ATTTGCTCAC AAATGAGAAA CTGGACCGAG AGAAGCTGTG 420
 TGGCCCTAAA GAGCCCTGTA TGCTGTATTT CCAAATTTTA ATGGATGATC CCTTTCAGAT 480
 TTACAGGGCC GAGCTCGAG 499

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT AAAATTTGAT TAGAAATGCA AGACTGGATG CCAAGATTGA | 60 |
| TTCTAAATTA GGTCATGTGG TTATGGGTAA CAATGCAGTC TCACCCTATC AGCAAGTGAT | 120 |
| TGAAAAGACC AAAAGCCTTT CCTTTAGAAG CCAGATGTTG GCCATGAATA TTGAGAAGAA | 180 |
| ACTTAATCAG AATAGCAGGT CAGAGGCTCC TAACTGGGCA ACTCAAGATT CTGGCTTCTA | 240 |
| CTGAAGAACC ATAAAGAAAA GATGAAAAAA AAAACTATCA AAGAAAGATG AAATAATAAA | 300 |
| ACTATTATAT AAAGGGTGAC TTAECTGAG | 329 |

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 607 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

| | |
|--|-----|
| GAATTCGGCC AAAGAGGCCT AACAGAGGAA ACCACCCTTC AACTGGAAGA TATCATTA | 60 |
| CAGAGGATAA GAGATCAGGC TTGGGATGAT GTAGTACGTA AAGAAAAACC TAAAGAGGAT | 120 |
| GTCATATGAAT ATAAAAAGCG TTTAACCTTA GACCATGAGA AGAGTAAATT GAGCCTTGCT | 180 |
| GAAATTTATG AACAGGAGTA CATCAAACTC AACCAGCAAA AAACAGCAGA AGAAGAAAAT | 240 |
| CCAGAACATG TAGAAATTCA GAAGATGATG GATTCCCTCT TCTTAAATTT GGATGCCNTC | 300 |
| TCAAACCTTC ACTTTATCCC TAAACCGCCT GTACCAGAGA TTAAAGTTGT GTCAAATCTG | 360 |
| CCAGCCATAA CCATGGAGGA AGTAGCCCCA GTGAGTGTTA GTGATGCAGC TCTCCTGGCC | 420 |
| CCAGAGGAGA TCAAGGAGAA AAATAAAGCT GGACATATAA AAACAGCTGC TGAAAAACA | 480 |
| GCTACAGAAC AACTCGAGGT GTGGGGAAAA GAAAGAGAGA TCAGATTGTT ACTGTGTCTG | 540 |
| TATAGAAAGA AGTAGACATA GGAGACTCCA TTTTGTCTG TACTAAGAAA AATTCTTCTG | 600 |
| CCTCGAG | 607 |

(2) INFORMATION FOR SEQ ID NO:1447:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

| | |
|---|-----|
| CTGCTGCAGC AATATTCAGA TTGAAAAAA TAGGTTTGGG TTCACTGAGT TTAAAGGGAT | 60 |
| GATGATAAAA AGGAGGTTCT TCTTCCTCTT CATCCGAAAC ATGAGGTTTA TTCACTATTA | 120 |
| CATCATCATC TTCTTTACTC TGTGCGATCT GTTTACATTT CTCAGTTAGT TCTTCTATAG | 180 |
| TAGTCTCTCC TGACTTTTGA GCAACTTTCT CTTCTATAGT AGGTGGAGGT GCAGGCTTTA | 240 |
| GGTTTGGTGG TAAAGGGACA CCAGCCTTAG CACACATGGC AGCTGCATTA GCTTTGGCTA | 300 |
| TTTCAAGTAA TTGAGCCTTA TCCAATCTG TCAGACGTTT GGGTGATCTG CCTCGTTCAG | 360 |

AAGACCTGGA TCTTTACGA CGGATGGGAG ATCTGCTAAA CCTTCTTCTT AAGGGTGTTT 420
 TTGATCGCCT TAATCTGACT GGTGAGTAGG CCTCTTTAGC CGAATTC 467

(2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GAATTCGGCC AAAGAGGCCT AGACACTTAT AGGCTTTTAA AGAAGCATTG ATCAATTTGC 60
 AAACCTTAGT CTACATCAGA CTGTGGAGCG TATTCATGTG GGCAAAAAAT ACGGTGATAT 120
 TCCTCGAG 128

(2) INFORMATION FOR SEQ ID NO:1449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

GAATTCGGCC ACNGAGGCCT ATTTAAATGA AAATNATTTG AATGTTTAAT ACTCTTCCCT 60
 TCTTCAATTG TAGAAACATT ACCCTTTTGC ACTATCTCAT CACTATTGTG GAAAATAAGT 120
 ACCCCAGTGT TCTCAATCTA AATGAAGAAT TGGGAGATAT TCTCAAGCT GCGAAAGTAA 180
 ACATGACTGA GCTGGACAAA GAAATAAGTA CCTTGAGAAG TGGCTTGAAA GCAGTAGAGA 240
 CAGAGCTGGA ATATCAGAAG TCTCAGCCCC CACAGCCCGG AGATAAGTTT GTGTCTGTTG 300
 TCAGCCATCT CGAG 314

(2) INFORMATION FOR SEQ ID NO:1450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

GGAATTCGGC CAAAGAGGCC TAGTGGTTTT CCCAGGAGGA AAGAGAGCTG CAGGGATACA 60
 GATGCCTTCC TGAGCAGAGA AAATAGAATA CTTGAGCCAA TTTTCATGTA AAATGGATTA 120
 TTTTCTGGC GTTTCCTGTC CTTCAAGTAA AAGGTTCTGG AATGAGTACT TCACTGCTGT 180
 AATGGAGACA CTAATATTTT ATGAATGCAG TTTTACAGTT TGCAGTAATG CCAGGCCTTT 240
 GGCTGTTTTT CATTAGATGG TGCCTTGGC TGGAAGCATA TACTCTTGTA GCTTTGATTT 300
 TAAATTTAAC TTTCAAGTTG AAAGAGCAGT GACTCATCCA AAGGACAGGT GATATTATT 360
 TATTTTTTCT TGAAATGCA GCACGGGTAT GTTGTTATCA CACGTTTAGG GGAATTGCCA 420
 CACTTCCTCG AG 432

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

```

GAATTCGGCC AAAGAGGCCT AGGATTGAAC GCTTTCACCC TGTGCCCCGC GCCTGGCGTA      60
ACGCGTGGCC CCAGACCACA CGCTGTAACC CGGGGTGAGA GGGAGTGAGG TGGGACTTCG      120
TACCGGACCC GGAGCGCCGG CCTCGCCCGC GCGGGCAGCG TTCCTGTGG GGAGTGCTCA      180
CTCAGCCTAG GCGGGCCCGG GAGGACTGCC GGGAGGAGGG AGTCGGCCTT GAATTGAGGC      240
CTCAGCCTTG AATAGGGTAG GGAGGCAAGC CTAGCCGAGA GTTTCAGCA AGCAAAAGCC      300
TGGAGGCACC AGGGTCTGCC CTAAGAACTG CAGCGCCTCT CCTCTGGCTG GGATTTAACG      360
CATTACGTCT CTGCTGTTTA TAGGTGTTGT GTTTGGTCTT ACCACTTCGT ATTCTATAGT      420
TTTTATTTAT TCCTGTTTTC TGAATTTTCC CACTTTGCTC GAG                          463

```

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 407 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

```

GAATTCGGCC AAAGAGGCCT AATGCAAGTC TGGACCGTTT AAAAGCTGGT AATTAAACAC      60
TTTATTCAT ATCAGAATAA AAGTCAACTA GTTGAATATT TCTAGGTGAG ATGTGGTACT      120
ACTTTTTTTT TNGCTGTTAT TTTATGTCTG TATCTAAAAT ATCTTACTGC ACTCTTTTTT      180
CAGGTTGCAG CAGATCCTTG AGTTTTGAAC CTGACGGGCA AATCAGAGCT TCTTCCTCAT      240
GGCAGTCGGT CAATGAGAGT GGAGACCAAG TTCACTGGTC TCCTGGCCAA GCCCGACTTC      300
AGGACCAAGG CCCATCATGG GCTTCGGGCG ACAGTAGCAA CAACCACAAA CCACGAGAGT      360
GGCTGGAGAT CGATTGGGGG GAGAAAAAGA AAATAACAGG ACTCGAG                          407

```

(2) INFORMATION FOR SEQ ID NO:1453:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

```

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTATAG GCCTCTTTGG CCGGAAATCA      60
TGGTGTTATA GATCAAAAGA TAAAAGTTTC ACAGAAGAGG TGGGATTGTA ACTAAGCTGT      120
TCATGCTCAG TAAGATTAGA GGAGGTGAAG CAAATGGGGG AATGTGTGCC AGAAGAGGAC      180
AGGTGCAAAG ATAAGCACTG GTGCTTGATC TTGACTGAAT TTTCAACCAA ACCAGCTGAC      240
TCTCAGGATA GTTGAAGGTC ACTTCTGCT GTTTAAAGAA AGATTCTAAA GTTACTTAAG      300
AAATATTTGG CAAAAGACTC AAAAGGAAGG ATTCCAATTA CAATATAAAT AAAGTAAGAA      360

```

ACCTCGAG

368

(2) INFORMATION FOR SEQ ID NO:1454:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

```

GAATTCGGCC TTCATGGCCT ACCGTGCTCT ATGCTGATCC TTTTCTCGT GAGAAAACGC      60
TGGCCTGTTA TTATTAGCTA AGGTCACACC CGCTGGGCAG CTCCTGGGAT TTTTGGATTG      120
CTCCCCACTC CAGAGGGAAG GCTATTTCTA GTGGCTTCTT TTCTTTGAGT CCTCCCTTCT      180
GTCTGTCTCT CTCCTGTTCC TCCTCTTTAC CAGTAGGGCT TCCTCAATGC TGACAGCCCT      240
GTGAAAAAAG GGGAGACATG CCGAGCTCCG GCAGGAAACT GCTGGCCCAG GACCTGGCTT      300
CTGGGGCACA AAGGAGAATT TCTGTGTTTG GAAAAGTACA GACTGAGCAG GTGACCCCCG      360
CACAGCCCCT TGGGGGAAAC ACTTGTGCCC TTGAGTCTG ACTGATATAA ACACAGACTC      420
TCTTGACTGT CCCATAAAGG CCAAAGCCAG AGAACCTCAG AAAGGGACTT GCAAATTGTG      480
AGTGAGGCAT ATCAGCTGGT GCTTTCTTTT CTCTGTGGGC TGCCATTTAT GAATCTCTTG      540
GTTTCTCTCT GTCTCTGTCC CTCCACTTTT CTCTCCTTTG CTGGTGTGTG CATTCCCTCT      600
GACGCGCTGG CTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1455:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

```

GAATTCGGCC TTCATGGCCT AGCCTTTTTG AAATCAGGA AAGACAAAGG TTCAATTACA      60
CCACTTTTGT CAATAAGCAA ACCAGGTATT TTTTCTTCT CCTGTTGTCT GGATATGGCA      120
ATAAATTTT TAAATTGCTG TGAGAACCA TATATGAAA GAGAGGAGTT GAATTGTGTG      180
TGCCTTTTAT GTCTTGAGAT TTATATGTGG AAAAGACGAC ATCTACTTCA AACTGTATTT      240
TTTTCGTTTT TTTTCTTTT TGGGGAAGGG GGGAGAACGG GGTCTTGCTC TGTCGCCAG      300
GCTGAACTCG AG

```

(2) INFORMATION FOR SEQ ID NO:1456:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

```

GAATTCGCCT TCATGGCCTA GCTTAATCTT ACAGTCATTT AAAATAATTT CAGAAATGTT      60
CCTTTCATAC CATTGTCTCC ACCCCCAAAC CAGCTTACTA AAAATGGCTT AGGATTGTG      120

```

TTCAGTCCTT CCTCTTCCTC TCCCCTGCTC CCAGACAAGG GTGTGTACTC AATACTGTAT 180
 TCAGAAGTTA CTTGGGTTAG TTCTTTTTTT CCGATCTTTC AGTGTGATTA TTTTATTCAT 240
 TTGAAATACA ATTGGATTCA TTCGTTTCCG TATGCTTTCA GTTTTAGCTT TTTTCCACTA 300
 TCTTTGTTGA TATAATTGCA TTTTGTGATA GGGGGATATT AATATACTTC ACAAAGTCAG 360
 AATAACATAA GGGTTTACTC AGATGTAACC TGTTATCTTA GCCCGTGATC TCGAG 415

(2) INFORMATION FOR SEQ ID NO:1457:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC 60
 AGTTGTATAT TCCCCCCTT TATACAGAAA TTTTACAATA ATTTTCAGATT TTTCTGAGTT 120
 TTTTCAGATT TTTGATTCTA TAATATGAGA TTATCTTTC TTCCTCTTAT TTTTATAGTT 180
 TATTTATTTT TTCTTTTCTT TTTAATTTGC TCATACAGGT TTAATCTCGA G 231

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

GAATTCTGTT CATATTTTAA AATGTTTCTT TTTTCAACA TTCAGCAAAA TATTATGTGC 60
 TAGGAAGTCT CCCAGACGCT TGTTAACATC TATGAATACA ACAAAGATTC TGCCCTCCTG 120
 GGCCTCTTTT CTGATGGGGA AGCAAAAATC TCGAG 155

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

GAATTCGGCC TTCATGGCCT AGGTGACTAA GTACAAAAAA ATAGTTTTCT CATTGTATTC 60
 AAAATAGTGA GTAGGTTCCC TGGATAATAC ACAGTGAGTAG TTGACATATT TTCTCAAAAC 120
 ACAACCAGAA AACCCTCTC CGGTATTTGT AAATCACCTT TCAAGGGAAA AAGTGAACAC 180
 GTATTCCTTG TATTTCTAGT TTGATTACCA AACCTGATGT TACAAAGAAA CCTCCGTTCT 240
 GTAGACAGAA TTTCTTTTAT TTTTCTTCTT TTAATCTCTA CAATCACTTT CCCAGTGCCA 300
 CCACCGCTCG AG 312

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

```
GAATTCGGCC TTCATGGCCT AGTCTCCCTC GGCCTGTGCC GCCGCCGACG CCGCTTGTGG      60
GCCCCACTCC GCTCTGTCTG CTTCCGCCACC TTCTCCCCGA GCACTGCCCG GCCGGCCGCC      120
ATGGCTAACG TGGCTGACAC GAAGCTGTAC GACATCCTGG CGTCCCGCCC GCGCGCCAGCG      180
AGAACGAGCT GAAGAAGGCA TACAGAAAGT TAGCCAAGGA ATATCATCCT GATAAGAATC      240
CAAATGCAGG AGACAAATTT AAAGAAATAA GTTTTGCATA TGAAGTACTA TCAAATCCTG      300
AGAAGCGTGA GTTATATGAC AGATACGGAG AGCAAGGTCT TCGGGAAGGC AGCGGCGGAG      360
GTGGTGGCAT GGATGATATT TTCTCTCACA TTTTGGTGG GGGATTGTTC GGCTTCATGG      420
GCAATCAGAG TAGAACTCGA AATGGCAGAA GAACTCGAG                                459
```

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

```
GAATTCGGCC TTCATGGCCT ACGAGATCAA GGACAAGAGG CAGCTTATAG ACAACCGCAA      60
GCTCATTGAG ACGCAAATGG AACGGTTCAA ACTTGTGGAA CGAGAGACCA AAACCAAAGC      120
TTACAGCAAA GAGGGCCTGG GCCTGGCCCA GAAGGTAGAT CCTGCCCGA AGGAGAAGGA      180
AGAGGTGGC CAGTGGCTCA CGAATACCAT CGACACGCTC AACATGCAGG TGGACCAATT      240
TGAGAGTGAA GTGGAGTCAC TGTCAGTGCA GACACGCAAG AAGAAGGGCG ACAAGGATAA      300
GCAGGACCGG ATTGAGGGCT TGAAGCGGCA CATCGAGAAG CACCGCTACC ACGTGCAGCAT      360
GCTAGAGACC ATCCTGCGCA TGCTGGACAA TGACTCCATC CTCGTTGACG CCATCCGCAA      420
GATCAAGGAC GACGTTGAGT ACTATGTTGA CTCATCCAG GACCCCGACT TCGAGGAGAA      480
CGAGTTTCTC TACGATGACC TGGACCTCGA G                                511
```

(2) INFORMATION FOR SEQ ID NO:1462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

```
GAATTCGGCC AAAGAGGCCT ATTTGTTTTG TGGTTTTAAA ATTTTCTT CGCATAAAGG      60
GTAACATCTT GCAACTTGAT TCTTCACTT CATGATATGC CTTAGATTTC TTTCCTTCCC      120
AATACTCGAG                                130
```

(2) INFORMATION FOR SEQ ID NO:1463:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

```

GAATTCGGCC AAAGAGGCCT ACTTGTAAG TGCTTTTGAA TTAATAAAAT ATTAGCATAA      60
TTGTGTTAG TCAGTTGAAC CCACTGTTAC CATGTTCTT ATCCCATGGG AAGCAGTTGG      120
TTACACGATT CTTATTTTAT AAGAAACAGC TGAGAGGCAC TATGGATTAG TCTTCTGAAG      180
TGAAGGAAAT ATAGATGTCT CCTAAGTGAT AGTTAACCCA TTTT TTTT TTTTAGGCAT      240
AGAAGCCAGT TCAGGGTCCA TAATATTAG TGACCAACAT TTTAAAGTAT AGCAGCAACC      300
TGGTTCTTAA ACACAAAGTA AGTTGCCCAT TAACAAATGG CTTTATCTT TAGCATGAAA      360
ACTTTCCACA CGTCTCGAG                                         379
  
```

(2) INFORMATION FOR SEQ ID NO:1464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

```

GAATTCGGCC AAAGAGGCCT ANAANAACT TTTTCTGGG AGCAAGGTAG TTATTTCAAA      60
GCACAGAAAA AGGCGGCGGG GGGCACAGAG AAGCACAGAG AAGCGGGGGC AGTTGCACAG      120
GTAAACATT CATCTGGCT TTTCTTTTA AAAGATAAAC TTTGTCCAC GTAAAGAGGA      180
ANACTGCATA GATATTCATT GAGATTATCT GATTGTGTCAC TGTGCCAAA GAAAAACAA      240
AGGTAAATA CACGAGTTC NNCATTCAGA AGAAAGTATT TCAGGTAAAA ATTAAGTATT      300
AAGCAACTTT TCTCAGCAGA AGAAATGCC AAATTCTTAA GGACAGTACT CGAG          354
  
```

(2) INFORMATION FOR SEQ ID NO:1465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

```

GAATTCGGCC AAAGAGGCCT AACTGCTCC AGCTCTGACT CCCTCATCCC TTGCCTGGAC      60
CATGGTAATT GACCCTAGCT GGTCTCCTTT TCTCCTCTCA TCAGTCTCTC ACATTGCTGC      120
TGTTTTCATC TTTGTGACAT ACAAATGTGT TGCTTTCCCG TCTAAAACCC TGCTTGTCCC      180
TCCCCATTTT GACTGCCTGC CCCCAGCAGC CACACACACA AACTCGAG          229
  
```

(2) INFORMATION FOR SEQ ID NO:1466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

| | |
|---|-----|
| GAATTCGGCC AAAGAGGCCT ATTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTAAATTTAT | 60 |
| AAGGAATAGA AATTTATTGG CTCACAGTTC TGGGGGCTGG GAAGTCCCAG AGTAAGGTGC | 120 |
| CAGCGTCTGG TGCAATCCTT CTTGTTGTGT CACTGTGGAA GGTGGAAGGG CAAGAGAGGG | 180 |
| CCAAGCTCAT CTTATTATAC CAGCACCCAT TCCAACATCA TCCTCGAAGG ATCCCAATTT | 240 |
| TGAAAGAAAA AGCATGTGAG ACACAGAACA GCGGAGAGAG TGAGGGCCCG GCATGCCCCC | 300 |
| AAGTCCCCAC CACCGCACCT GCTCGAG | 327 |

(2) INFORMATION FOR SEQ ID NO:1467:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGAGAGAGAG AGAGAAAAGG AGGGGGTGGT GGAGAAGCGG | 60 |
| GAGCGAAGGA AAGGAGGCAA AAGGCAAAGT GAAGGAAAGC TGGATAGCTC GGCCTCTCCA | 120 |
| AACTGATTGA TTAGTCATGA TCCCCGCACT TTTAACAGGG ACTCATTCAA TTGGGAAGGT | 180 |
| GGAGCGCTGG GGAGCAGATT AGCATACGCT TGTTTACTCA TCTTCTGAGG GATTTTTTCC | 240 |
| CCCTCTTTCC TTTCATTTTG AGAAGAAGGA GGGAGGGGAG GGGGGACTTG GGGGGGAGA | 300 |
| AGGGGGCTGT GGCTTGTGTT ATAAAGGACG CAAAAATAA ATAAATTAGA GCATCTTTTG | 360 |
| GGGGGAGGGA ATTCAGCGGA TCAGTCTTAA GATGGAGCTC GAG | 403 |

(2) INFORMATION FOR SEQ ID NO:1468:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACACGAGGTC AGACGTCACA CATGTTTTTT TGGCTTGTTT | 60 |
| TTTGAAGTT TTTACGACTT GTCATGAGTC TCGGCCTGGC TTCTGTTTTT CACTGTCCGG | 120 |
| AAGAGTGTGG TCCTTCTGCA TTGACCTTC CTTACCCTC ATCCAGTCCT CCCAGTGTGG | 180 |
| CCGGTCTCAT TTCGTGTCGT CAGCTGGGTC AGCTGGCTCG GTGTGGAGTT TGGATTTTCC | 240 |
| GTGATCCATC CCATGCTTTT TTTTCTTTT TTTCTTTTTT CCTTTTCTTT TCTTTTCTT | 300 |
| TTTTTTCAGT TTTCTCCCCA ACTCTCGAG | 329 |

(2) INFORMATION FOR SEQ ID NO:1469:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | ACAGGAAAAT | TCTTCTGGCG | TATTCATTG | TGATGTTTAT | 60 |
| AGTATATGCC | TTTGAAGTGG | CATCTTGAT | CACAGCAGCA | ACACAACGAG | ACTTTATGCT | 120 |
| AGAGAGGTAC | CAAAACAACA | GCCCTCCAAA | CGATGATGAC | CAGTGGAAAA | ACAATGGAGT | 180 |
| CACCAAAACC | TGGGACAGGC | TCATGCTCCA | GGACAATTGC | TGTGGCGTAA | ATGGTCCATC | 240 |
| AGACTGGCAA | AAATACACAT | CTGCCTTCCG | GACTGAGAAT | AATGATGCTG | ACTATCCCTG | 300 |
| GCCTCGTCAA | TGCTGTGTTA | TGAACAATCT | TAAAGAATCT | CTCACCTCG | AG | 352 |

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AGAGCCGTCC | TATCAGATTA | TCTTAACAAG | AAAACCAACT | 60 |
| GGAAAAA | ATGAAATTCC | TTATCTTCGC | ATTTTTCGGT | GGTGTTCACC | TTTATCCCT | 120 |
| GTGCTCTGGG | AAAGCTATAT | GCAAGAATGG | CATCTCTAAG | AGGACTTTTG | AAGAAATAAA | 180 |
| AGAAGAAATA | GCCAGCTGTG | GAGATGTTGC | TAAAGCAATC | ATCAACCTAG | CTGTTTATGG | 240 |
| TAAAGCCCAG | AACAGATCCT | ATGAGCGATT | GGCACTTCTG | GTTGATACTG | TTGGACCCAG | 300 |
| ACTGAGTGGC | TCCAAGAACT | AGAAAAAGCC | ATCCAAATTA | TGTACCAAAA | CCTGCAGCAA | 360 |
| GATGGGCTGG | AGAAAGTTCA | CCTGGAGCCA | GTGAGAATAC | CCCACTGGGA | GAGGGGAGAA | 420 |
| GAATCAGCTG | TGATGCTGGA | GCCAAGAATT | CATAAGATAG | CCATCCTGGG | TCTTGGCAGC | 480 |
| AGCATTGGGA | CTCCTCCAGA | AGGCATTACA | GCAGAAGTTC | TGCTGGTGAC | CTCTTTCGAT | 540 |
| GAAGTGCAGA | GAAGGGCCTC | AGAAGCAAGA | GGAAGATTG | TGTTTATAA | CCAACCTTAC | 600 |
| AACCTCGAG | | | | | | 609 |

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCC | TTCATGGCCT | AATTGAATTC | TAGACCTGCC | TCGAGCCTGG | GCAATAGAAT | 60 |
| GAGGCTCCAT | CTCATAATAA | TAATAAGCAG | CAGCGGCAGC | TCTGGTAGAT | TTTTTTGTGT | 120 |
| GCTTGCTCTC | ATGAAGACTT | AAGCCTGCTC | TTTCAATTG | AAACCTAGGC | ACTTGGACTA | 180 |
| ACTTAAAGA | TCATGTAAAA | AATTTAATTT | TGTTTGGTA | TAGATTAAAT | TGTGGTTTTT | 240 |
| TTTTTCTCTT | TTAGATATAA | TTGATCTGT | TGCTTTAGAA | ATTCCATTAT | CCAAAAACCT | 300 |
| TCTGGCACAG | ATTAGTGCTC | TTGCTCTTCA | GCTGGATTCA | GAAGATCTTC | ATAATTATTC | 360 |
| AGGAAGCCAA | CTATTTGAAA | TGCACGAGAA | AACCTCGAG | | | 399 |

(2) INFORMATION FOR SEQ ID NO:1472:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACAGGTTTAA AACTGGTTTT TTGCATACTG CTATATAATT | 60 |
| CTCTGTCTCT CTCTGTTTAT CTCTCCCTC CCTCCCCTCC CTTTCTTCTC CATCTCCATT | 120 |
| CTTTTGAATT TCCTCATCCC TCCATCTCAA TCCCGTATCT ACGCACCCCC CCCCCAGGC | 180 |
| AAAGCAGTGC TCTGAGTATC ACATCACACA AAAGGAACAA AAGCGAAACA CACAAACCAG | 240 |
| CCTCAACTTA CACTTGGTTA CTCAAAGAA CAAGAGTCAA TGGTACTTGT CCTAGCGTTT | 300 |
| CTCGAG | 306 |

(2) INFORMATION FOR SEQ ID NO:1473:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

| | |
|--|-----|
| GAATTCGGCC TCATGGCCTA CAACTCCGCA GCAAACAACCT CCGCAAACGG AAAAAGAACG | 60 |
| ACATGATGCA ATCTTCAGGA AAGTAAGAGG CATACTAAAT AAGCTTACTC CTGAAAAGTT | 120 |
| TGACAAGCTA TGCCTTGAGC TCCTCAATGT GGGTGTAGAG TCTAACTCA TCCTTAAAGG | 180 |
| GGTCATACTG CTGATTGTGG ACAAAGCCCT AGAAGAGCCA AAGTATAGCT CACTGTATGC | 240 |
| TCAGCTATGT CTGCGATTGG CAGAAGATGC ACCAACTTT GATGGCCAG CAGCAGAGGG | 300 |
| TCAACCAGGA CAGAAGCAAA GCACCACATT CAGACGCCTC CTAATTTCCA AATTACAAGA | 360 |
| TGAATTTGAA AACCGAACGC TCGAG | 385 |

(2) INFORMATION FOR SEQ ID NO:1474:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 428 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGATCCCTT ATTTTGCCAA AAAGTGTCT CAATTCATTT | 60 |
| GGATAACTTT TATGTTTTAG GAACGTGGCC TCTCTTTTAA TTACTGAGAA CTTACAAAAT | 120 |
| GGTTCAGAAA GTTTATATTT TTAAAGCTTT CATTCAATGA TATATTGAAC ATCTAAGGCT | 180 |
| TAACATCTT TCCACTGGA CAAAAACAGA ATTCCTAAAA ATGAGGAGGA GGGCCCCAGTG | 240 |
| TGGTGGCTTA CACCTGGAAT TCCAGTGCTT TGGGAGTCCA AGGTAGGAGA ACTGCTTGAG | 300 |
| GCCAGGGGTT TGAGACCAGC CTGGGCAACA CAGCAAGACA ACTCTACAAA AAATTAAAAA | 360 |
| AACAATCCAG GGCCGAGCAT AGTGGTTCAC ACCTGTAATC CCAGCACTTT AGGAGGCCAA | 420 |
| GCCTCGAG | 428 |

(2) INFORMATION FOR SEQ ID NO:1475:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

```

GAATTCGGCC TTCATGGCCT ACTGGGATGT ATATGAGAGA CAGTGCTTTC AATTAAATCC      60
TTGGGTATAT TTTTATTAAT TTCCTCCAGA TTTTCTTTT AAGGCCTTTT CTAAGTTATA      120
CTGCATATCA AACTTCCCTG TTATTGAAGG ATATAAGGTA GAAGGTAAAA GCCATTTTCC      180
TATAAGTAAC TTGGGCATTT GCAAAGATT TTCTCAAGTG CAGTTGTAAC TATACTAAAA      240
TATACTAATA TTGTGTTATG ATATACCTTG CTTTTTTTCT TTTATTTTTT CTTTGTAGAC      300
AGAGTTTTCG TCTTGTTCCT CAGGCTGAAG CGCTCGAG      338

```

(2) INFORMATION FOR SEQ ID NO:1476:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

```

GAATTCGGCC TTCATGGCCT ACAAAGAGCT AGAAGCCATT GAAAGTCGGC TAGAAAAGAC      60
AGAATTCCTT CTAAGAGAGG ATTTAACTAA ACTGAAAACA TTAAGTGTGA TGTTTGTAGA      120
TGAACGGAAA ACAATGAGTG AAAAATTAAA GAAACTGAA GATAAATTAC AAGCTGCTTC      180
TTCTCAGCTT CAAGTGGAGC AAAATAAAGT AACACAGTT ACTGAGAAGT TAATTGAGGA      240
AACTAAAAGG GCGCTCAAGT CCAAACCGA TGTAGAAGAA AAGATGTACA GCGTAACCAA      300
GGAGAGAGAT GATTAAAAAA ACAAATTGAA AGCGGCAGAA CTCGAG      346

```

(2) INFORMATION FOR SEQ ID NO:1477:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

```

GAATTCGGCC TTCATGGCCT ACAGGTTTTC ATTTTATATT ATTTTCCTTT AGCCTGAAAA      60
ATTTATTTAT TTTTCTCTT AGTACAAGTC TGCTGGTGGT AAATCTCTT AGTTTTTGTG      120
TATTGAAAGA TATTTTATTT TTGCCTTCAT TCCAGAAGGT TGCTTTTGCT GGATATAGGA      180
TTCTACAAC TTTGCCTTTA ACATGTTATG GATGCCATTC CTCTGTCTTT TAGCTTCCAT      240
TGTTTCTGAT GCTAAATCTT CAGTCATTTT ATCATTGATC CTCTGTAATG TACTCGAG      298

```

(2) INFORMATION FOR SEQ ID NO:1478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

| | |
|--|-----|
| CGGAAGTAGC CCAAATGCAC CTAGGAACAT TGTGCTTCA GGACCAGTTA TTTCTGACCT | 60 |
| TCCAGTTGTT CCTGACTGTG AAGGGTGACC GCTTCCCGGG ACTCGAG | 107 |

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT ACTTATATTC TTTATTATTA TTTAGTACAA AAATAGATTC | 60 |
| CCAGTAGATA TCCACAAGCA ATATTAGCAG GGCTTCTGTT TCTAAGTGAC CACAGACTAA | 120 |
| CCCTTTCTAG GCTTTAACAT TGTAAATAAT CCTATAAACA GTTTGATTTT TTAAGATGAT | 180 |
| TTTTGATTTG AAGAGACAGG CTTTACATAA GCCTTCATTC CTTCAAAAGG TCCTGACAAA | 240 |
| ATACTTGGGT TTTTTTCTCT TTTTTTCATT CTGGTATGCT TTGCAGCATT TCAGCTGCTT | 300 |
| TGGTGGGGAC ACAGATAACC CCTTCGCTTC CAGACTCGAG | 340 |

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

| | |
|---|-----|
| GCGATTATTG TAAGTTGACA ATTTATAATT GTATAAAAGT ATGAGGTACA AAGTGATGTT | 60 |
| ATAGCTTAAG AATACAGTAT GGTATGATTA AATCAAGTTA TTAACCTATC CTTACGTTA | 120 |
| AATGCTTAAA TTTTGTGATG AGAACATTTG AAATTTACTC TTGGAAGGTA AAAAAAATC | 180 |
| TCAGGACCCC CCAAATTAAA GCCATGAAGC TGAATTGTGC AACATCCTC GAG | 233 |

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

```

GAATTCGGCC TTCATGGCCT AGATAACTAT TGCTCCCACT ACCCTTTCAG CTATCTCACA      60
TAACTTTGAT ATATATTATT TTTATTATCG TTTATTAAGT GTCTAATTTT CATTGTGAAG      120
TCTCCTTGGA CCTATAAGGC TGAAAATAAAA TAATTTAAAA TTTATTTTCT TATTGTTTCT      180
AATTCAATTT CATTATAGTT AATGCAAGTG GTCATTGTGC TATTGAGTTT GGTACTTTGG      240
AGGTTTCTTT TTCTGGCTAT CTCGAG                                           266

```

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

```

GAATTCGGCC TTCATGGCCT AAGAAATGTT CACTTTTCCA ACTTAAAAGG ATTTTAAAA      60
ATACAAACAT AATGACCTA CCTGGTCAA AGAACAGAAG TGAGGAGAAC TTGCTTAAAG      120
GTATTGATGT TATATTTTCT CTTGACTGAG TGCTTGAAAA AAAATTTTAT TGAACATATG      180
TTCTCCTTCC GTGGCTTTT TGTCTTGCT TTTTGTGTT GTTTGTGTT TTTTCTTCTT      240
GAGATGGAGT CTCACTCTCT GCTCGAG                                           267

```

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

```

GAATTCGGCC TTCATGGCCT AAATTAGCAT CTAGTGTCAC AGGTAAAAGA ATTTCAGGAC      60
CAGGTTTAAA CTTTATTTTA AATATTTTTA TACTTAGGTC TCTTTTCTCT GCCTCTCCCC      120
AAAGAAGAGC CACTGGCCTT AGTTGTTTGA GCTTACTGCT TATATTATAG AGTGTAATA      180
GGTAACTAGA GACTAAAATT TTATTAACCA GCATGTTTGG TATATTAAAA GCAGTTCTCG      240
AG                                           242

```

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

```

GAATTCGGCC TTCATGGCCT ACAGAGTGTG GTTCTGTAG CAACACTTCT CATGACCATC      60
TGTTTTGTGT TTATGATGAT TTTTTCAGGT CTGTTGGTCA ATCTCACAAC CATTGCATCT      120
TGGCTGTCAT GGCTTCAGTA CTTGAGCAT CCACGATATG GATTTACGGC TTTGCAGCAT      180
AATGAATTTT TGGGACAAAA CTTCTGCCCA GGAATCAATG CAACAGGAAA CAATCCTTGT      240
AACTATGCAA CATGTACTGG CGAAGAATAT TTGTTAAAGC AAGGGCTCGA G                                           291

```


(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

```

GAATTCGGCC TTCATGGCCT AGTAATTTTT GATAGTAAGG GCTTTTTATT GTCATTTTTT    60
GTTAATCGTT TCCTGTCTGT TTTGTATTC TTTTGTTCCT CTCTTCCTCG CTTGGTATCA    120
TCTTTGCAAT TTGATAATTT TTGTTGTGAT ATACTTTGAT TCTTTCTATT TATCTCTTCT    180
GAATCTAATA TTAGTTTTTT TTATCTTTTC TGTATCTATT ATTAGTTTTT TTTCTTTGTG    240
GTTATCATGA GGCTTCCACT CGAG                                           264

```

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

```

GAATTCGGCC TTCATGGCCT ACCAGTGCCT TCCTCTTCCC TATATTCTGT GTGTCTTAAC    60
GGAATTATTT TTCCAAATCA TTGTGTGCAA AGAACTAAT GACATCATAA GTATGATTTC    120
TGTACACATT TTAGTTGTAA TTGCTAGGTT TTCCAAGATT TCACAGTCAT CAAGTCATCT    180
GTTCCCAGAC ATCCCAACAA GTACTTATCA AGTGTCTCCA TOTGCTGCCT TCATCTCTCT    240
CAGGTGCCAT TCCAGTGACA TTGCTATAGC CTCTTGCTGT ACCCCCCTCG AG           292

```

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

```

GAATTCGGCC TTCATGGCCT AATGGATATA GAATCCAGG TTGATAAACA TTTTCTGTCA    60
CAACTTTACA ACTGAAGGCA TTGCCCTTTT GTCTTTTACC GTTCATTGA TAAAAAGTCT    120
GGTGGAATC TAATTCTTAC ACCTTTGTAG GTGAGCATTT TTTCTTTCC TGTGACACAT    180
TTGTGATTAT CTGATCCTTA GAGATCTGAA GTTTTATCAT TTGTATCTAT GAGATCTTTT    240
CCCATCCTCC TGGTGCTCGA G                                           261

```

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

| | |
|--|-----|
| GAATTCGGCC TTCATGGCCT AATTTTCTGT ATATTTTAC ATGAATTTCA GTACTATATT | 60 |
| GAACAGCTAT GTTTAAGGAT AATCAAAAGA TGACTGTGAC AGGGAGAATT TGGAAATATT | 120 |
| AGCCCAAGTC TAGTCAATTG TGATTGTTGT TGCCTTGGTA CTAGTTTAAA TTGGGGCTAA | 180 |
| ATTTAGAGCC ACTGGGACTG AGTACCTCGG TTGATCTCCA ATGATTCCAA TTGCTAAAAA | 240 |
| GTAAAGGGCA ACCACACATA CGTACCAATT CTGAAGTCCT AGGAAATTTT TAAAAGAATG | 300 |
| TAAGAGAATA AGAAAATGTA AAAGGGAGAA GAGTTTATAT GTCATGACGT AAGTTTATA | 360 |
| GTTATTACT TGTAACTGG ACCTTCTCTG CTTCTTCCAA TGTGTTTATT AAGACCTGTC | 420 |
| TGAAAAATGA CCTTCCAACCT CCCCTGAGTA ATTATTTAAG ACCCTTTCAT CTTACCAACC | 480 |
| CTCTCGAG | 488 |

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAATCAA AATAAAAGTA AAAGTAAGAA | 60 |
| GATGGAAATT TGCTTAGCTG TGAAAGGAAA GGCGATCTGT CTGATGTCCT GTGTTTGGTG | 120 |
| CCTAGGTGGG CTGGGTGCTT GCATTTCTTG CTTGCACTG TCAGGATTTT TCAGGGATCA | 180 |
| GCCTTGGCAC TGGAGACCTT CACATTTTCC ATCTGGTTAC TATGGCACAC AACTCGAG | 238 |

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

| | |
|--|-----|
| GAATTACTCT GGAAGATATG CTCTATGCTG CTTTCATCCAT AAAGAGTAAT TATTTGGTGT | 60 |
| TCATGGCGGA ACTGTTCTGG TGTTTGAAG TGGTGAAGCC GTCTTTTGTA CAGCCTCGTG | 120 |
| TTGTTCTGTC ACAAGGAGCT GAACCTGTAA AAGATATGCC TTCAATTCCT GTCTTGAATG | 180 |
| CTGCCAAAAG AAATGTCTTA GATAGTAGT CTGACTTCCC TTCAAGTGGG GAAGGAGCTA | 240 |
| CATTTACACA GTCTCATCTC GAG | 263 |

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

| | |
|---|-----|
| GCGATTGAAT TCTAGACCTG CCTCGAGCTC ACACCTGGAT TATCTCAGTA GTTCCCAAC | 60 |
| TGGTTTCCTT GTTCCATTC TTGCCTCCTT CTGTCTACTC TCAATATAAC AGCTAGAACA | 120 |
| ATCCTTTTAC AATGGAATTC AGATCATGTT TACCCCTCTG TTCAAATTCT CCAGTGACTT | 180 |
| TCCAGTTTTT ACATGATCTG GCTCCTACTA CCTGTCTCAC TGTGTTTCCT ACTACTCTCC | 240 |
| TGCCCTTTCT CCTCGAG | 257 |

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

| | |
|---|-----|
| GAATTAAAGA GGGCGATATC ATCACACTCA CTAACCAAAT TGATGAGAAC TGGTATGAGG | 60 |
| GGATGCTGCA TGGCCATTCA GGCTTCTTCC CCATCAATTA TGTGGAATTT CTGGTTGCC | 120 |
| TGCCCCATTA GGATGTTATG CTGGCTGGCT CGCCTCCTCT TGACCCAGAT AGTTACGGTT | 180 |
| AACCACTGCT TTGGCAATGC TGCTTATAAC ACATCCCAAG TGAGGCCCGC AGTGGTCCAC | 240 |
| GTCACTCCAGC CCCACCAAGT GACTTTGGTT GACTTGTGGG CTCCACAGG ACTCGAG | 297 |

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

| | |
|---|-----|
| GAATTCGGCC TTCATGGCCT AAAAAGAAAG AAAAAGAAAA GAAAAAACCT TGGAGAAGTA | 60 |
| AGGGATTCTG TAAAAAATTT CCCCAATTC ACTAGAGAGA TTGACATATA AATTAGAAA | 120 |
| ATTGAGATAA CCTATGTAAG ATGCTATGTA AGACAACCAT TGCAGAGACA CAAAGTAATC | 180 |
| AGATTCTTGA AGGTCAATGC AAAAGAAAAA AATATTAAAG GCACTCGAG | 229 |

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

| | |
|---|----|
| GAATTCGGCC TTCATCTGAC AATTAAAAAC ACTACCTTAG TTTGTTTTTC TGTAATTGAA | 60 |
|---|----|

```

TTTGACAGT TCTATTTTAC TTGAATTAGT CTTTTTATAT ATATATAGGC AGAAGTACTT      120
AAATAAATCT TCCCTTAAGT ATCAAAAGCA AAAGAATAAC ATTCATAGAA GTCTAACATG      180
TTCAAACGTG TAAATATACT ACAATTGTTT ATTCACATTA TAAATGCAGC TAAAATGACT      240
AACCTTTCAG ATCAACCCCT CGAG                                         264

```

(2) INFORMATION FOR SEQ ID NO:1495:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

```

GAATTCGGCC TTCATGGCCT ACCTTCCTTC CTCCTTCCT TCCTTTCCTT CCTTCTCTCC      60
TTCCTTCCTT TCCTTCCTTT CTTTCCTTTC CTCTCTTCT CTCTTCTGT CATGGTCTGG      120
CTCTGTACC CAGGCTGGAG TGCAGGGGTG CAATCTCAGC TCGCTGCAAC TTCTTCCCCC      180
CCAACTCGAG                                         190

```

(2) INFORMATION FOR SEQ ID NO:1496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

```

GGCCTTCATG GCCTACTAAG CTATTGATT CTAAGTGAAT ATGTTATCTC TTATTAGAGG      60
ATATGTTAAT TTTCTGTCAT TTTATTCATT TATTAACCTA ACATCTCTGA TTGCCTACCA      120
TGTGTCAGGC TCTGTACTAA GGATTGAGGA CCCAAAGATG AACAAAACAT GGGGCCTAAT      180
TCAAAGATT CACAACTGG AGAGAAAGTC AGCCACATAC AAAAGCCTCG AG              232

```

(2) INFORMATION FOR SEQ ID NO:1497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

```

GTAGAATTGT ACAGTGCTTA TGAGTTATGC ATGTGTTCTT GGTCTTGTG CTAGGATTTT      60
TTTTTTTTT TGATTGCTGC TCCAGTTGCC TTAATTACTT TGACATTGGA GTTGACCACA      120
TGATGGTGT CCACACTTCC CCTAGGCTCG AG                                         152

```

(2) INFORMATION FOR SEQ ID NO:1498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

| | |
|---|-----|
| GCGATTGAAT TCTAGACCTG CCTCGATCTC TTGTATTCAG TATTTTGTGG GGGAGGTACT | 60 |
| TTGAAACTGT GTAAATATAC CATTCTCAT TAACTTTTC AATTTATTCC CTTATTTAGA | 120 |
| TGCGTATGAA CTCATGGCTT CTTGTTTAT TTGATGGATC CAAATCTGTT AATATCCTTA | 180 |
| CTGATTTGGA TGCTCAGACT GCCCCAGATT TGGCCAGTGG AAGCCCTTTC AGGCTTGCTC | 240 |
| CCATGTCCTT CGAG | 254 |

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

| | |
|--|-----|
| GAATTCGGCC TTTCATGGCC TAGAGAGCGC GGTGGGCTGC CATTAAACG CGGCCATCGG | 60 |
| TCCGGCCATC ATCCCTTCA CGGTACTAGA CTCCGGGATG GTGAGATCCT TCTCATCCTT | 120 |
| TGGGGGCCGA CCCCCTTCC GGGGACTTTG CTCTTGGGCT CTTTTCAGAG GGGATTGGA | 180 |
| GCCTCTCTCT GAAGAGCCTG AAGACACCCT CTTCTTTCCT TCTCCCATGT TCTTCTTCAC | 240 |
| CTTCCCTTCA GACAGGCTAA GTTTGCGCTT CTCATCACCT GAGTTTGGCC TACTTCTCTC | 300 |
| CTCACTGGAA TTACGTCGAT TCTGTTCATC AGAAGAATTG TGGGATGACG TCTGGTCTTT | 360 |
| CCCTTTGGCT CTCCTGTAGG CCATGAAGGC CCGGCCTTCA TGGCCTACCA TTTCTTACAC | 420 |
| ACACTGCCAG AGATACTCTA GGCATGTAAA GCACAAACAT ACATATAAAA TCTGCGGGCT | 480 |
| TCAAAAAATA TAAGTAGGAT GTCATCTATA CTGTACATACA CTTTGTTTTT TATCACTTAC | 540 |
| TTAATGTTAT ATCTTGATA TTGTATTACC CTGGGTATTA AAAAGAACTC CTTTCACATT | 600 |
| TTAAAATAAC AATCTGAGCA CTTCAATAAT CCAATGCGT ATCTCCAGTC TGCTCGAG | 658 |

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

| | |
|---|-----|
| GAATTCTAGA CCTGTCTCGA GAAACCAGAG GACTTTTCTG CTTTGTGTTT TCTTTTAGGA | 60 |
| GGTAATAAAA CCGTGAATTT ATTTAAATGC TAATGTGTAG GATCTCACTC GAG | 113 |

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,

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or a complement of said sequence.

2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ

ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,

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4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
or to a complement of said sequence.

5. An isolated protein encoded by an isolated polynucleotide of claim 1.
6. An isolated protein encoded by an isolated polynucleotide of claim 2.
7. An isolated protein encoded by an isolated polynucleotide of claim 3.
8. An isolated protein encoded by an isolated polynucleotide of claim 4.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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|---|-----------|--|
| (51) International Patent Classification ⁶ : C12N 15/12, 5/10, C07K 14/47, C12Q 1/68, A61K 38/17. | A3 | (11) International Publication Number: WO 98/45435 (43) International Publication Date: 15 October 1998 (15.10.98) |
| (21) International Application Number: PCT/US98/06954 (22) International Filing Date: 10 April 1998 (10.04.98) (30) Priority Data: 08/835,913 10 April 1997 (10.04.97) US (71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US). (72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). (74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US). | | (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 12 November 1998 (12.11.98) |
| (54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs) (57) Abstract Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided. | | |

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A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N5/10 C07K14/47 C12Q1/68 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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| A | WO 97 07198 A (GENETICS INSTITUT) 27 February 1997 see the whole document --- | 1-8 |
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

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Date of the actual completion of the international search

3 July 1998

Date of mailing of the international search report

3 0. 09. 98

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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| A | JACOBS K ET AL: "A NOVEL METHOD FOR ISOLATING EUKARYOTIC CDNA CLONES ENCODING SECRETED PROTEINS" JOURNAL OF CELLULAR BIOCHEMISTRY - SUPPLEMENT, vol. 21A, 10 March 1995, page 19 XP002027246 see abstract --- | 1-8 |
| A | WO 90 14432 A (GENETICS INST) 29 November 1990 see the whole document --- | 1-8 |
| A | WO 96 17925 A (IMMUNEX CORP) 13 June 1996 see the whole document ----- | 1-8 |

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 06954

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: (1-8) partially

An isolated polynucleotide comprising a nucleotide sequence selected from SEQ ID no.1, consisting of a nucleotide sequence selected from SEQ ID no.1, consisting essentially of a nucleotide sequence selected from SEQ ID no.1; an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence consisting of SEQ ID no.1; an isolated protein encoded by said isolated polynucleotides;

Inventions 2 to 1500. Claims: (1-8) partially

Idem as subject 1 but limited to SEQ ID nos.2 to 1500 respectively clone ID nos. B11 to BV29. (Invention 2 is limited to SEQ ID. no. 2; Invention 3 is limited to SEQ ID no. 3;.....Invention 1500 is limited to SEQ ID no. 1500);

| Patent document cited in search report | Publication date | Patent family member(s) | Publication date |
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